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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No. 107196.135

First Inventor or Application Identifier WEINSTOCK et al.

Title NUCLEIC ACID . . . THERAPEUTICS

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02/18/99

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

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1. ☐ * Fee Transmittal Form (e.g., PTO/SB/17)
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(preferred arrangement set forth below)
 - Descriptive title of the Invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to Microfiche Appendix
 - Background of the Invention
 - Brief Summary of the Invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
3. ☐ Drawing(s) (35 U.S.C. 113) [Total Sheets]
4. Oath or Declaration [Total Pages]
 - a. ☐ Newly executed (original or copy)
 - b. ☐ Copy from a prior application (37 C.F.R. § 1.63(d))
(for continuation/divisional with Box 16 completed)
 - i. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

5. ☐ Microfiche Computer Program (Appendix)
6. Nucleotide and/or Amino Acid Sequence Submission
(if applicable, all necessary)
 - a. ☒ Computer Readable Copy - CD ROM
 - b. ☒ Paper Copy (identical to computer copy) 6196 pages
 - c. ☐ Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

7. ☐ Assignment Papers (cover sheet & document(s))
8. ☐ 37 C.F.R. § 3.73(b) Statement of Power of Attorney
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12. ☐ Return Receipt Postcard (MPEP 503)
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Title Of The Invention

**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROBACTER CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS**

5

Cross-Reference to Related Applications

This application is converted from U.S. provisional application Serial Number
10 60/074,787, filed February 18, 1998 and U.S. provisional application Serial Number
60/094,145 filed July 24, 1998.

Field Of The Invention

The invention relates to isolated nucleic acids and polypeptides derived from
15 *Enterobacter cloacae* that are useful as molecular targets for diagnostics, prophylaxis
and treatment of pathological conditions, as well as materials and methods for the
diagnosis, prevention, and amelioration of pathological conditions resulting from
bacterial infection.

20 Background Of The Invention

Enterobacter cloacae (*E. cloacae*) belongs to the bacterial family
Enterobacteriaceae, whose diverse members are Gram-negative rods that are glucose
fermenters and nitrate reducers. These organisms are found free-living in nature and
as part of the indigenous flora of human and animals. They grow rapidly under
25 aerobic and anaerobic conditions and are metabolically active, utilizing a variety of
substrates. Most species are opportunistic pathogens (Kenneth Ryan,
Enterobacteriaceae, Chap. 20, Medical Microbiology, An Introduction to Infectious
Diseases, Second Edition, Editor, John C. Sherris, Elsevier, New York, 1990).

E. cloacae is an ornithine-positive, lysine-negative pathogen that can be
30 associated with urinary tract and respiratory tract infections. The bacteria produces

endotoxins which as aerosols can penetrate into the lungs causing fever, coughing, difficulty in breathing and wheezing (Fairley, T. and Gislason, S., 1986-1997, Environmed Research Inc). *E. cloacae* is becoming progressively common in newborns in Neonatal Intensive Care Units (NICU) (Shi, Z.Y., et al, 1996, J. Clin. Microbiol. 34:2784-2790; Cordero, L., et al, 1997, Pediatr. Infect. Dis. J. 16:18-23; Acolet, D., et al, 1994, J. Hosp. Infect. 28:273-286). A study at Children's Hospital in Michigan showed a four-fold increase in *Enterobacter* in patients with bacteremia between 1989 and 1992. *E. cloacae* accounted for 74% of the isolates. Twenty eight percent of the infected children went into shock and six percent died (Andresen, J., et al, 1994, Pediatr. Infect. Dis. J. 13: 787-792). An outbreak of multidrug-resistant *E. cloacae* lasted for 4 months in the NICU in China (Shi, Z.Y., et al, 1996, J. Clin. Microbiol. 34:2784-2790). Outbreaks have also occurred in surgical wards (Burchard, K.W., et al, 1986, Surgery 100:857-862) and burn units (Markowitz, S. M., et al, 1983, J. Infect. Dis. 148:18-23). *E. cloacae* has also been shown to be the causative agent in a case of gas gangrene (Fata, F., et al, 1996, South Med. J. 89:1095-1096).

Epidemiology of *E. cloacae* is not completely understood, although studies of infection and colonization point to the endogenous flora of the patients. Molecular typing results of 141 strains of *E. cloacae* from broad geographic areas in the United States (from the National Surveillance Program: SCOPE) indicated that although clonal spread of a single strain was observed within a given institution most of the episodes of bacteremia were caused by strains unique to the individual patients. Therefore, selection of mutant subpopulations within each endogenous infection can be caused by drug exposure (Pfaller, M.A., 1997, Diagn. Microbiol. Infect. Dis. 28:211-219).

Antibiotic resistance is a major problem in the control of infectious diseases. Strains of *E. cloacae* resistant to broad-spectrum penicillins and beta-lactamase-stable

cephalosporins occurs at a frequency of 10^7 to 10^6 (Kadima, T.A. and Weiner, J.H., 1997, Antimicrobiol. Agents Chemother. 41:2177-2183; Lampe, M.F., et al, Antimicrob. Agents Chemother. 21:655-660; Lindberg, F., et al, Rev. Infect. Dis. 8 [Suppl 3]:S292-S304). Selected fluoroquinolones have often been successfully
5 administered to patients with urinary tract infections; however, *E. cloacae* has become resistant to many of them (Deguchi, T., et al, 1997, Antimicrobiol. Agents Chemother. 41: 2544-2546). Some resistance has been attributed to plasmid-containing *E. cloacae* and some to the *E. cloacae* chromosome. In Holland, two different resistant strains of *E. cloacae* have been identified. The Amsterdam strain (resistant to ceftotaxim and
10 piperacillin) exhibits depressed chromosomal Class 1 beta-lactamase, whereas the Rotterdam strain (resistant to cefuroxime) favors the spread of a plasmid encoding TEM-2 beta-lactamase (Namavar, F., 1997, BIO 99-53 99-606615). Resistant strains of *E. cloacae* developed within 6 days in nearly 50% of the *E. cloacae*-infected intensive care patients with pulmonary complications treated with cefotaxime (Fussle,
15 et al., 1994, Clin. Investig. 72:1015-1019). While several antimicrobial agents retain potent activity against the highly resistant organisms (Pfaller, M.A., 1997, Diagn. Microbiol. Infect. Dis. 28:211-219), constant exposure to these agents may eventually result in resistance.

E. cloacae has been shown to be beneficial to plants in the control of diseases
20 caused by bacteria (Bacon, C.W., et al., PCT publication WO 97/24433). As a biocontrol agent, *E. cloacae* coated onto cucumber seed has protected the seed from a lethal infection of the fungus *Pythium ultimum* (Nelson, E.B., et al, 1992, Can. J. Plant Pathol. 14:106-114). Nutritional mutants of *E. cloacae* were also protective and it has been suggested that mutant strains would be beneficial for an environmental
25 containment strategy (Roberts, D.P., et al, 1994, Plant Science [Limerick], 10183-89).

Summary Of The Invention

The present invention fulfills the need for diagnostic tools and therapeutics by providing bacterial-specific compositions and methods for detecting *Enterobacter* species including *E. cloacae*, as well as compositions and methods useful for treating and preventing *Enterobacter* infection, in particular, *E. cloacae* infection, in vertebrates including mammals.

The present invention encompasses isolated nucleic acids and polypeptides derived from *E. cloacae* that are useful as reagents for diagnosis of bacterial disease, components of effective antibacterial vaccines, and/or as targets for antibacterial drugs including anti-*E. cloacae* drugs. They can also be used to detect the presence of *E. cloacae* and other *Enterobacter* species in a sample; and in screening compounds for the ability to interfere with the *E. cloacae* life cycle or to inhibit *E. cloacae* infection. They also have use as biocontrol agents for plants.

In one aspect, the invention features compositions of nucleic acids corresponding to entire coding sequences of *E. cloacae* proteins, including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *E. cloacae* proteins to block protein translation, and methods for producing *E. cloacae* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *E. cloacae* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *E. cloacae* are within the scope of this invention.

The nucleotide sequences provided in SEQ ID NO: 1 - SEQ ID NO: 5662, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 5662 may be "provided" in a variety of medias to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide

sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO: 1 - SEQ ID NO: 5662, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 5662. Uses for and methods for providing nucleotide sequences in a variety of media is well known in the art (see e.g., EPO Publication No. EP 0 756 006).

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage media, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A person skilled in the art can readily appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable media having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable media. A person skilled in the art can readily adopt any of the presently known methods for recording information on computer readable media to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a person skilled in the art for creating a computer readable media having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable media. The sequence

information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A person skilled in the art can readily adapt any
5 number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable media having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NO: 1 - SEQ ID NO: 5662, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to SEQ ID
10 NO: 1 - SEQ ID NO: 5662 in computer readable form, a person skilled in the art can routinely access the coding sequence information for a variety of purposes. Computer software is publicly available which allows a person skilled in the art to access sequence information provided in a computer readable media. Examples of such computer software include programs of the "Staden Package", "DNA Star",
15 "MacVector", GCG "Wisconsin Package" (Genetics Computer Group, Madison, WI) and "NCBI Toolbox" (National Center For Biotechnology Information). Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New*
20 *Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Computer algorithms enable the identification of *E. cloacae* open reading frames (ORFs) within SEQ ID NO: 1 - SEQ ID NO: 5662 which contain homology to ORFs or proteins from other organisms. Examples of such similarity-search
25 algorithms include the BLAST [Altschul et al., J. Mol. Biol. 215:403-410 (1990)] and Smith-Waterman [Smith and Waterman (1981) *Advances in Applied Mathematics*,

2:482-489] search algorithms. Suitable search algorithms are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular*

5 *Research*, American Society for Microbiology, Washington, D.C. (1997). Such algorithms are utilized on computer systems as exemplified below. The ORFs so identified represent protein encoding fragments within the *E. cloacae* genome and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

10 The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *E. cloacae* genome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the

15 present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A person skilled in the art can readily appreciate that any one of the currently available computer-based systems is suitable for use in the present invention. The computer-based systems of the present invention comprise a

20 data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the

25 nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *E. cloacae* genome which are similar to, or "match", a particular target sequence or target motif. A variety of known algorithms are known in the art and have been disclosed publicly, and a variety of commercially available software for conducting homology-based similarity searches are available and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, FASTA (GCG Wisconsin Package), Bic_SW (Compugen Bioccelerator), BLASTN2, BLASTP2, BLASTX2 (NCBI) and Motifs (GCG). Suitable software programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). A person skilled in the art can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A person skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that many genes are longer than 500 amino acids, or 1.5 kb in length, and that commercially important fragments

of the *E. cloacae* genome, such as sequence fragments involved in gene expression and protein processing, will often be shorter than 30 nucleotides.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are
5 chosen based on a specific functional domain or three-dimensional configuration which is formed upon the folding of the target polypeptide. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites, membrane-spanning regions, and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin
10 structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *E. cloacae* genome possessing varying degrees of homology to the target sequence or target
15 motif. Such presentation provides a person skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *E.*
20 *cloacae* genome. In the present examples, implementing software which implement the BLASTP2 and bic_SW algorithms (Altschul et al., J Mol. Biol. 215:403-410 (1990); Compugen Biocellator) was used to identify open reading frames within the *E. cloacae* genome. A person skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search means for the
25 computer-based systems of the present invention. Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition,

Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

The invention features *E. cloacae* polypeptides, preferably a substantially pure
5 preparation of an *E. cloacae* polypeptide, or a recombinant *E. cloacae* polypeptide. In
preferred embodiments: the polypeptide has biological activity; the polypeptide has an
amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99%
identical to an amino acid sequence of the invention contained in the Sequence
Listing, preferably it has about 65% sequence identity with an amino acid sequence of
10 the invention contained in the Sequence Listing, and most preferably it has about 92%
to about 99% sequence identity with an amino acid sequence of the invention
contained in the Sequence Listing; the polypeptide has an amino acid sequence
essentially the same as an amino acid sequence of the invention contained in the
Sequence Listing; the polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino
15 acid residues in length; the polypeptide includes at least about 5, preferably at least
about 10, more preferably at least about 20, still more preferably at least about 50,
100, or 150 contiguous amino acid residues of the invention contained in the
Sequence Listing. In yet another preferred embodiment, the amino acid sequence
which differs in sequence identity by about 7% to about 8% from the *E. cloacae*
20 amino acid sequences of the invention contained in the Sequence Listing is also
encompassed by the invention.

In preferred embodiments: the *E. cloacae* polypeptide is encoded by a nucleic
acid of the invention contained in the Sequence Listing, or by a nucleic acid having at
least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid
25 of the invention contained in the Sequence Listing.

In a preferred embodiment, the subject *E. cloacae* polypeptide differs in amino acid sequence at about 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *E. cloacae* polypeptide exhibits an *E. cloacae* biological activity, e.g., the *E. cloacae* polypeptide retains a biological activity of a naturally occurring *E. cloacae* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

In yet other preferred embodiments, the *E. cloacae* polypeptide is a recombinant fusion protein having a first *E. cloacae* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *E. cloacae*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

In a preferred embodiment, the encoded *E. cloacae* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at about 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *E. cloacae* encoded polypeptide exhibits an *E. cloacae* biological activity, e.g., the

encoded *E. cloacae* enzyme retains a biological activity of a naturally occurring *E. cloacae*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

The *E. cloacae* strain, 15842, from which genomic sequences have been sequenced, has been deposited on August 22, 1997, in the American Type Culture Collection and assigned the ATCC designation # 202023.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridize under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *E. cloacae* polypeptides, especially by antisera to an active site or binding domain of *E. cloacae* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *E. cloacae* polypeptide analogs or variants.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

In preferred embodiments, the subject *E. cloacae* nucleic acid will include a transcriptional regulatory sequence, e.g., at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *E. cloacae* gene sequence,

e.g., to render the *E. cloacae* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *E. cloacae* polypeptide of the invention, hybridizes under stringent conditions to a
5 nucleic acid probe corresponding to at least about 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 12 consecutive nucleotides of the invention contained in the Sequence Listing; still more preferably to at least about 20 consecutive nucleotides of the invention contained in the Sequence Listing; most preferably to at least about 40 consecutive nucleotides of
10 the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *E. cloacae* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%,
15 98% or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least about 5, preferably at least about
20 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *E. cloacae* polypeptide or an *E. cloacae* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a
25 recombinant *E. cloacae* polypeptide or *E. cloacae* polypeptide variant; including

culturing the cell, e.g., in a cell culture medium, and isolating an *E. cloacae* or *E. cloacae* polypeptide variant, e.g., from the cell or from the cell culture medium.

One embodiment of the invention is directed to substantially isolated nucleic acids. Nucleic acids of the invention include sequences comprising at least about 8
5 nucleotides in length, more preferably at least about 12 nucleotides in length, even more preferably at least about 15-20 nucleotides in length, that correspond to a subsequence of any one of SEQ ID NO: 1 - SEQ ID NO: 5662 or complements thereof. Alternatively, the nucleic acids comprise sequences contained within any ORF (open reading frame), including a complete protein-coding sequence, of which
10 any of SEQ ID NO: 1 - SEQ ID NO: 5662 forms a part. The invention encompasses sequence-conservative variants and function-conservative variants of these sequences. The nucleic acids may be DNA, RNA, DNA/RNA duplexes, protein-nucleic acid (PNA), or derivatives thereof.

In another aspect, the invention features a purified recombinant nucleic acid
15 having at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing

The invention also encompasses recombinant DNA (including DNA cloning and expression vectors) comprising these *E. cloacae*-derived sequences; host cells comprising such DNA, including fungal, bacterial, yeast, plant, insect, and mammalian
20 host cells; and methods for producing expression products comprising RNA and polypeptides encoded by the *E. cloacae* sequences. These methods are carried out by incubating a host cell comprising an *E. cloacae*-derived nucleic acid sequence under conditions in which the sequence is expressed. The host cell may be native or recombinant. The polypeptides can be obtained by (a) harvesting the incubated cells
25 to produce a cell fraction and a medium fraction; and (b) recovering the *E. cloacae*

polypeptide from the cell fraction, the medium fraction, or both. The polypeptides can also be made by *in vitro* translation.

In another aspect, the invention features nucleic acids capable of binding mRNA of *E. cloacae*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *E. cloacae*. A further aspect features a nucleic acid which is capable of binding specifically to an *E. cloacae* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *E. cloacae* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *E. cloacae* nucleic acid.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *E. cloacae* polypeptide or an *E. cloacae* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *E. cloacae* polypeptide or *E. cloacae* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *E. cloacae* or *E. cloacae* polypeptide variant, e.g., from the cell or from the cell culture medium.

In yet another embodiment of the invention encompasses reagents for detecting bacterial infection, including *E. cloacae* infection, which comprise at least one *E. cloacae*-derived nucleic acid defined by any one of SEQ ID NO: 1 - SEQ ID NO: 5662, or sequence-conservative or function-conservative variants thereof. Alternatively, the diagnostic reagents comprise nucleotide sequences that are contained within any open reading frames (ORFs), including preferably complete protein-coding sequences, contained within any of SEQ ID NO: 1 - SEQ ID NO: 5662, or polypeptide sequences contained within any of SEQ ID NO: 5663 - SEQ ID NO:

11324, or polypeptides of which any of the above sequences forms a part, or antibodies directed against any of the above peptide sequences or function-conservative variants and/or fragments thereof.

The invention further provides antibodies, preferably monoclonal antibodies, which specifically bind to the polypeptides of the invention. Methods are also provided for producing antibodies in a host animal. The methods of the invention comprise immunizing an animal with at least one *E. cloacae*-derived immunogenic component, wherein the immunogenic component comprises one or more of the polypeptides encoded by any one of SEQ ID NO: 1 - SEQ ID NO: 5662 or sequence-conservative or function-conservative variants thereof; or polypeptides that are contained within any ORFs, including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 5662 forms a part; or polypeptide sequences contained within any of SEQ ID NO: 5663 - SEQ ID NO: 11324; or polypeptides of which any of SEQ ID NO: 5663 - SEQ ID NO: 11324 forms a part. Host animals include any warm blooded animal, including without limitation mammals and birds. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *E. cloacae*-specific antigens.

In yet another aspect, the invention provides diagnostic methods for detecting *E. cloacae* antigenic components or anti-*E. cloacae* antibodies in a sample. *E. cloacae* antigenic components may be detected by known processes, including but not limited to detection by a process comprising: (i) contacting a sample suspected to contain a bacterial antigenic component with a bacterial-specific antibody, under conditions in which a stable antigen-antibody complex can form between the antibody and bacterial antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of at least one bacterial antigenic component in the

sample. In different embodiments of this method, the antibodies used are directed against a sequence encoded by any of SEQ ID NO: 1 - SEQ ID NO: 5662 or sequence-conservative or function-conservative variants thereof, or against a polypeptide sequence contained in any of SEQ ID NO: 5663 - SEQ ID NO: 11324 or

5 function-conservative variants thereof.

In yet another aspect, the invention provides a method for detecting antibacterial-specific antibodies in a sample, which comprises: (i) contacting a sample suspected to contain antibacterial-specific antibodies with an *E. cloacae* antigenic component, under conditions in which a stable antigen-antibody complex can form

10 between the *E. cloacae* antigenic component and antibacterial antibodies in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of antibacterial antibodies in the sample. In different embodiments of this method, the antigenic component is encoded by a sequence contained in any of SEQ ID NO: 1 - SEQ ID

15 NO: 5662 or sequence-conservative and function-conservative variants thereof, or is a polypeptide sequence contained in any of SEQ ID NO: 5663 - SEQ ID NO: 11324 or function-conservative variants thereof.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *E. cloacae*. The method includes: immunizing a

20 subject with an *E. cloacae* polypeptide, e.g., a surface or secreted polypeptide, or a combination of such peptides or active portion(s) thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind

25 an *E. cloacae* polypeptide. The method includes contacting the compound to be evaluated with an *E. cloacae* polypeptide and determining if the compound binds or

otherwise interacts with the *E. cloacae* polypeptide. Compounds which bind or otherwise interact with *E. cloacae* polypeptides are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

- 5 In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *E. cloacae* nucleic acid, e.g., DNA or RNA. The method includes contacting the compound to be evaluated with an *E. cloacae* nucleic acid and determining if the compound binds or otherwise interacts with the *E. cloacae* nucleic acid. Compounds
- 10 which bind *E. cloacae* are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

- A particularly preferred embodiment of the invention is directed to a method of screening test compounds for anti-bacterial activity, which method comprises:
- selecting as a target a bacterial specific sequence, which sequence is essential to the
- 15 viability of a bacterial species; contacting a test compound with said target sequence; and selecting those test compounds which bind to said target sequence as potential anti-bacterial candidates. In one embodiment, the target sequence selected is specific to a single species, or even a single strain, such as, for example, the strain *E. cloacae* 15842. In a second embodiment, the target sequence is common to at least two
- 20 species of bacteria. In a third embodiment, the target sequence is common to a family of bacteria. The target sequence may be a nucleic acid sequence or a polypeptide sequence. Methods employing sequences common to more than one species of microorganism may be used to screen candidates for broad spectrum anti-bacterial activity.

- 25 The invention also provides methods for preventing or treating disease caused by certain bacteria, including *E. cloacae*, which are carried out by administering to an

animal in need of such treatment, in particular a warm-blooded vertebrate, including but not limited to birds and mammals, a compound that specifically inhibits or interferes with the function of a bacterial polypeptide or nucleic acid. In a particularly preferred embodiment, the mammal to be treated is human.

5

DETAILED DESCRIPTION OF THE INVENTION

The sequences of the present invention include the specific nucleic acid and amino acid sequences set forth in the Sequence Listing that forms a part of the present specification, and which are designated SEQ ID NO:1 - SEQ ID NO: 11324. Use of
10 the terms "SEQ ID NO: 1 - SEQ ID NO: 5662 ", " SEQ ID NO: 5663 - SEQ ID NO: 11324, "the sequences depicted in Table 2", etc., is intended, for convenience, to refer to each individual SEQ ID NO *individually*, and is not intended to refer to the genus of these sequences unless such reference would be indicated. In other words, it is a shorthand for listing all of these sequences individually. The invention encompasses
15 each sequence individually, as well as any combination thereof.

Definitions

"Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or
20 polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

A nucleic acid or polypeptide sequence that is "derived from" a designated
25 sequence refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or

complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to, replacement of an amino acid with one having similar physico-chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants also include any polypeptides that have the ability to elicit antibodies specific to a designated polypeptide.

An "*E. cloacae*-derived" nucleic acid or polypeptide sequence may or may not be present in other bacterial species, and may or may not be present in all *E. cloacae* strains. This term is intended to refer to the source from which the sequence was originally isolated. Thus, an *E. cloacae*-derived polypeptide, as used herein, may be used, e.g., as a target to screen for a broad spectrum antibacterial agent, to search for homologous proteins in other species of bacteria or in eukaryotic organisms such as bacteria humans, etc.

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least about 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains sufficient polypeptide to allow protein sequencing; at least about 1, 10, or preferably 100 mg of polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least about 10%, more preferably at least about 50%, of the subject cells.

5 A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is
10 derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment
15 produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *E. cloacae* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

20 An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into
25 messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are

determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

"Homologous" refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two

sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC
5 and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which
10 hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires
15 that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C) require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.
20 As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

A polypeptide has *E. cloacae* biological activity if it has one, two or preferably more of the following properties: (1) if when expressed in the course of an *E.*
25 *cloacae* infection, it can promote, or mediate the attachment of *E. cloacae* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *E.*

cloacae protein; (3) the gene which encodes it can rescue a lethal mutation in an *E. cloacae* gene. A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *E. cloacae* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *E. cloacae* polypeptides, e.g., one or more of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO (Chinese Hamster Ovary) cells. Because peptides such as *E. cloacae* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *E. cloacae* fragment or *E. cloacae* analog is one which exhibits a biological activity in any biological assay for *E. cloacae* activity. The fragment or analog possesses about 10%, preferably about 40%, more preferably about 60%, 70%, 80% or 90% or greater of the activity of *E. cloacae*, in any *in vivo* or *in vitro* assay.

Analogous can differ from naturally occurring *E. cloacae* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogs include *E. cloacae* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *E. cloacae* polypeptide.

Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, 5 tyrosine. Other conservative substitutions can be made in view of the table below.

TABLE 1

CONSERVATIVE AMINO ACID REPLACEMENTS

	For Amino Acid	Code	Replace with any of
	Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
10	Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met,
	Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
	Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
	Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
	Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
15	Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
	Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
	Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
	Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
	Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met,
20	Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-
	Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-
	Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-
	Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O),
	Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O),
25	Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
	Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *E. cloacae* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *E. cloacae* polypeptides can be generated by methods known to those skilled in the art. The ability of an *Enterobacter* fragment to exhibit a biological activity of *E. cloacae* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *E. cloacae* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

An "immunogenic component" as used herein is a moiety, such as an *E. cloacae* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *E. cloacae* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *E. cloacae* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in

specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of increased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences

differs depending upon the host organism; in prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended
5 to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably
10 linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The "metabolism" of a substance, as used herein, means any aspect of the expression, function, action, or regulation of the substance. The metabolism of a
15 substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution
20 of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

25 Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains,

unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. The practice of the invention will employ, unless

5 otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See e.g.*, Sambrook, Fritsch, and Maniatis, *Molecular Cloning: Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 10 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.); *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991); *Immunology*, 2d Edition, 1989, Roitt *et al.*, C.V. Mosby Company, and New York; *Advanced Immunology*, 2d Edition, 1991, Male *et al.*,

15 Grower Medical Publishing, New York.; *DNA Cloning: A Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis*, 1984, (M.L. Gait ed); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *Animal Cell Culture*, 1986 (R.I. Freshney ed.); *Immobilized Cells and Enzymes*, 1986 (IRL Press); Perbal, 1984, *A Practical Guide to Molecular Cloning*; *Gene Transfer Vectors for*

20 *Mammalian Cells*, 1987 (J. H. Miller and M. P. Calos eds., Cold Spring Harbor Laboratory); Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

25 Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention; however, preferred materials and/or methods are

described. Materials, reagents and the like to which reference is made in the following description and examples are obtainable from commercial sources, unless otherwise noted.

5 *E. cloacae* Genomic Sequence

This invention provides nucleotide sequences of the genome of *E. cloacae* which thus comprises a DNA sequence library of *E. cloacae* genomic DNA. The detailed description that follows provides nucleotide sequences of *E. cloacae*, and also
10 describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are compositions and methods of using the disclosed *E. cloacae* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *E. cloacae*.

15 To determine the genomic sequence of *E. cloacae*, DNA from strain 15842 of *E. cloacae* was isolated after Zymolyase digestion, sodium dodecyl sulfate lysis, potassium acetate precipitation, phenol:chloroform extraction and ethanol precipitation (Soll, D.R., T. Srikantha and S.R. Lockhart: Characterizing Developmentally Regulated Genes in *E. cloacae*. In Microbial Genome Methods. K.W. Adolph, editor.
20 CRC Press. New York. p 17-37.). DNA was sheared hydrodynamically using an HPLC (Oefner, et. al., 1996) to an insert size of 2000-3000 bp. After size fractionation by gel electrophoresis the fragments were blunt-ended, ligated to adapter oligonucleotides and cloned into the pGTC (Thomann) vector to construct a "shotgun" subclone library.

DNA sequencing was achieved using established ABI sequencing methods on ABI377 automated DNA sequencers. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The cloning and sequencing procedures are described in more detail in the Exemplification.

10 A variety of approaches may be used to order the contigs so as to obtain a continuous sequence representing the entire *E. cloacae* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *E. cloacae* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that
15 contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *E. cloacae* sequences were analyzed for the presence of open reading
20 frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *E. cloacae* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *E. cloacae* polypeptide. Such start codons within the ORFs
25 provided herein were identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *E. cloacae* polypeptide is within the scope of this

invention. For example, within the ORFs a codon such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis were identified and the portion of an ORF corresponding to a naturally-occurring *E. cloacae* polypeptide was recognized. The predicted coding regions were defined by
5 evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and McIninch, 1993, *Comp. .* 17:123).

Each predicted ORF amino acid sequence was compared with all sequences found in current GENBANK, SWISS-PROT, and PIR databases using the BLAST algorithm. BLAST identifies local alignments occurring by chance between the ORF
10 sequence and the sequence in the databank (Altschall et al., 1990, *L Mol. Biol.* 215:403-410). Homologous ORFs (probabilities less than 10^{-5} by chance) and ORF's that are probably non-homologous (probabilities greater than 10^{-5} by chance) but have good codon usage were identified. Both homologous, sequences and non-homologous sequences with good codon usage, are likely to encode proteins and are encompassed
15 by the invention.

E. cloacae Nucleic Acids

The present invention provides a library of *E. cloacae*-derived nucleic acid
20 sequences. The libraries provide probes, primers, and markers which are used as markers in epidemiological studies. The present invention also provides a library of *E. cloacae*-derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

The nucleic acids of this invention may be obtained directly from the DNA of
25 the above referenced *E. cloacae* strain by using the polymerase chain reaction (PCR). See "*PCR, A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press,

Oxford, UK, 1991) for details about the PCR. High fidelity PCR is used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products is verified by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening the libraries
5 by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *E. cloacae* polypeptides
10 from a cDNA library in accordance with protocols herein described. A cDNA encoding an *E. cloacae* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes
15 encoding *E. cloacae* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using
20 standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by
25 reference herein).

In another example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide
5 cassettes comprising pairs of synthetic oligonucleotides, as described below.

Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes,
10 primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products) of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

15 Probes

A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *E. cloacae*. With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired
20 inclusivity and exclusivity with respect to *E. cloacae*, and extraneous nucleic acids likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least about twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

25 Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will

readily recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect
5 homologous regions (especially homologous genes) of other *Enterobacter* species using appropriate stringency hybridization conditions as described herein.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described
10 above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *E. cloacae* nucleic acid from one strain from the nucleic acid of other another strain as well as from other organisms. Nucleic acid
15 having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Enterobacter* species from each other and from other organisms. Preferably, the sequence will comprise at least about twenty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000
20 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences
25 described herein have utility as primers for the amplification of *E. cloacae* nucleic acid. These nucleic acids may also have utility as primers for the amplification of

nucleic acids in other *Enterobacter* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of ≥ 10 -15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *E. cloacae* nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *E. cloacae* and/or other *Enterobacter* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

The nucleic acids of the present invention find use as templates for the recombinant production of *E. cloacae*-derived peptides or polypeptides

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *E. cloacae* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Enterobacter* species.

In one embodiment, nucleic acid or derivatives corresponding to *E. cloacae* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more

nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid
5 having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

The present invention encompasses isolated polypeptides and nucleic acids
10 derived from *E. cloacae* that are useful as reagents for diagnosis of bacterial infection, components of effective anti-bacterial vaccines, and/or as targets for anti-bacterial drugs, including anti-*E. cloacae* drugs.

Expression of *E. cloacae* Nucleic Acids

15

Table 2, which is appended herewith and which forms part of the present specification, provides a list of open reading frames (ORFs) in both strands and a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of
20 the predicted polypeptide with known proteins encoded by ORFs in other organisms. An ORF is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and was determined from stop to stop codons. The first column contains a designation for the contig from which each ORF was identified (numbered arbitrarily). Each contig represents a
25 continuous stretch of the genomic sequence of the organism. The second column lists the ORF designation. The third and fourth columns list the SEQ ID numbers for the

nucleic acid and amino acid sequences corresponding to each ORF, respectively. The fifth and sixth columns list the length of the nucleic acid ORF and the length of the amino acid ORF, respectively. The nucleotide sequence corresponding to each ORF begins at the first nucleotide immediately following a stop codon and ends at the nucleotide immediately preceding the next downstream stop codon in the same reading frame. It will be recognized by one skilled in the art that the natural translation initiation sites will correspond to ATG, GTG, or TTG codons located within the ORFs. The natural initiation sites depend not only on the sequence of a start codon but also on the context of the DNA sequence adjacent to the start codon. Usually, a recognizable ribosome binding site is found within 20 nucleotides upstream from the initiation codon. In some cases where genes are translationally coupled and coordinately expressed together in "operons", ribosome binding sites are not present, but the initiation codon of a downstream gene may occur very close to, or overlap, the stop codon of the an upstream gene in the same operon. The correct start codons can be generally identified without undue experimentation because only a few codons need be tested. It is recognized that the translational machinery in bacteria initiates all polypeptide chains with the amino acid methionine, regardless of the sequence of the start codon. In some cases, polypeptides are post-translationally modified, resulting in an N-terminal amino acid other than methionine *in vivo*. The seventh and eighth columns provide metrics for assessing the likelihood of the homology match (determined by the BLASTP2 algorithm), as is known in the art, to the genes indicated in the eleventh column when the designated ORF was compared against a non-redundant comprehensive protein database. Specifically, the seventh column represents the "Blast Score" for the match (a higher score is a better match), and the eighth column represents the "P-value" for the match (the probability that such a match can have occurred by chance; the lower the value, the more likely the match is

valid). If a BLASTP2 score of less than 46 was obtained, no value is reported in the table the "P-value". Column nine provides the name of the organism that was identified as having the closest homology match. The tenth column provides, where available, either a public database accession number or our own sequence name. The
5 eleventh column provides, where available, the Swissprot accession number (SP),(SP), the locus name (LN), the Organism (OR), Source of variant (SR), E.C. number (EC), the gene name (GN), the product name (PN), the Function Description (FN), Left End (LE), Right End (RE), Coding Direction (DI), and the description (DE) or notes (NT) for each ORF. Information that is not preceded by a code designation
10 in the eleventh column represents a description of the ORF. This information allows one of ordinary skill in the art to determine a potential use for each identified coding sequence and, as a result, allows to use the polypeptides of the present invention for commercial and industrial purposes.

Using the information provided in SEQ ID NO: 1 - SEQ ID NO: 5662, SEQ
15 ID NO: 5663 - SEQ ID NO: 11324 and in Table 2 together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all the nucleic acid fragments of interest including open reading frames (ORFs) encoding a large variety of proteins of *E. cloacae*.

Nucleic acid isolated or synthesized in accordance with the sequences
20 described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in SEQ ID NO: 1 - SEQ ID NO: 5662 and in Table 2 or fragments of said nucleic acid encoding active portions of *E. cloacae* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

25 The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by

the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in
5 a strain that does not produce the same gene product(s). This includes, but is not limited to, Eucaryotic species such as the yeast *Saccharomyces cerevisiae*, *Methanobacterium* strains or other Archaea, and Eubacteria such as *E. coli*, *B. Subtilis*, *S. Aureus*, *S. Pneumonia* or *Pseudomonas putida*. In some cases the expression host will utilize the natural *E. cloacae* promoter whereas in others, it will
10 be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *E. cloacae* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory
15 sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to
20 produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

25 In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression

plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

- 5 A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press (1989)), and other laboratory textbooks.

- For example, a host cell transfected with a nucleic acid vector directing
10 expression of a nucleotide sequence encoding an *E. cloacae* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange
15 chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such polypeptides.

Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

- 20 In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction.
25 Chromatographic techniques which can be used in the final purification step are

known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *E. cloacae* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically
5 cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128).

Another strategy would be to alter the nucleic acid encoding an *E. cloacae* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al.,
10 (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide
15 synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

The present invention provides a library of *E. cloacae*-derived nucleic acid
20 sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *E. cloacae*-derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

Nucleic acids comprising any of the sequences disclosed herein or sub-
25 sequences thereof can be prepared by standard methods using the nucleic acid sequence information provided in SEQ ID NO: 1 - SEQ ID NO: 5662. For example,

DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 764:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of
5 synthetic oligonucleotides, as described below.

Of course, due to the degeneracy of the genetic code, many different nucleotide sequences can encode polypeptides having the amino acid sequences defined by SEQ ID NO: 5663 - SEQ ID NO: 11324 or sub-sequences thereof. The codons can be selected for optimal expression in prokaryotic or eukaryotic systems.

10 Such degenerate variants are also encompassed by this invention.

Insertion of nucleic acids (typically DNAs) encoding the polypeptides of the invention into a vector is easily accomplished when the termini of both the DNAs and the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-
15 stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific
20 oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki *et al.*, 1988, *Science* 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids of the invention may be isolated directly from cells.
25 Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic

material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

- 5 The nucleic acids of the present invention may be flanked by natural *E. cloacae* regulatory sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'- noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such
- 10 modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more
- 15 additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage.
- 20 Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

 The invention also provides nucleic acid vectors comprising the disclosed *E. cloacae*-derived sequences or derivatives or fragments thereof. A large number of

25 vectors, including plasmid and bacterial vectors, have been described for replication

and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for cloning or protein expression.

The encoded *E. cloacae* polypeptides may be expressed by using many known vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or
5 pRSET or pREP (Invitrogen, San Diego, CA), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g.
10 antibiotic resistance, and one or more expression cassettes. The inserted *E. cloacae* coding sequences may be synthesized by standard methods, isolated from natural sources, or prepared as hybrids, etc. Ligation of the *E. cloacae* coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by known methods. Suitable host cells may be
15 transformed/transfected/infected as appropriate by any suitable method including electroporation, CaCl_2 mediated DNA uptake, bacterial infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *E.*
20 *cloacae*, *E. coli*, *B. Subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination
25 regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these

regions, methods of isolation, manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced *E. cloacae*-derived peptides and polypeptides.

Advantageously, vectors may also include a transcription regulatory element (i.e., a promoter) operably linked to the *E. cloacae* portion. The promoter may optionally contain operator portions and/or ribosome binding sites. Non-limiting examples of bacterial promoters compatible with *E. coli* include: b-lactamase (penicillinase) promoter; lactose promoter; tryptophan (*trp*) promoter; araBAD (arabinose) operon promoter; lambda-derived P₁ promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the *trp* and *lac* UV5 promoters. Non-limiting examples of yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactose epimerase promoter, and alcohol dehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limitation viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences, polyA addition sequences and enhancer sequences to increase expression. Sequences which cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or prohormone pro region sequences, may also be included. These sequences are well described in the art.

Nucleic acids encoding wild-type or variant *E. cloacae*-derived polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene.

Other recombination-based methods such as nonhomologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

The nucleic acids of the present invention find use as templates for the recombinant production of *E. cloacae*-derived peptides or polypeptides.

5

Identification and Use of *E. cloacae* Nucleic Acid Sequences

The disclosed *E. cloacae* polypeptide and nucleic acid sequences, or other sequences that are contained within ORFs, including complete protein-coding
10 sequences, of which any of the disclosed *E. cloacae*-specific sequences forms a part, are useful as target components for diagnosis and/or treatment of *E. cloacae*- caused infection

It will be understood that the sequence of an entire protein-coding sequence of which each disclosed nucleic acid sequence forms a part can be isolated and identified
15 based on each disclosed sequence. This can be achieved, for example, by using an isolated nucleic acid encoding the disclosed sequence, or fragments thereof, to prime a sequencing reaction with genomic *E. cloacae* DNA as template; this is followed by sequencing the amplified product. The isolated nucleic acid encoding the disclosed sequence, or fragments thereof, can also be hybridized to *E. cloacae* genomic libraries
20 to identify clones containing additional complete segments of the protein-coding sequence of which the shorter sequence forms a part. Then, the entire protein-coding sequence, or fragments thereof, or nucleic acids encoding all or part of the sequence, or sequence-conservative or function-conservative variants thereof, may be employed in practicing the present invention.

25 Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and

antibody-based methods for detecting bacterial infection. Therapeutic applications include without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are both unique to bacteria and essential for growth and/or replication of bacteria.

5

Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *E. cloacae*

The disclosed *E. cloacae* genome sequence includes segments that direct the
10 synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *E. cloacae*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences,
15 which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences:

Computer-assisted comparison of the disclosed *E. cloacae* sequences with
20 previously reported sequences present in publicly available databases is useful for identifying functional *E. cloacae* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess
25 some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in

transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *E. cloacae* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

10 Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *E. cloacae* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

15 Targets for therapeutic drugs according to the invention include, but are not limited to, polypeptides of the invention, whether unique to *E. cloacae* or not, that are essential for growth and/or viability of *E. cloacae* under at least one growth condition. Polypeptides essential for growth and/or viability can be determined by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout".

20 Alternatively, genetic footprinting can be used (Smith *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92:5479-6433; Published International Application WO 94/26933; U.S. Patent No. 5,612,180). Still other methods for assessing essentiality includes the ability to isolate conditional lethal mutations in the specific gene (e.g., temperature sensitive mutations). Other useful targets for therapeutic drugs, which include
25 polypeptides that are not essential for growth or viability *per se* but lead to loss of viability of the cell, can be used to target therapeutic agents to cells.

Strain-specific sequences:

Because of the evolutionary relationship between different *E. cloacae* strains, it is believed that the presently disclosed *E. cloacae* sequences are useful for identifying, and/or discriminating between, previously known and new *E. cloacae* strains. It is

5 believed that other *E. cloacae* strains will exhibit at least about 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *E. cloacae* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *E. cloacae*

10 strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *E. cloacae*. Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively recognize one or more *E. cloacae* strains.

15 In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *E. cloacae* strains but are not found in other bacterial species.

E. cloacae Polypeptides

20

This invention encompasses isolated *E. cloacae* polypeptides encoded by the disclosed *E. cloacae* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least about 5 amino acid residues in length. Using the DNA sequence information

25 provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood

that the sequence of an entire nucleic acid encoding an *E. cloacae* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain
5 reaction with genomic *E. cloacae* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the present invention, including function-conservative variants of the disclosed ORFs, may be isolated from wild-type or mutant *E. cloacae* cells, or from heterologous organisms or cells (including, but not limited to, bacteria,
10 fungi, insect, plant, and mammalian cells) including *E. cloacae* into which an *E. cloacae*-derived protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

E. cloacae polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein , including,
15 without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* 85:2149. The synthesis is carried out with amino acids that are protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are
20 also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the polypeptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take place at the amino-terminus. The conditions for the removal of the alpha-amino protecting group do not remove the side-chain protecting groups.

25 Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC,

reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the *E. cloacae* protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against an *E. cloacae* protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The present invention also encompasses derivatives and homologues of *E. cloacae*-encoded polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

To identify *E. cloacae*-derived polypeptides for use in the present invention, essentially the complete genomic sequence of a virulent, methicillin-resistant isolate of *Enterobacter cloacae* isolate was analyzed. While, in very rare instances, a nucleic acid sequencing error may be revealed, resolving a rare sequencing error is well

within the art, and such an occurrence will not prevent one skilled in the art from practicing the invention.

Also encompassed are any *E. cloacae* polypeptide sequences that are contained within the open reading frames (ORFs), including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 5662 forms a part. Table 2, which is appended herewith and which forms part of the present specification, provides a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. As a result, one skilled in the art can use the polypeptides of the present invention for commercial and industrial purposes consistent with the type of putative identification of the polypeptide.

The present invention provides a library of *E. cloacae*-derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences that are contemplated for use as components of vaccines. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended herewith and which forms part of the present specification.

The present invention also provides a library of *E. cloacae*-derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences lacking homology to any known prokaryotic or eukaryotic sequences. Such libraries provide probes, primers, and markers which can be used to diagnose *E. cloacae* infection, including use as markers

in epidemiological studies. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended

The present invention also provides a library of *E. cloacae*-derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the

5 polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise targets for therapeutic drugs.

Specific Example: Determination Of *Enterobacter* Protein Antigens For Antibody
And Vaccine Development

10

The selection of *Enterobacter* protein antigens for vaccine development can be derived from the nucleic acids encoding *E. cloacae* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the discriminant analysis described by Klein, et al. (Klein, P.,
15 Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted
20 ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities lower than 1×10^{-6} that the homology is only due to
25 random chance) to membrane or exported proteins represent protein antigens for

vaccine development. Possible functions can be provided to *E. cloacae* genes based on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

10

Production of Fragments and Analogs of *E. cloacae* Nucleic Acids and Polypeptides

Based on the discovery of the *E. cloacae* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure of *E. cloacae* genes, e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *E. cloacae* polypeptides. Such screens are useful for the identification of inhibitors of *E. cloacae*.

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for

a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNAs which encode an array of fragments. DNAs which encode fragments of a protein can
5 also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of
10 desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random
15 mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

20

PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase
25 chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to

the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

Saturation Mutagenesis

5 Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by
10 modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

15

Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into
20 an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.*
25 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al.

(1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

5 Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

15 Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be

predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

5

Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide
10 encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein
15 DNA. Generally, oligonucleotides of at least about 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using
20 techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the
25 technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The

codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate

5 locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard
10 techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

15 Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned
20 sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or
25 alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

Other Modifications of *E. cloacae* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *E. cloacae* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and
5 resistance to proteolytic degradation *in vivo*). A modified *E. cloacae* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *E. cloacae* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to
10 minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *E. cloacae* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the
15 protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *E. cloacae* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Sehon and co-workers (Wie et al., *supra*) to produce a protein conjugated with
20 PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *E. cloacae* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San
25 Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *E. cloacae* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988)

5 *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *E. cloacae* polypeptide, canonical protease sensitive sites can be engineered between regions,
10 each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or
15 more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene
20 products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *E. cloacae* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the
25 gene whose product was detected. Each of the techniques described below is

amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

Two Hybrid Systems

- 5 Two hybrid assays such as the system described below (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *E. cloacae* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *E. cloacae* protein. (The *E. cloacae* domain is used as the bait protein and the library of variants are
- 10 expressed as prey fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind an *E. cloacae* polypeptide.

Display Libraries

- 15 In one approach to screening assays, the Enterobacter peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected
- 20 by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to
- 25 be visually inspected and separated under a fluorescence microscope, or, where the

morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can
5 be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be
10 amplified by another round of infection. The group of almost identical *E. coli* filamentous phages, M13, fd., and f1, are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes
15 recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

20 A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an
25 immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE

(Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al.

5 (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et
10 al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus* protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the
15 physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull et al. (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing
20 the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell
25 contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the

DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic

activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not
5 a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of
10 transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction
15 of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled
20 transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant
25 peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round

of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as
5 a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one
10 sequences the DNA produced by the phagemid host.

Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one
15 skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated though one of the primary screens described
20 above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *E. cloacae* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *E. cloacae* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its
5 counter ligand, e.g., in the case of an *E. cloacae* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *E. cloacae* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *E. cloacae*-derived peptidomimetics which competitively or noncompetitively inhibit binding of the *E. cloacae* polypeptide with an interacting polypeptide (see, for
10 example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *E. cloacae* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide,
15 and which therefore can inhibit binding of an *E. cloacae* polypeptide to an interacting polypeptide and thereby interfere with the function of *E. cloacae* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see
20 Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of
25 the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), b-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al.

(1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and et al. (1986) *Biochem Biophys Res Commun* 134:71).

5 Vaccine Formulations for *E. cloacae* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *E. cloacae* or for treatment of *E. cloacae* infection. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *E. cloacae*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *E. cloacae* surface proteins. Any nucleic acid encoding an immunogenic *E. cloacae* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

15 One aspect of the invention provides a vaccine composition for protection against infection by *E. cloacae* which contains at least one immunogenic fragment of an *E. cloacae* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *E. cloacae* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *E. cloacae* peptide in association with appropriate MHC molecules to T cells in conjunction with the necessary co-stimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be

employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

- 5 Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.
- 10 Vaccine compositions of the invention containing immunogenic components (e.g., *E. cloacae* polypeptide or fragment thereof or nucleic acid encoding an *E. cloacae* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it
- 15 is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or
- 20 effectiveness of the antibody. For vaccines of the invention containing *E. cloacae* polypeptides, the polypeptide is co-administered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or

25 DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration

5 include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *E. cloacae*. Cain et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose,

10 magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-

15 sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or

20 genetically engineered fusions of the *E. cloacae* polypeptide with cholera toxin or its B subunit, procholeraenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*E. cloacae* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or

25 immuno-stimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant

(chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 mg to 50 mg, for example 10 mg to 35 mg. When used in the form of microcapsules, the amount used will depend on
5 the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *E. cloacae*
10 polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *E.*
15 *cloacae* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *E. cloacae*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 mg to 10 g, preferably 10 mg to 100 mg. A suitable dosage for adults will also be in the range
20 of 5 mg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine
25 based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.*

150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary
5 immunization schedule over 1 month (Boedecker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *E. cloacae* protein of the invention expressed on its surface or it can be based on an *E.*
10 *coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *E. cloacae* infection, some are useful only for treating *E. cloacae* infection, and some are useful for both preventing and treating *E. cloacae* infection. In a preferred embodiment, the vaccine
15 composition of the invention provides protection against *E. cloacae* infection by stimulating humoral and/or cell-mediated immunity against *E. cloacae*. It should be understood that amelioration of any of the symptoms of *E. cloacae* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *E. cloacae*-caused disease, or an increase in the production of antibodies in the serum
20 or mucous of patients.

Antibodies Reactive With *E. cloacae* Polypeptides

The invention also includes antibodies specifically reactive with the subject *E. cloacae* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can
25 be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a

mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *E. cloacae* polypeptide can be administered in the presence of
5 adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *E. cloacae* polypeptides of the invention, e.g. antigenic
10 determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least about 95% homologous). In yet a further preferred embodiment of the invention, the anti-*E. cloacae* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80%
15 percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most preferred
20 embodiment, there is no cross-reactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *E. cloacae* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂
25 fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The

antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*E. cloacae* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *E. cloacae* polypeptides or *E. cloacae* polypeptide variants, and antibody fragments such as Fab`
5 and F(ab`)₂, can be used to block the action of *E. cloacae* polypeptide and allow the study of the role of a particular *E. cloacae* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *E. cloacae* and by microinjection of anti-*E. cloacae* polypeptide antibodies of the present invention.

10 Antibodies which specifically bind *E. cloacae* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *E. cloacae* antigens. Anti-*E. cloacae* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *E. cloacae* levels in tissue or bodily fluid as part of a clinical
15 testing procedure. Likewise, the ability to monitor *E. cloacae* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *E. cloacae* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-
20 *E. cloacae* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *E. cloacae* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *E. cloacae* antigens.

Another application of anti-*E. cloacae* polypeptide antibodies of the invention
25 is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type,

having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *E. cloacae* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*E. cloacae* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *E. cloacae* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

Bio chip Technology

The nucleic acid sequence of the present invention may be used to detect *E. cloacae* or other species of *Enterobacter* acid sequence using bio chip technology. Bio chips containing arrays of nucleic acid sequence can also be used to measure expression of genes of *E. cloacae* or other species of *Enterobacter*. For example, to diagnose a patient with a *E. cloacae* or other *Enterobacter* infection, a sample from a human or animal can be used as a probe on a bio chip containing an array of nucleic acid sequence from the present invention. In addition, a sample from a disease state can be compared to a sample from a non-disease state which would help identify a gene that is up-regulated or expressed in the disease state. This would provide valuable insight as to the mechanism by which the disease manifests. Changes in gene expression can also be used to identify critical pathways involved in drug transport or metabolism, and may enable the identification of novel targets involved in virulence or host cell interactions involved in maintenance of an infection. Procedures using such techniques have been described by Brown *et al.*, 1995, *Science* 270: 467-470.

Bio chips can also be used to monitor the genetic changes of potential therapeutic compounds including, deletions, insertions or mismatches. Once the therapeutic is added to the patient, changes to the genetic sequence can be evaluated for its efficacy. In addition, the nucleic acid sequence of the present invention can be used to determine essential genes in cell cycling. As described in Iyer *et al.*, 1999 (*Science*, 283:83-87) genes essential in the cell cycle can be identified using bio chips. Furthermore, the present invention provides nucleic acid sequence which can be used with bio chip technology to understand regulatory networks in bacteria, measure the response to environmental signals or drugs as in drug screening, and

study virulence induction. (Mons *et al.*, 1998, *Nature Biotechnology*, 16: 45-48.

Patents teaching this technology include U.S. Patents 5445934, 5744305, and 5800992.

Drug Screening Assays Using *E. cloacae* Polypeptides

- 5 By making available purified and recombinant *E. cloacae* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *E. cloacae* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *E.*
- 10 *cloacae* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the person skilled in the art.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in

15 cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system,

20 the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *E. cloacae* polypeptide.

- 25 Screening assays can be constructed *in vitro* with a purified *E. cloacae* polypeptide or fragment thereof, such as an *E. cloacae* polypeptide having enzymatic

activity, such that the activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound.

Moreover, a control assay can also be performed to provide a baseline for comparison.

- 5 Suitable products include those with distinctive absorption, fluorescence, or chemiluminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *E. cloacae* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote
- 10 membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *E. cloacae* cells.

Overexpression Assays

- Overexpression assays are based on the premise that overproduction of a
- 15 protein would lead to a higher level of resistance to compounds that selectively interfere with the function of that protein. Overexpression assays may be used to identify compounds that interfere with the function of virtually any type of protein, including without limitation enzymes, receptors, DNA- or RNA-binding proteins, or any proteins that are directly or indirectly involved in regulating cell growth.
- 20 Typically, two bacterial strains are constructed. One contains a single copy of the gene of interest, and a second contains several copies of the same gene. Identification of useful inhibitory compounds of this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of the two strains. The method involves constructing a nucleic acid vector that directs
- 25 high level expression of a particular target nucleic acid. The vectors are then transformed into host cells in single or multiple copies to produce strains that express

low to moderate and high levels of protein encoding by the target sequence (strain A and B, respectively). Nucleic acid comprising sequences encoding the target gene can, of course, be directly integrated into the host cell.

Large numbers of compounds (or crude substances which may contain active
5 compounds) are screened for their effect on the growth of the two strains. Agents which interfere with an unrelated target equally inhibit the growth of both strains. Agents which interfere with the function of the target at high concentration should inhibit the growth of both strains. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the
10 compound is affecting the particular target that is being tested, it should be possible to inhibit the growth of strain A at a concentration of the compound that allows strain B to grow.

Alternatively, a bacterial strain is constructed that contains the gene of interest under the control of an inducible promoter. Identification of useful inhibitory agents
15 using this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of this strain under both inducing and non-inducing conditions. The method involves constructing a nucleic acid vector that directs high-level expression of a particular target nucleic acid. The vector is then transformed into host cells that are grown under both non-inducing and inducing conditions
20 (conditions A and B, respectively).

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on growth under these two conditions. Agents that interfere with the function of the target should inhibit growth under both conditions. It should be possible, however, to titrate out the inhibitory effect of the
25 compound in the overexpressing strain. That is, if the compound is affecting the

particular target that is being tested, it should be possible to inhibit growth under condition A at a concentration that allows the strain to grow under condition B.

Ligand-binding Assays

5 Many of the targets according to the invention have functions that have not yet been identified. Ligand-binding assays are useful to identify inhibitor compounds that interfere with the function of a particular target, even when that function is unknown. These assays are designed to detect binding of test compounds to particular targets. The detection may involve direct measurement of binding. Alternatively, indirect
10 indications of binding may involve stabilization of protein structure or disruption of a biological function. Non-limiting examples of useful ligand-binding assays are detailed below.

A useful method for the detection and isolation of binding proteins is the Biomolecular Interaction Assay (BIAcore) system developed by Pharmacia Biosensor
15 and described in the manufacturer's protocol (LKB Pharmacia, Sweden). The BIAcore system uses an affinity purified anti-GST antibody to immobilize GST-fusion proteins onto a sensor chip. The sensor utilizes surface plasmon resonance which is an optical phenomenon that detects changes in refractive indices. In accordance with the practice of the invention, a protein of interest is coated onto a chip and test
20 compounds are passed over the chip. Binding is detected by a change in the refractive index (surface plasmon resonance).

A different type of ligand-binding assay involves scintillation proximity assays (SPA, described in U.S. Patent No. 4,568,649).

Another type of ligand binding assay, also undergoing development, is based
25 on the fact that proteins containing mitochondrial targeting signals are imported into isolated mitochondria *in vitro* (Hurt *et al.*, 1985, *Embo J.* 4:2061-2068; Eilers and

Schatz, *Nature*, 1986, 322:228-231). In a mitochondrial import assay, expression vectors are constructed in which nucleic acids encoding particular target proteins are inserted downstream of sequences encoding mitochondrial import signals. The chimeric proteins are synthesized and tested for their ability to be imported into isolated mitochondria in the absence and presence of test compounds. A test compound that binds to the target protein should inhibit its uptake into isolated mitochondria *in vitro*.

Another ligand-binding assay is the yeast two-hybrid system (Fields and Song, 1989, *Nature* 340:245-246). The yeast two-hybrid system takes advantage of the properties of the GAL4 protein of the yeast *Saccharomyces cerevisiae*. The GAL4 protein is a transcriptional activator required for the expression of genes encoding enzymes of galactose utilization. This protein consists of two separable and functionally essential domains: an N-terminal domain which binds to specific DNA sequences (UAS_G); and a C-terminal domain containing acidic regions, which is necessary to activate transcription. The native GAL4 protein, containing both domains, is a potent activator of transcription when yeast are grown on galactose media. The N-terminal domain binds to DNA in a sequence-specific manner but is unable to activate transcription. The C-terminal domain contains the activating regions but cannot activate transcription because it fails to be localized to UAS_G. In the two-hybrid system, a system of two hybrid proteins containing parts of GAL4: (1) a GAL4 DNA-binding domain fused to a protein 'X' and (2) a GAL4 activation region fused to a protein 'Y'. If X and Y can form a protein-protein complex and reconstitute proximity of the GAL4 domains, transcription of a gene regulated by UAS_G occurs. Creation of two hybrid proteins, each containing one of the interacting proteins X and Y, allows the activation region of UAS_G to be brought to its normal site of action.

The binding assay described in Fodor *et al.*, 1991, *Science* 251:767-773, which involves testing the binding affinity of test compounds for a plurality of defined polymers synthesized on a solid substrate, may also be useful.

Compounds which bind to the polypeptides of the invention are potentially
5 useful as antibacterial agents for use in therapeutic compositions.

Pharmaceutical formulations suitable for antibacterial therapy comprise the antibacterial agent in conjunction with one or more biologically acceptable carriers. Suitable biologically acceptable carriers include, but are not limited to, phosphate-buffered saline, saline, deionized water, or the like. Preferred biologically acceptable
10 carriers are physiologically or pharmaceutically acceptable carriers.

The antibacterial compositions include an antibacterial effective amount of active agent. Antibacterial effective amounts are those quantities of the antibacterial agents of the present invention that afford prophylactic protection against bacterial infections or which result in amelioration or cure of an existing bacterial infection.
15 This antibacterial effective amount will depend upon the agent, the location and nature of the infection, and the particular host. The amount can be determined by experimentation known in the art, such as by establishing a matrix of dosages and frequencies and comparing a group of experimental units or subjects to each point in the matrix.

20 The antibacterial active agents or compositions can be formed into dosage unit forms, such as for example, creams, ointments, lotions, powders, liquids, tablets, capsules, suppositories, sprays, aerosols or the like. If the antibacterial composition is formulated into a dosage unit form, the dosage unit form may contain an antibacterial effective amount of active agent. Alternatively, the dosage unit form may include less
25 than such an amount if multiple dosage unit forms or multiple dosages are to be used to administer a total dosage of the active agent. Dosage unit forms can include, in

addition, one or more excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), bactericide(s), or the like.

For general information concerning formulations, see, e.g., Gilman et al. (eds.), 1990, *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, 8th ed., Pergamon Press; and *Remington's Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co., Easton, PA; Avis et al. (eds.), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman et al (eds.), 1990, *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

10 The antibacterial agents and compositions of the present invention are useful for preventing or treating *E. cloacae* infections. Infection prevention methods incorporate a prophylactically effective amount of an antibacterial agent or composition. A prophylactically effective amount is an amount effective to prevent *E. cloacae* infection and will depend upon the specific bacterial strain, the agent, and the
15 host. These amounts can be determined experimentally by methods known in the art and as described above.

E. cloacae infection treatment methods incorporate a therapeutically effective amount of an antibacterial agent or composition. A therapeutically effective amount is an amount sufficient to ameliorate or eliminate the infection. The prophylactically
20 and/or therapeutically effective amounts can be administered in one administration or over repeated administrations. Therapeutic administration can be followed by prophylactic administration, once the initial bacterial infection has been resolved.

The antibacterial agents and compositions can be administered topically or systemically. Topical application is typically achieved by administration of creams,
25 ointments, lotions, or sprays as described above. Systemic administration includes both oral and parental routes. Parental routes include, without limitation,

subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation and intranasal administration.

EXEMPLIFICATION

5

Cloning and Sequencing *E. cloacae* Genomic Sequence

This invention provides nucleotide sequences of the genome of *E. cloacae* which thus comprises a DNA sequence library of *E. cloacae* genomic DNA. The
10 detailed description that follows provides nucleotide sequences of *E. cloacae*, and also describes how the sequences were obtained and how ORFs (Open Reading Frames) and protein-coding sequences can be identified. Also described are methods of using the disclosed *E. cloacae* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and
15 comparison of medically important sequences in this and other strains of *E. cloacae* as well as other species of *Enterobacter*.

Chromosomal DNA from strain 15842 of *E. cloacae* was isolated after Zymolyase digestion, sodium dodecyl sulfate lysis, potassium acetate precipitation, phenol:chloroform extraction and ethanol precipitation (Soll, D.R., T. Srikantha and
20 S.R. Lockhart: Characterizing Developmentally Regulated Genes in *E. cloacae*. In Microbial Genome Methods. K.W. Adolph, editor. CRC Press. New York. p 17-37.). Genomic *E. cloacae* DNA was hydrodynamically sheared in an HPLC and then separated on a standard 1% agarose gel. Fractions corresponding to 2500-3000 bp in length were excised from the gel and purified by the GeneClean procedure (Bio101,
25 Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique *Bst*XI-linker adapters (5'-GTCTTCACACGGGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar excess). These linkers are complimentary to the *Bst*XI-cut pGTC vector, while the
5 overhang is not self-complimentary. Therefore, the linkers will not concatermerize nor will the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adapted inserts were then ligated to *Bst*XI-cut vector to construct a "shotgun" subclone libraries.

10 Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Transformants were then used for plating of clones and picking for sequencing. The cultures were grown
15 overnight at 37°C. DNA was purified using a silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 μ g of DNA was obtained per clone.

These purified DNA samples were then sequenced using primarily ABI dye-terminator chemistry. All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The ABI dye terminator sequence reads were
20 run on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. Base calls and quality scores were determined using the program PHRED (Ewing et al., 1998, Genome Res. 8: 175-185; Ewing and Green, 1998, Genome Res. 8: 685-734). Reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan.
25 1996, p.157) with default program parameters and quality scores. The initial assembly was done at 6-fold coverage and yielded 513 contigs.

Finishing can follow the initial assembly. Missing mates (sequences from clones that only gave reads from one end of the *Enterobacter* DNA inserted in the plasmid) can be identified and sequenced with ABI technology to allow the identification of additional overlapping contigs.

5 End-sequencing of randomly picked genomic lambda was also performed. Sequencing on a both sides was done for all lambda sequences. The lambda library backbone helped to verify the integrity of the assembly and allowed closure of some of the physical gaps. Primers for walking off the ends of contigs would be selected using pick_primer (a GTC program) near the ends of the clones to
10 facilitate gap closure. These walks can be sequenced using the selected clones and primers. These data are then reassembled with PHRAP. Additional sequencing using PCR-generated templates and screened and/or unscreened lambda templates can be done in addition.

To identify *E. cloacae* polypeptides the complete genomic sequence of *E.*
15 *cloacae* were analyzed essentially as follows: First, all possible stop-to- stop open reading frames (ORFs) greater than 180 nucleotides in all six reading frames were translated into amino acid sequences. Second, the identified ORFs were analyzed for homology to known (archeabacter, prokaryotic and eukaryotic) protein sequences. Third, the coding potential of non-homologous sequences were evaluated with the
20 program GENEMARKTM (Borodovsky and McIninch, 1993, Comp. Chem. 17:123).

Identification, Cloning and Expression of *E.cloacae* Nucleic Acids

Expression and purification of the *E.cloacae* polypeptides of the invention can
25 be performed essentially as outlined below.

To facilitate the cloning, expression and purification of membrane and secreted proteins from *E.cloacae*, a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, is selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence.

PCR Amplification and Cloning of Nucleic Acids Containing ORF's Encoding

10 Enzymes

Nucleic acids chosen (for example, from the nucleic acids set forth in SEQ ID NO: 1 - SEQ ID NO: 5662 for cloning from the 15842 strain of *E.cloacae* are prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers specific for the 5' and 3' ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies (Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) are designed to include an NcoI cloning site at the extreme 5' terminus. These primers are designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *E.cloacae* DNA sequence. All reverse primers (specific for the 3' end of any *E.cloacae* ORF) include a EcoRI site at the extreme 5' terminus to permit cloning of each *E.cloacae* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag.

Genomic DNA prepared from the 15842 strain of *E.cloacae* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *E.cloacae* ORF, genomic DNA (50
5 nanograms) is introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *E.cloacae* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100
10 microliters.

Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly,
15 MA, USA)(Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in
20 slices isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of *E. cloacae* Nucleic Acids Into an Expression Vector

The pET-28b vector is prepared for cloning by digestion with restriction
25 endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). The pET-28a vector, which

encodes a His-Tag that can be fused to the 5' end of an inserted gene, is prepared by digestion with appropriate restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously
5 digested pET-28b expression vector. Products of the ligation reaction are then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation Of Competent Bacteria With Recombinant Plasmids

10

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), are transformed with recombinant pET expression plasmids carrying the cloned *E. cloacae* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction
15 is mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight.
20 Transformed colonies of BL21 are then picked and analyzed to evaluate cloned inserts as described below.

Identification Of Recombinant Expression Vectors With *E. cloacae* Nucleic Acids

25

Individual BL21 clones transformed with recombinant pET-28b *E. cloacae* ORFs are analyzed by PCR amplification of the cloned inserts using the same forward

and reverse primers, specific for each *E. cloacae* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the *E. cloacae* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

5

Isolation and Preparation of Nucleic Acids From Transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *E. cloacae* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml
10 kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression Of Recombinant *E. cloacae* Sequences In *E. coli*

15 The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda
20 derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

25 To express recombinant *E. cloacae* sequences, 50 nanograms of plasmid DNA isolated as described above is used to transform competent BL21(DE3) bacteria as

described above (provided by Novagen as part of the pET expression system kit).

The lacZ gene (beta-galactosidase) is expressed in the pET-System as described for the *E. cloacae* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25

5 micrograms/ml kanamycin sulfate. The following day, bacterial colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *E. cloacae* recombinant DNA constructions .

10 After induction of gene expression with IPTG, bacteria are pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells are then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets are weighed and frozen at -80°C until ready for protein
15 purification.

A variety of methodologies known in the art can be utilized to purify the isolated proteins. (Current Protocols in Protein Science, John Wiley and Sons, Inc., J. E. Coligan et al., eds., 1995). For example, the frozen cells may be thawed, resuspended in buffer and ruptured by several passages through a small volume
20 microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate may be centrifuged to yield a clear supernatant (crude extract) and following filtration the crude extract may be fractionated over columns. Fractions may be monitored by absorbance at OD₂₈₀ nm. and peak fractions may analyzed by SDS-PAGE

25 The concentrations of purified protein preparations may be quantified spectrophotometrically using absorbance coefficients calculated from amino acid

content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

- 5 SDS-polyacrylamide gels of various concentrations may be purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin
- 10 inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more
5 than routine experimentation, many equivalents to the specific embodiments and
methods described herein. The specific embodiments described herein are offered by
way of example only, and the invention is to limited only by the terms of the
appended claims, along with the full scope of equivalents to which such claims are
entitled.

10

TABLE 2

Contig	Orf	nt ID	aa ID	nt Length	aa Length	Blast Score	Blast Probability	Subject Taxonomy	Subject Name	Subject Description
CONTIG1	31892515_f2_2	1	5663	432	144	264	6.2(10)-23	Salmonella typhimurium	U94729	[de:salmonella typhimurium oxd-6 operon, putative substrate-binding protein (oxd-6a), putative transmembrane protein (oxd-6), putative transmembrane protein (oxd-6c), putative atpase (oxd-6d), and putative atpase (oxd-6e)]
CONTIG1	32542792_c2_6	2	5664	231	77	92	0.0016	Plasmodium falciparum	P09346	knob-associated histidine-rich protein precursor (kahrp).
CONTIG10	22066424_c1_4	3	5665	490	163	262	3.2(10)-22	Escherichia coli	b1006	[pn:hypothetical protein] [gn:ycdg]
CONTIG100	30752167_c1_6	4	5666	267	89	390	2.7(10)-36	Escherichia coli	b4162	[pn:hypothetical 23.5 kd protein in psd-amib intergenic region] [gn:yier]
CONTIG100	15735381_c3_7	5	5667	393	131	542	2.2(10)-52	Escherichia coli	b4162	[pn:hypothetical 23.5 kd protein in psd-amib intergenic region] [gn:yier]
CONTIG101	3222031_f1_1	6	5668	675	225	797	2.1(10)-79	Escherichia coli	b1047	[pn:hypothetical protein]
CONTIG101	6261469_c2_6	7	5669	647	215	621	9.3(10)-61	Escherichia coli	b1045	[pn:hypothetical protein]
CONTIG102	4535155_c2_13	8	5670	924	308	1137	1.8(10)-115	Escherichia coli	b0433	[pn:ampg protein] [gn:ampg]
CONTIG103	19719827_f1_1	9	5671	1005	335	120	0.00079	Human herpesvirus 6 (strain Uganda-1102)	AF015297	[de:human herpesvirus 6 (strain uganda-1102) ie2hom mma, complete cds.] [pn:ie2hom] [gn:ie2hom] [nt:similar to the immediate-early 2 protein of human]
CONTIG105	24245287_c1_5	10	5672	1170	390	1142	5.7(10)-116	Escherichia coli	b4261	[pn:hypothetical 40.4 kd protein in pepa-gntv intergenic region] [gn:yjgp]
CONTIG106	15104766_f3_7	11	5673	756	252	518	7.7(10)-50	Escherichia coli	P06615	resolvase (protein d).
CONTIG108	35269762_f2_2	12	5674	951	317	131	4.0(10)-6	Bacillus subtilis	yojN	[pn:hypothetical protein]

CONTIG109	7240778_f2_2	13	5675	519	173	224	1.1(10)-18	Haemophilus influenzae	HI1415	[pn:hypothetical protein]
CONTIG11	29877090_c2_8	14	5676	345	115	191	1.2(10)-14	Cloning vector pCMVLacl	U64448	or:cloning vector penvlaci pn:lae repressor gn:laci le:2685 re:3803 di:direct
CONTIG11	3328900_c3_9	15	5677	342	114	203	1.8(10)-16	Haemophilus influenzae	HI0522	[pn:sp]
CONTIG110	4084392_f2_1	16	5678	1110	370	154	2.1(10)-8	Escherichia coli	P07620	plasmid partition par a protein.
CONTIG111	25803317_f2_3	17	5679	1056	352	1446	3.5(10)-148	Escherichia coli	b2392	[pn:hypothetical protein]
CONTIG113	34192257_f2_1	18	5680	1071	357	805	3.0(10)-80	Escherichia coli	b3589	[pn:hypothetical 40.2 kd protein in avia-selb intergenic region] [gn:yiaj]
CONTIG115	26750793_f3_3	19	5681	537	179	799	1.3(10)-79	Escherichia coli	b3279	[pn:hypothetical protein] [gn:yida]
CONTIG115	16175299_c1_5	20	5682	199	66	275	4.2(10)-24	Escherichia coli	b3281	[pn:shikimate dehydrogenase] [gn:aroC]
CONTIG115	22938215_c3_7	21	5683	357	119	311	6.5(10)-28	Escherichia coli	b3280	[pn:hypothetical 10.0 kd protein in rmd-aroC intergenic region]
CONTIG116	19713405_c3_8	22	5684	198	66	180	5.0(10)-14	Escherichia coli	b1972	[pn:hypothetical protein]
CONTIG116	24033587_c3_9	23	5685	522	174	479	1.0(10)-45	Haemophilus influenzae	HI0970	[pn:3-dehydroquinate dehydratase] [gn:aroG]
CONTIG117	13852211_f1_1	24	5686	591	197	647	1.6(10)-63	Escherichia coli	b1988	[pn:nitrogen assimilation regulatory protein] [gn:nac]
CONTIG117	21690876_f2_2	25	5687	240	80	224	1.1(10)-18	Escherichia coli	b1990	[pn:31.6 kd protein in cobt 3'''region precursor] [gn:erfK]
CONTIG117	29942556_f2_4	26	5688	342	114	250	1.8(10)-21	Escherichia coli	b1988	[pn:nitrogen assimilation regulatory protein] [gn:nac]
CONTIG118	14225431_c1_13	27	5689	492	164	558	4.4(10)-54	Erwinia carotovora subsp. carotovora	JC4729	mob protein c - erwinia carotovora subsp. carotovora a cis-acting locus, orit and trans-acting locus, mob are involved in mobilization of pec3, a non-self-transmissible multiple-copy plasmid. the mob consists of five proteins
CONTIG118	5163340_c2_16	28	5690	696	232	938	2.3(10)-94	Plasmid pSW200	L42525	or:plasmid psw200 gn:moba le:1657 re:3156 di:direct sr:plasmid psw200 dna

CONTIG119	36072216_c2_6	29	5691	1392	464	2041	3.1(10)-211	Escherichia coli	b0930	[pn:asparaginyl-tRNA synthetase] [gn:asns]
CONTIG120	2394707_f1_1	30	5692	567	189	629	1.3(10)-61	Escherichia coli	b3983	[pn:50s ribosomal subunit protein 111] [gn:rplk]
CONTIG120	23572188_f1_2	31	5693	708	236	959	1.3(10)-96	Escherichia coli	b3984	[pn:50s ribosomal subunit protein 11] [gn:rpla]
CONTIG120	31651642_f2_4	32	5694	315	105	295	3.2(10)-26	Escherichia coli	b3985	[pn:50s ribosomal subunit protein 110] [gn:rplj]
CONTIG121	23552216_f2_1	33	5695	384	128	612	8.4(10)-60	Escherichia coli	b3310	[pn:50s ribosomal subunit protein 114] [gn:rpln]
CONTIG121	20117711_f2_2	34	5696	600	200	779	1.7(10)-77	Escherichia coli	b3308	[pn:50s ribosomal subunit protein 15] [gn:rple]
CONTIG121	2037562_f3_3	35	5697	357	119	512	3.2(10)-49	Escherichia coli	b3309	[pn:50s ribosomal subunit protein 124] [gn:rplx]
CONTIG122	16411425_f1_2	36	5698	1055	352	1187	9.8(10)-121	Escherichia coli	b2965	[pn:ornithine decarboxylase, constitutive] [gn:spec]
CONTIG122	24229836_c2_9	37	5699	531	177	571	1.8(10)-55	Escherichia coli	b2966	[pn:hypothetical protein] [gn:yqga]
CONTIG123	34484627_f2_2	38	5700	516	172	188	7.0(10)-15	Escherichia coli	b3335	[pn:type 4 prepilin-like protein specific leader peptidase] [gn:hofd]
CONTIG123	32032906_c2_6	39	5701	519	173	732	1.6(10)-72	Escherichia coli	b3336	[pn:bacterioferritin] [gn:bfr]
CONTIG125	24335430_c2_7	40	5702	1173	391	1749	2.7(10)-180	Escherichia coli	b0094	[pn:cell division protein ftsa] [gn:ftsa]
CONTIG125	10020833_c3_8	41	5703	255	85	309	1.1(10)-27	Escherichia coli	b0093	[pn:cell division protein ftsq] [gn:ftsq]
CONTIG126	26582352_f1_1	42	5704	657	219	1051	2.5(10)-106	Escherichia coli	b3229	[pn:stringent starvation protein] [gn:sspa]
CONTIG126	31338512_f3_4	43	5705	216	72	243	1.1(10)-20	Escherichia coli	b3228	[pn:stringent starvation protein b] [gn:sspb]
CONTIG127	4891510_f1_1	44	5706	333	111	387	5.7(10)-36	Escherichia coli	b1060	[pn:hypothetical protein] [gn:hypothetical protein]
CONTIG127	33255311_f2_4	45	5707	699	233	774	5.7(10)-77	Escherichia coli	b1059	[pn:hypothetical protein] [gn:sola]
CONTIG128	25781411_f2_1	46	5708	474	158	646	2.1(10)-63	Escherichia coli	b3342	[pn:30s ribosomal subunit protein s12] [gn:rpsl]
CONTIG128	23714561_f2_2	47	5709	411	137	637	1.8(10)-62	Escherichia coli	b3341	[pn:30s ribosomal subunit protein s7] [gn:rpsg]

CONTIG128	46907_c3_4	48	5710	339	113	158	1.1(10)-11	Eikenella corrodens	P35648	hemagglutinin 2.
CONTIG129	16178312_fl_2	49	5711	555	185	706	9.9(10)-70	Escherichia coli	P08504	transposase for transposon tn2501.
CONTIG129	22386375_c1_6	50	5712	636	212	691	3.6(10)-68	Escherichia coli	b1374	[pn: hypothetical protein]
CONTIG130	16016405_f2_1	51	5713	402	134	349	6.2(10)-32	Escherichia coli	b0339	[pn: cyanate permease] [gn: cym]
CONTIG130	1150468_c2_7	52	5714	909	303	970	9.6(10)-98	Escherichia coli	b1668	[pn: hypothetical protein]
CONTIG131	395662_fl_2	53	5715	380	127	208	5.4(10)-17	Haemophilus influenzae	HI1053	[pn: gb]
CONTIG131	35806526_f3_3	54	5716	357	119	91	0.00013	Mycoplasma genitalium	MG427	[pn: hypothetical protein mg427]
CONTIG131	23601436_f3_4	55	5717	624	208	134	2.7(10)-8	Escherichia coli	b1649	[pn: hypothetical protein]
CONTIG132	22667830_fl_1	56	5718	786	262	331	5.0(10)-30	Bacillus subtilis	pdhD	[pn: dihydrolipoamide dehydrogenase e3 subunit of both pyruvate dehydrogenase and 2- oxoglutarate dehydrogenase]
CONTIG132	34410768_f2_2	57	5719	249	83	301	7.5(10)-27	Escherichia coli	b1994	[pn: insertion element is5 hypothetical 39.3 kd protein]
CONTIG134	10651717_c1_6	58	5720	498	166	777	2.7(10)-77	Plasmid pSW200	L42525	or: plasmid psw200 gn: mobb le: 2345 re: 2830 di: direct sr: plasmid psw200 dna
CONTIG134	26681336_c1_7	59	5721	219	73	328	1.0(10)-29	Erwinia carotovora subsp. carotovora	JC4730	mob protein d - erwinia carotovora subsp. carotovora a cis-acting locus, orit and trans-acting locus, mob arc involved in mobilization of pec3, a non-self-transmissible multiple-copy plasmid. the mob consists of five proteins.
CONTIG134	12897806_c3_9	60	5722	861	287	1188	7.7(10)-121	Plasmid pSW200	L42525	or: plasmid psw200 gn: moba le: 1657 re: 3156 di: direct sr: plasmid psw200 dna
CONTIG135	964590_fl_2	61	5723	627	209	824	2.8(10)-82	Escherichia coli	b0434	[pn: hypothetical lipoprotein in ampg 5''' region] [gn: yajg]
CONTIG135	30722826_fl_3	62	5724	372	124	458	1.7(10)-43	Escherichia coli	b0433	[pn: ampg protein] [gn: ampg]

CONTIG135	34626891_c1_5	63	5725	237	79	316	1.8(10)-28	Escherichia coli	b0435	[pn:bola protein] [gn:bola]
CONTIG136	5954207_f1_1	64	5726	765	255	828	1.1(10)-82	Escherichia coli	b2511	[pn:hypothetical protein]
CONTIG136	32500050_f3_3	65	5727	606	202	891	2.2(10)-89	Escherichia coli	b2512	[pn:hypothetical protein]
CONTIG137	14506503_f1_1	66	5728	462	154	166	2.8(10)-12	Escherichia coli	b4396	[pn:right origin-binding protein] [gn:rob]
CONTIG137	30667937_f3_3	67	5729	192	64	121	2.8(10)-7	Escherichia coli	b1790	[pn:hypothetical protein]
CONTIG137	1189430_f3_4	68	5730	360	120	100	1.5(10)-5	Escherichia coli	b1112	[pn:hypothetical protein]
CONTIG137	14743832_c3_6	69	5731	216	72	228	4.0(10)-19	Escherichia coli	b2106	[pn:hypothetical protein]
CONTIG138	25392331_f1_1	70	5732	312	104	378	5.2(10)-35 %	Escherichia coli	b1852	[pn:glucose 6-phosphate 1 dehydrogenase] [gn:zwf]
CONTIG138	16695877_f3_6	71	5733	885	295	1346	1.3(10)-137	Escherichia coli	b1851	[pn:phosphogluconate dehydratase] [gn:edd]
CONTIG139	32314061_f2_4	72	5734	387	129	130	1.0(10)-8	Escherichia coli	b1569	[pn:repressor protein of division inhibition gene dicb] [gn:dicc]
CONTIG139	14470637_c2_8	73	5735	423	141	401	1.8(10)-37	Escherichia coli	b1570	[pn:repressor protein of division inhibition gene dicb] [gn:dica]
CONTIG140	35949137_f3_4	74	5736	1260	420	211	1.5(10)-14	Pseudomonas putida	S27611	agglutination protein - pseudomonas putida
CONTIG142	35835092_f1_1	75	5737	1197	399	1652	5.2(10)-170	Escherichia coli	b3544	[pn:periplasmic dipeptide transport protein precursor] [gn:dppa]
CONTIG144	16054202_f1_4	76	5738	336	112	528	6.7(10)-51	Escherichia coli	b1827	[pn:hypothetical protein]
CONTIG144	10314637_c2_10	77	5739	987	329	1049	4.0(10)-106	Escherichia coli	b1828	[pn:hypothetical protein]
CONTIG145	33239137_f2_2	78	5740	711	237	1012	3.3(10)-102	Escherichia coli	b0571	[pn:hypothetical protein] [gn:ylea]
CONTIG145	11117780_f3_4	79	5741	342	114	242	6.0(10)-20	Escherichia coli	b0570	[pn:hypothetical protein] [gn:ybcz]
CONTIG145	35569027_c3_10	80	5742	603	201	287	4.5(10)-25	Escherichia coli	b0572	[pn:hypothetical protein] [gn:yldb]
CONTIG146	3906875_f3_4	81	5743	1296	432	1799	1.3(10)-185	Escherichia coli	b3702	[pn:chromosomal replication initiator protein dnaa] [gn:dnaa]

CONTIG147	32610875_f3_3	82	5744	288	96	278	2.1(10)-24	Escherichia coli	b1916	[pn:regulatory protein] [gn:sdia]
CONTIG147	16413907_f3_5	83	5745	461	154	500	6.2(10)-48	Escherichia coli	b1914	[pn:23.9 kd protein in uvrc-sdia intergenic region] [gn:uvry]
CONTIG147	12614702_c1_7	84	5746	225	75	299	1.2(10)-26	Escherichia coli	b1915	[pn:yeef]
CONTIG148	22746011_f1_1	85	5747	366	122	199	4.9(10)-16	Escherichia coli	b1166	[pn:hypothetical protein]
CONTIG148	5250378_c2_7	86	5748	888	296	464	4.0(10)-44	Klebsiella pneumoniae	I23111	or:klebsiella pneumoniae pn:fimbrial adhesin gn:fimk le:1139 rc:2380 di:direct sr:klebsiella pneumoniae
CONTIG149	3954682_c2_4	87	5749	558	186	555	9.1(10)-54	Bacteriophage lambda	A14086	repressor protein ci - phage lambda repressor protein ci allows phage lambda to reside inactively in the chromosome of its host bacterium. this lysogenic state is maintained by binding of regulatory protein ci to the or and ol operators, preventing
CONTIG15	36406937_f1_1	88	5750	467	156	168	9.9(10)-12	Escherichia coli	b3066	[pn:dna primase] [gn:dnag]
CONTIG15	9784375_f2_2	89	5751	330	110	113	8.3(10)-6	Haemophilus influenzae	HI0532	[pn:dna primase] [gn:dnag]
CONTIG150	24485818_f1_1	90	5752	195	65	160	4.0(10)-11	Escherichia coli	b1184	[pn:umuc protein] [gn:umuc]
CONTIG150	24042892_c1_5	91	5753	258	86	104	0.00018	Methanococcus jannaschii	MJ1643	[pn:chromosome segretation protein]
CONTIG151	4485693_c1_4	92	5754	825	275	1160	7.0(10)-118	Escherichia coli	b0197	[pn:hypothetical 29.4 kd lipoprotein in rcsf-rnh intergenic region]
CONTIG152	32285024_c1_7	93	5755	931	310	1152	5.0(10)-117	Escherichia coli	A25937	arsenical pump-driving atpase (ec 3.6.1.-) - escherichia coliplasmid r773 this anion-transporting atpase catalyzes the extrusion of the oxyanions arsenite, antimonite, and arsenate, thus lowering the intracellular concentration of these toxic oxyanions.
CONTIG153	14258412_f1_1	94	5756	183	61	101	1.2(10)-5	Haemophilus influenzae	HI0598	[pn:hypothetical protein]

CONTIG153	1461540_f1_2	95	5757	945	315	633	5.0(10)-62	Escherichia coli	b0626	[pn:hypothetical protein] [gn:yhem]
CONTIG153	14850461_c2_8	96	5758	396	132	588	2.8(10)-57	Escherichia coli	b0624	[pn:hypothetical 13.8 kd protein in cspe-lipa intergenic region] [gn:ybei]
CONTIG154	24645175_c1_1	97	5759	456	152	183	2.3(10)-14	Escherichia coli	S70162	,
CONTIG155	29394584_c2_9	98	5760	839	279	1123	5.9(10)-114	Escherichia coli	b0031	[pn:dihydrodipicolinate reductase] [gn:dapb]
CONTIG155	23632260_c3_10	99	5761	390	130	567	4.9(10)-55	Escherichia coli	b0032	[pn:carbamoyl-phosphate synthase small chain] [gn:caral]
CONTIG156	1384665_f2_1	100	5762	1269	423	1956	3.2(10)-202	Escherichia coli	b4260	[pn:aminopeptidase a/1] [gn:pepa]
CONTIG157	16303956_f2_2	101	5763	2103	701	2013	2.8(10)-208	Escherichia coli	b1102	[pn:outer-membrane receptor for fe] [gn:fhue]
CONTIG158	10563465_f3_3	102	5764	492	164	102	9.3(10)-6	Escherichia coli	b2861	[pn:insertion element is2 hypothetical 13.4 kd protein]
CONTIG159	12991252_f1_1	103	5765	726	242	313	4.0(10)-28	Escherichia coli	b0752	[pn:hypothetical protein] [gn:ybgr]
CONTIG159	23938415_f3_4	104	5766	390	130	102	9.3(10)-6	Bacillus subtilis	yozA	[pn:hypothetical protein]
CONTIG159	24660337_c3_8	105	5767	285	95	375	1.1(10)-34	Escherichia coli	b1994	[pn:insertion element is5 hypothetical 39.3 kd protein]
CONTIG16	4019806_c2_5	106	5768	435	145	108	2.1(10)-6	Escherichia coli	b1219	[pn:hypothetical 12.7 kd protein in chac-narl intergenic region] [gn:ychn]
CONTIG160	23728327_f1_1	107	5769	510	170	244	8.3(10)-21	Bacillus subtilis	gleR	[pn:transcriptional regulator] [gn:ywpi]
CONTIG160	35253527_f2_3	108	5770	1143	381	824	2.8(10)-82	Escherichia coli	b1624	[pn:hypothetical protein]
CONTIG161	12694182_c1_9	109	5771	762	254	426	4.2(10)-40	Escherichia coli	b0897	[pn:hypothetical 23.1 kd protein in dm5c 3'''region] [gn:ycacl]
CONTIG161	26616641_c3_11	110	5772	582	194	222	1.8(10)-18	Homo sapiens	Y07867	or:homo sapiens pn:pirin le:205 re:1077 di:direct sr:human
CONTIG162	7282255_f1_1	111	5773	372	124	450	1.2(10)-42	Escherichia coli	b0946	[pn:hypothetical protein]
CONTIG162	21741657_c2_12	112	5774	972	324	1313	4.4(10)-134	Escherichia coli	b0947	[pn:hypothetical protein]
CONTIG163	22949037_c1_12	113	5775	792	264	1273	7.5(10)-130	Escherichia coli	b2568	[pn:signal peptidase i] [gn:lepb]

CONTIG163	31880432_c1_13	114	5776	531	177	776	3.5(10)-77	Escherichia coli	b2566	[pn:gtp-binding protein] [gn:era]
CONTIG163	12203387_c2_15	115	5777	801	267	1059	3.6(10)-107	Escherichia coli	b2567	[pn:ribonuclease iii] [gn:rnac]
CONTIG165	20508557_fl_1	116	5778	1307	436	1915	7.0(10)-198	Escherichia coli	b4208	[pn:d-serine/d-alanine/glycine transporter] [gn:cycA]
CONTIG165	26386588_f2_2	117	5779	636	212	821	6.0(10)-82	Escherichia coli	b4207	[pn:probable fbp-type 22 kd peptidyl-prolyl cis- trans isomerase]
CONTIG167	31367263_fl_2	118	5780	1200	400	452	7.5(10)-43	Escherichia coli	AF005044	[PN:TraU] [GN:traU] [DE:Escherichia coli plasmid R100-1 TraV (traV), TraR (traR), OrfG1(orfG1), OrfI1 (orfH), OrfI (orfI), TraC (traC), TrbI (trbI), TraW(traW), TraU (traU), TrbC (trbC), 1 raN (traN), TrbE (trbE) and TraF(traF) genes, c
CONTIG168	34615936_c1_7	119	5781	879	293	1005	1.8(10)-101	Escherichia coli	b4174	[pn:hflk protein] [gn:hflk]
CONTIG168	26601532_c2_8	120	5782	333	111	516	1.2(10)-49	Escherichia coli	b4173	[pn:gtp-binding protein hflx] [gn:hflx]
CONTIG169	21657693_fl_2	121	5783	597	199	707	7.2(10)-70	Escherichia coli	b3639	[pn:dfp protein] [gn:dfp]
CONTIG169	32246000_f2_5	122	5784	204	68	151	4.0(10)-10	Escherichia coli	b3639	[pn:dfp protein] [gn:dfp]
CONTIG169	5953150_c3_14	123	5785	852	284	801	7.7(10)-80	Escherichia coli	b3638	[pn:dna repair protein radc] [gn:radc]
CONTIG170	1204702_fl_1	124	5786	336	112	523	2.2(10)-50	Escherichia coli	b0969	[pn:hypothetical protein in held-sert intergenic region] [gn:yccck]
CONTIG170	31462776_f2_4	125	5787	663	221	634	3.8(10)-62	Escherichia coli	b0970	[pn:hypothetical 23.4 kd protein in sert 5'''region] [gn:ycca]
CONTIG170	1210765_c2_13	126	5788	282	94	307	1.7(10)-27	Escherichia coli	b0968	[pn:hypothetical protein]
CONTIG170	32428439_c3_17	127	5789	1152	384	965	3.2(10)-97	Escherichia coli	b1243	[pn:periplasmic oligopeptide-binding protein precursor] [gn:oppa]
CONTIG171	11737962_f3_4	128	5790	948	316	104	0.01	Streptococcus phage phi7201	U89246	[de:streptococcus phage phi7201 orfX and orfY unknown protein genes,partial cds] [pn:unknown] [nt:orfY]

CONTIG173	26742882_f2_2	129	5791	555	185	144	1.5(10)-9	Pseudomonas sp.	P18896	increased glyphosate resistance protein.
CONTIG173	4164015_c3_8	130	5792	1047	349	1016	1.3(10)-102	Escherichia coli	b3001	[pn:hypothetical protein]
CONTIG174	5270268_f1_1	131	5793	1392	464	1809	1.2(10)-186	Escherichia coli	b0436	[pn:trigger factor] [gn:tig]
CONTIG175	22050143_f1_1	132	5794	1092	364	463	5.2(10)-44	Escherichia coli	b4287	[pn:ironiii dicitrate transport atp-binding protein fece] [gn:fece]
CONTIG175	4579201_f2_2	133	5795	558	186	304	3.6(10)-27	Bacillus subtilis	yvrB	[pn:hypothetical protein]
CONTIG175	35567462_c2_12	134	5796	402	134	324	8.5(10)-29	Escherichia coli	b1243	[pn:periplasmic oligopeptide-binding protein precursor] [gn:oppa]
CONTIG176	25938376_f2_2	135	5797	576	192	659	8.8(10)-65	Escherichia coli	b0199	[pn:abc] [gn:abc]
CONTIG176	23473562_f2_3	136	5798	483	161	767	3.1(10)-76	Escherichia coli	b0199	[pn:abc] [gn:abc]
CONTIG176	7270092_f3_8	137	5799	614	205	777	2.7(10)-77	Escherichia coli	b0198	[pn:hypothetical abc transporter permease protein yaee] [gn:yaec]
CONTIG176	29453308_c2_12	138	5800	630	210	892	1.8(10)-89	Escherichia coli	b0200	[pn:hypothetical 21.3 kd protein in abc-rrsh intergenic region] [gn:yaed]
CONTIG177	24848941_f2_2	139	5801	525	175	573	3.8(10)-55	Escherichia coli	b2216	[pn:probable sensor protein yojn] [gn:yojn]
CONTIG178	24253325_f1_1	140	5802	429	143	141	6.7(10)-10	Escherichia coli	b3097	[pn:hypothetical 14.5 kd protein in exur-tdec intergenic region]
CONTIG180	13066567_f1_1	141	5803	654	218	509	6.9(10)-49	Escherichia coli	b4121	[pn:hypothetical 23.4 kd protein in melb-fumb intergenic region] [gn:yjdf]
CONTIG180	30672151_f3_4	142	5804	189	63	270	1.5(10)-23	Escherichia coli	b4121	[pn:hypothetical 23.4 kd protein in melb-fumb intergenic region] [gn:yjdf]
CONTIG182	11814452_f1_1	143	5805	369	123	397	5.0(10)-37	Escherichia coli	b4372	[pn:dna polymerase iii psi subunit] [gn:hold]
CONTIG182	21991462_f2_3	144	5806	492	164	521	3.7(10)-50	Escherichia coli	b4373	[pn:ribosomal-protein-alanine acetyltransferase] [gn:rimi]
CONTIG182	5086063_f2_4	145	5807	351	117	461	8.4(10)-44	Escherichia coli	b4375	[pn:peptide-chain-release factor 3] [gn:prfc]
CONTIG182	34491258_f3_6	146	5808	786	262	999	8.1(10)-101	Escherichia coli	b4374	[pn:hypothetical 22.2 kd protein in rimi-prfc intergenic region] [gn:yjig]

CONTIG184	25969562_c1_6	147	5809	696	232	1038	6.0(10)-105	Escherichia coli	b3346	[pn:hypothetical protein] [gn:ytheo]
CONTIG184	4897691_c2_7	148	5810	684	228	837	1.2(10)-83	Escherichia coli	b3347	[pn:fkbp-type peptidyl-prolyl cis-trans isomerase] [gn:fkpa]
CONTIG185	30566284_c1_4	149	5811	1331	443	690	4.5(10)-68	Escherichia coli	b0544	[pn:hypothetical protein] [gn:ybok]
CONTIG186	4416343_f1_3	150	5812	669	223	1018	7.9(10)-103	Escherichia coli	b1180	[pn:hypothetical protein]
CONTIG186	2625761_f2_6	151	5813	402	134	443	6.7(10)-42	Escherichia coli	b1179	[pn:hypothetical protein]
CONTIG186	9805436_c1_12	152	5814	726	242	1038	6.0(10)-105	Escherichia coli	b1175	[pn:cell division inhibitor mind] [gn:mind]
CONTIG186	15681716_c3_17	153	5815	807	269	908	3.6(10)-91	Escherichia coli	b1176	[pn:cell division inhibitor minc] [gn:minc]
CONTIG187	962900_f3_2	154	5816	1848	616	1429	2.2(10)-146	Escherichia coli	b2395	[pn:yfea]
CONTIG188	676041_f2_3	155	5817	1506	502	1903	1.3(10)-196	Escherichia coli	b1603	[pn:pyridine nucleotide transhydrogenase subunit- alpha] [gn:pnta]
CONTIG189	24508336_f3_4	156	5818	579	193	573	1.1(10)-55	Escherichia coli	b1622	[pn:maly protein] [gn:maly]
CONTIG189	34569806_f3_5	157	5819	1011	337	1346	1.3(10)-137	Escherichia coli	b1623	[pn:adenosine deaminase] [gn:add]
CONTIG19	32204791_f1_1	158	5820	399	133	622	7.2(10)-61	Enterobacteria ceae	S07447	[pn:hypothetical protein, 13.1k]
CONTIG19	25522168_f2_3	159	5821	297	99	165	2.0(10)-12	Shigella flexneri	P04337	hypothetical mercuric resistance protein merc.
CONTIG19	12995781_f3_5	160	5822	339	113	114	5.0(10)-7	Shigella flexneri	P04336	mercuric transport protein.
CONTIG19	9901712_c1_6	161	5823	663	221	722	1.8(10)-71	Shigella flexneri	P07044	mercuric resistance operon regulatory protein.
CONTIG190	15651516_f1_1	162	5824	960	320	1514	2.2(10)-155	Escherichia coli	b1415	[pn:lactaldehyde dehydrogenase a] [gn:alda]
CONTIG190	12242930_f1_2	163	5825	444	148	521	3.7(10)-50	Escherichia coli	b1418	[gn:cybb]
CONTIG190	35662765_f2_5	164	5826	204	68	138	1.3(10)-9	Escherichia coli	b1418	[gn:cybb]
CONTIG190	35348277_c1_11	165	5827	345	115	111	1.3(10)-6	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr le:<1 re:588 di:direct

CONTIG190	16095807_c2_13	166	5828	390	130	135	2.8(10)-9	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:car le:59 re:580 di:direct nt:orf2
CONTIG191	25508265_c2_11	167	5829	735	245	920	1.8(10)-92	Escherichia coli	b1913	[pn:excinuclease abc subunit c] [gn:uvrc]
CONTIG191	6760811_c2_13	168	5830	240	80	316	1.8(10)-28	Escherichia coli	b1912	[pn:phosphotidylglycerophosphate synthetase] [gn:pgsa]
CONTIG191	30128300_c3_15	169	5831	1203	401	1726	7.5(10)-178	Escherichia coli	b1913	[pn:excinuclease abc subunit c] [gn:uvrc]
CONTIG192	29711561_c2_11	170	5832	522	174	322	4.5(10)-29	Escherichia coli	b1043	[pn:hypothetical protein] [gn:csgc]
CONTIG192	35548807_c3_12	171	5833	561	187	589	2.2(10)-57	Escherichia coli	b1041	[pn:nucleation component of curlin monomers] [gn:csgb]
CONTIG192	30331555_c3_13	172	5834	477	159	507	1.1(10)-48	Escherichia coli	b1042	[pn:major curlin subunit precursor] [gn:csga]
CONTIG193	3939087_f1_1	173	5835	891	297	1376	9.1(10)-141	Escherichia coli	b1829	[pn:heat shock protein htpx] [gn:htpx]
CONTIG193	33848575_f2_2	174	5836	1608	536	2343	3.1(10)-243	Escherichia coli	b1830	[pn:tail-specific protease precursor] [gn:prc]
CONTIG194	16019651_f1_2	175	5837	926	309	1434	6.5(10)-147	Escherichia coli	b1370	[pn:insertion element is5 hypothetical protein] [gn:yi52_5]
CONTIG194	30157255_f3_6	176	5838	279	93	94	0.00042	Escherichia coli	U95365	transposase, is5b,
CONTIG194	21775383_c1_8	177	5839	300	100	447	2.6(10)-42	Escherichia coli	D90774	or:escherichia coli gn:is5 le:13994 re:14362 di:direct sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:orf_id:o263#20; similar to [swissprot accession [pn:hypothetical protein]
CONTIG194	22458580_c1_9	178	5840	348	116	484	3.1(10)-46	Escherichia coli	b1371	[pn:hypothetical protein]
CONTIG195	16500153_c1_7	179	5841	1560	520	1825	2.3(10)-188	Escherichia coli	b2216	[pn:probable sensor protein yojn] [gn:yojn]
CONTIG196	34647280_f2_4	180	5842	414	138	558	4.4(10)-54	Escherichia coli	b4200	[pn:30s ribosomal subunit protein s6] [gn:rpstf]
CONTIG196	14884500_f2_5	181	5843	216	72	345	1.6(10)-31	Escherichia coli	b4201	[pn:primosomal replication protein n] [gn:prib]
CONTIG196	10632182_c1_8	182	5844	399	133	307	1.7(10)-27	Escherichia coli	b4199	[pn:hypothetical 10.1 kd protein in auid-rpsf intergenic region] [gn:yifv]
CONTIG197	1308262_f2_2	183	5845	564	188	655	2.2(10)-64	Escherichia coli	b3856	[pn:hypothetical protein]

CONTIG198	23687750_c1_6	184	5846	729	243	757	3.6(10)-75	Escherichia coli	b0629	[pn:hypothetical transcriptional regulator in lipa- lipb intergenic region] [gn:ybef]
CONTIG198	3242252_c1_7	185	5847	1011	337	1650	8.5(10)-170	Escherichia coli	b0628	[pn:lipic acid synthetase] [gn:lipa]
CONTIG199	29723842_c1_10	186	5848	561	187	102	0.0028	Haemophilus influenzae	HI0015	[pn:signal peptidase i] [gn:lepb]
CONTIG199	54140_c2_11	187	5849	813	271	93	0.027	Escherichia coli	AF005044	[PN:TrbC] [GN:trbC] [DE:Escherichia coli plasmid R100-1 TraV (traV), TraR (traR), OrfG1(orfG1), OrfH (orfH), OrfI (orfI), TraC (traC), TrbI (trbI), TraW(traW), TraU (traU), TrbC (trbC), TraN (traN), TrbE (trbE) and TraF(traF) genes, c
CONTIG199	32032827_c3_12	188	5850	741	247	93	0.20999	Vibrio cholerae	Y00557	[PN:protease] [GN:prtV] [DE:Vibrio cholerae DNA for hlyA, hlyB, lipA, lipB and prtV genes.] [LE:7537] [RE:10296] [DI:complement]
CONTIG2	16218928_c2_6	189	5851	417	139	129	1.3(10)-8	Escherichia coli	b1228	[pn:hypothetical protein]
CONTIG2	829150_c3_7	190	5852	336	112	115	3.8(10)-7	Escherichia coli	b1228	[pn:hypothetical protein]
CONTIG20	16620400_c2_3	191	5853	519	173	153	1.2(10)-10	Escherichia coli	b3816	[pn:magnesium and cobalt transport protein cora] [gn:cora]
CONTIG200	31875006_f1_1	192	5854	810	270	966	2.6(10)-97	Escherichia coli	b0761	[pn:molybdenum transport protein mode] [gn:mode]
CONTIG200	10634661_f2_2	193	5855	1164	388	1413	1.1(10)-144	Escherichia coli	b0760	[pn:putative molybdenum transport atp-binding protein modf] [gn:modf]
CONTIG201	5198443_c3_13	194	5856	792	264	490	7.0(10)-47	Bacillus subtilis	ymaE	[pn:hypothetical protein]
CONTIG202	4394533_c3_5	195	5857	831	277	993	3.5(10)-100	Escherichia coli	b0732	[pn:ybgg] [gn:ybgg]
CONTIG203	2375193_c1_4	196	5858	204	68	102	8.9(10)-5	Methanobacterium thermoautotrophicum	MTH104	[pn:multidrug transporter homolog]

CONTIG203	5164657_c1_5	197	5859	741	247	921	1.5(10)-92	Methanobacterium thermoautotrophicum	MTH104	[pn:multidrug transporter homolog]
CONTIG204	1962750_c1_5	198	5860	750	250	962	6.7(10)-97	Escherichia coli	b2055	[pn:hypothetical protein] [gn:wcae]
CONTIG204	4739068_c2_9	199	5861	351	117	558	4.4(10)-54	Escherichia coli	b2054	[pn:hypothetical protein] [gn:wcae]
CONTIG204	159627_c3_10	200	5862	228	76	355	1.3(10)-32	Escherichia coli	b2056	[pn:hypothetical protein] [gn:wcae]
CONTIG205	26694807_c1_5	201	5863	372	124	594	6.7(10)-58	Yersinia pestis	AF053945	[de:yersinia pestis plasmid ppcpl, complete plasmid sequence.]
CONTIG206	21683457_f1_1	202	5864	2127	709	3388	0	Escherichia coli	b3340	[pn:fusa] [gn:fusa]
CONTIG206	1069655_f1_2	203	5865	378	126	406	5.7(10)-38	Escherichia coli	b3339	[pn:elongation factor tu] [gn:tufa]
CONTIG206	510290_c1_4	204	5866	705	235	390	4.0(10)-36	Eikenella corrodens	P35649	hypothetical 66.3 kd protein in hag2 5'region.
CONTIG206	394215_c1_5	205	5867	1113	371	575	7.0(10)-56	Eikenella corrodens	P35649	hypothetical 66.3 kd protein in hag2 5'region.
CONTIG206	22352280_c2_10	206	5868	189	63	105	5.7(10)-5	Eikenella corrodens	P35649	hypothetical 66.3 kd protein in hag2 5'region.
CONTIG207	2376381_f1_4	207	5869	825	275	274	1.8(10)-33	Escherichia coli	b2106	[pn:hypothetical protein]
CONTIG207	21484653_f3_8	208	5870	447	149	168	9.4(10)-13	Escherichia coli	D90774	or:escherichia coli gn:is5 le:13994 re:14362 di:direct sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:orf_id:o263#20; similar to [swissprot accession]
CONTIG207	34410768_c2_13	209	5871	987	329	1308	1.5(10)-133	Escherichia coli	b1994	[pn:insertion element is5 hypothetical 39.3 kd protein]
CONTIG209	16506441_f1_1	210	5872	1032	344	1346	1.3(10)-137	Escherichia coli	b4175	[pn:hflc protein] [gn:hflc]
CONTIG209	25839843_f2_2	211	5873	504	168	450	1.2(10)-42	Escherichia coli	b4174	[pn:hflk protein] [gn:hflk]
CONTIG21	32445803_f2_1	212	5874	909	303	1213	1.7(10)-123	Escherichia coli	P03008	transposase for transposon tn3.

CONTIG210	34188287_f2_4	213	5875	2229	743	1836	1.7(10)-189	Pseudomonas aeruginosa	X9514	or:pseudomonas aeruginosa gn:mexf le:1439 re:4627 di:direct
CONTIG210	4867075_f2_5	214	5876	279	93	92	0.00011	Saccharomyces cerevisiae	YNL259C	[pn:antioxidant protein and metal homeostasis factor] [gn:atx1]
CONTIG211	5944581_c2_13	215	5877	1152	384	545	1.1(10)-52	Escherichia coli	AF044506	[de:escherichia coli strain ec50 hep gene, partial cds; rhsg accessorygenetic element vrg protein gene, complete cds; and core proteingene, partial cds.] [pn:vgrg protein]
CONTIG211	36147260_c2_14	216	5878	1092	364	100	0.12	Mycobacterium tuberculosis	AL021246	[de:mycobacterium tuberculosis sequence v008.] [pn:pgrs-family] [gn mtv008 46c] [nt mtv008.46c, member of the m. tuberculosis]
CONTIG212	13880212_f2_2	217	5879	390	130	462	6 5(10)-44	Escherichia coli	b3501	[pn:arsenical resistance operon arsefg repressor] [gn:arsf]
CONTIG212	16600136_f2_3	218	5880	393	131	463	5 2(10)-44	Escherichia coli	A25937	arsenical pump-driving atpase (cc 3 6.1.-) - escherichia coli plasmid r773 this anion-transporting atpase catalyzes the extrusion of the oxyanions arsenite, animonite, and arsenate, thus lowering the intracellular concentration of these toxic oxyanions.
CONTIG212	31284383_c2_8	219	5881	333	111	494	2 7(10)-47	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn:tnpa gn:tnpa le:10303 re:11307 di:complement
CONTIG213	4494000_f1_1	220	5882	954	318	90	0.23	Drosophila melanogaster	M19537	or:drosophila melanogaster gn:rp1215 le:join(<1 re:133,379 di:direct sr.d.melanogaster dna, clone p4.1 nt:description: ma polymerase ii 215kd subunit; ma

CONTIG213	24478907_f1_2	221	5883	1770	590	150	2.5(10)-15	Escherichia coli	AF005044	[PN:TraC] [GN:traC] [DE:Escherichia coli plasmid R100-1 TraV (traV), TraR (traR), OrfG1(orfG1), OrfH (orfH), OrfI (orfI), TraC (traC), TrbI (trbI), TraW(traW), FraU (traU), TrbC (trbC), TraN (traN), TrbE (trbE) and TraF(traF) genes, c
CONTIG214	22770005_f3_5	222	5884	1548	516	2262	1.2(10)-234	Escherichia coli	b2149	[pn:galactoside transport atp-binding protein mglA] [gn:mglA]
CONTIG214	3417013_f3_6	223	5885	1026	342	1311	7.0(10)-134	Escherichia coli	b2148	[pn:galactoside transport system permease protein mglC] [gn:mglC]
CONTIG215	5078300_f3_6	224	5886	876	292	1456	3 (10)-149	Escherichia coli	b4192	[pn:hypothetical 40.3 kd protein in aidb-rpsf intergenic region] [gn:yjfr]
CONTIG215	22367036_c1_8	225	5887	804	268	1175	1.8(10)-119	Escherichia coli	b4193	[pn:hypothetical 52.9 kd protein in aidb-rpsf intergenic region] [gn:yjfs]
CONTIG216	10411407_f1_3	226	5888	388	130	195	1.3(10)-15	Rhizobium sp.	S34667	hypothetical protein 140 - rhizobium sp.
CONTIG216	10563465_f2_6	227	5889	420	140	102	9.3(10)-6	Escherichia coli	b2861	[pn:insertion element is2 hypothetical 13.4 kd protein]
CONTIG216	6383505_c3_17	228	5890	633	211	232	1.6(10)-19	Bacillus subtilis	soj	[pn:hypothetical protein]
CONTIG217	4301907_f1_1	229	5891	1212	404	1634	4.2(10)-168	Escherichia coli	b2393	[pn:nucleoside permease nupC] [gn:nupC]
CONTIG217	4900012_c1_11	230	5892	651	217	505	4.5(10)-48	Escherichia coli	b2395	[pn:yfea]
CONTIG218	21697135_f2_2	231	5893	873	291	1293	5.7(10)-132	Escherichia coli	b4396	[pn:right origin-binding protein] [gn:rob]
CONTIG22	34587776_c1_4	232	5894	201	67	315	2.5(10)-28	Escherichia coli	b3232	[pn:hypothetical 43.1 kd protein in rplm-rhoa intergenic region] [gn:yhcm]
CONTIG220	13775768_f2_1	233	5895	432	144	675	1.8(10)-66	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn.tnpa gn:tnpa le:10303 re:11307 di:complement
CONTIG220	1977312_c1_7	234	5896	882	294	91	0.031	Bacillus subtilis	ydcM	[pn:hypothetical protein]
CONTIG221	23609515_f1_1	235	5897	294	98	419	2.3(10)-39	Enterobacter agglomerans	A38965	hypothetical protein a (insertion sequence is1222) -enterobacter agglomerans

CONTIG221	9896067_f3_4	236	5898	185	62	185	1.5(10)-14	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG221	190787_c1_6	237	5899	513	171	143	4.2(10)-10	Rhizobium sp.	P55623	hypothetical 18.8 kd protein y4qb,
CONTIG222	29744052_f3_7	238	5900	1122	374	165	6.0(10)-10	Methanococcus jannaschii	MJ1187	[pn:dinitrogenase reductase activating glycohydrolase] [gn:drag]
CONTIG223	34486000_f1_1	239	5901	249	83	341	4.4(10)-31	Escherichia coli	b2833	[pn:hypothetical protein]
CONTIG223	12699062_f1_2	240	5902	459	153	704	1.5(10)-69	Escherichia coli	b2834	[pn:hypothetical protein]
CONTIG223	15898537_f1_3	241	5903	324	108	320	7.2(10)-29	Escherichia coli	b2834	[pn:hypothetical protein]
CONTIG223	10425262_f2_5	242	5904	729	243	954	4.7(10)-96	Escherichia coli	b2831	[pn:muth] [gn:muth]
CONTIG223	24720916_f2_8	243	5905	375	125	504	2.2(10)-48	Escherichia coli	b2834	[pn:hypothetical protein]
CONTIG223	32550407_c3_17	244	5906	354	118	393	1.3(10)-36	Escherichia coli	b2835	[pn:hypothetical protein in muth-aas intergenic region] [gn:yged]
CONTIG224	35447642_c1_15	245	5907	915	305	1424	7.5(10)-146	Escherichia coli	S70160	,
CONTIG224	4110291_c1_16	246	5908	420	140	639	1.2(10)-62	Escherichia coli	S70161	,
CONTIG224	3907697_c2_17	247	5909	1473	491	2437	3.3(10)-253	Escherichia coli	S70159	,
CONTIG224	3939017_c2_20	248	5910	273	91	434	6.0(10)-41	Escherichia coli	S70163	,
CONTIG225	24301557_f1_2	249	5911	1362	454	1668	1.0(10)-171	Escherichia coli	b3502	[pn:arsenical pump membrane protein] [gn:arsb]
CONTIG225	4110263_f1_3	250	5912	279	93	416	4.9(10)-39	Escherichia coli	b3503	[pn:arsenate reductase] [gn:arsc]
CONTIG225	36135812_f3_6	251	5913	336	112	431	1.3(10)-40	Escherichia coli	A25937	arsenical pump-driving atpase (cc 3.6.1.-) - escherichia coli plasmid r773 this anion-transporting atpase catalyzes the extrusion of the oxyanions arsenite, antimonite, and arsenate, thus lowering the intracellular concentration of these toxic oxyanions

CONTIG225	15661513_c1_10	252	5914	639	213	359	1.1(10)-32	Rhizobium sp.	P50360	hypothetical 29.3 kd protein in region 2 of sym plasmid (no1265).
CONTIG226	22760817_f1_1	253	5915	426	142	472	5.7(10)-45	Escherichia coli	b4206	[pn:hypothetical protein] [gn:ytfb]
CONTIG226	7220463_c1_13	254	5916	462	154	536	9.5(10)-52	Escherichia coli	b4203	[pn:50s ribosomal subunit protein 19] [gn:rplj]
CONTIG226	15056377_c2_16	255	5917	246	82	385	9.5(10)-36	Escherichia coli	b4202	[pn:30s ribosomal subunit protein s18] [gn:rpsr]
CONTIG226	38537_c3_22	256	5918	957	319	151	9.0(10)-9	Escherichia coli	b1533	[pn:hypothetical 28.7 kd protein in marb-dcp intergenic region] [gn:yded]
CONTIG227	3382959_c2_10	257	5919	287	95	231	2.0(10)-19	Escherichia coli	b1099	[pn:dna polymerase iii, delta''' subunit] [gn:holb]
CONTIG227	19800956_c3_11	258	5920	873	291	1259	2.2(10)-128	Escherichia coli	b1100	[pn:hypothetical protein in holb-ptsg intergenic region] [gn:yeth]
CONTIG227	24010937_c3_12	259	5921	1467	489	2174	2.5(10)-225	Escherichia coli	b1101	[pn:pts system, glucose-specific ilbc component] [gn:ptsg]
CONTIG228	15814663_c2_11	260	5922	531	177	144	9.0(10)-10	Methanobacterium thermoautotrophicum	MTH806	[pn:protease iv]
CONTIG228	26598393_c3_13	261	5923	738	246	95	0.024	Methanobacterium thermoautotrophicum	MTH466	[pn:unknown]
CONTIG229	12927341_f2_3	262	5924	825	275	1127	2.2(10)-114	Escherichia coli	b2741	[pn:rna polymerase sigma subunit rpos] [gn:rpos]
CONTIG229	15673942_f3_4	263	5925	1095	365	1130	1.1(10)-114	Escherichia coli	b2742	[pn:lipoprotein nlpd precursor] [gn:nlpd]
CONTIG23	24634555_c1_3	264	5926	390	130	100	1.5(10)-5	Escherichia coli	b4283	[pn:insertion element is911 hypothetical 11.6 kd protein] [gn:y191]
CONTIG230	9860003_f2_4	265	5927	1815	605	277	3.3(10)-21	Bacteriophage T7	P03692	dna primase, chains a and b (cc 2.7 7.-).
CONTIG230	32505283_f3_6	266	5928	1029	343	272	2.2(10)-23	Escherichia coli	b1149	[pn hypothetical protein]
CONTIG231	11963255_f2_3	267	5929	546	182	382	2.0(10)-35	Escherichia coli	b0633	[pn:rare lipoprotein a precursor] [gn:rlpa]

CONTIG231	12363162_f2_5	268	5930	318	106	371	2.8(10)-34	Escherichia coli	b0631	[pn:hypothetical 9.8 kd protein in lipb-daca intergenic region]
CONTIG231	15723956_f3_6	269	5931	270	90	204	3.7(10)-16	Escherichia coli	b0633	[pn:rare lipoprotein a precursor] [gn:rlpa]
CONTIG231	25563161_f3_7	270	5932	1305	435	1920	2.1(10)-198	Escherichia coli	b0632	[pn:d-alanine carboxypeptidase] [gn:daca]
CONTIG231	32516510_f3_9	271	5933	687	229	858	7.2(10)-86	Escherichia coli	b0630	[pn:lipoate-protein ligase b] [gn:lipb]
CONTIG232	25839831_f1_1	272	5934	1161	387	1782	8.6(10)-184	Escherichia coli	b0677	[pn:n-acetylglucosamine-6-phosphate deacetylase] [gn:naga]
CONTIG232	3009677_f3_5	273	5935	804	268	1338	9.8(10)-137	Escherichia coli	b0678	[pn:glucosamine-6-phosphate isomerase] [gn:nagb]
CONTIG232	34174053_f3_7	274	5936	1197	399	1782	8.6(10)-184	Escherichia coli	b0676	[pn:n-acetylglucosamine repressor] [gn:nagc]
CONTIG233	26445952_c1_13	275	5937	345	115	285	3.7(10)-25	Escherichia coli	b0551	[pn:hypothetical protein] [gn:ybcq]
CONTIG233	36366038_c3_18	276	5938	636	212	159	8.4(10)-12	Escherichia coli	b0798	[pn:hypothetical 18.7 kd protein in rhle-ding/rarb intergenic region] [gn:ybia]
CONTIG236	4166305_c1_17	277	5939	651	217	174	2.2(10)-13	Escherichia coli	b2846	[pn:hypothetical protein]
CONTIG236	5353400_c3_22	278	5940	2436	812	3750	0	Escherichia coli	b0221	[pn:hypothetical protein]
CONTIG236	4191068_c3_23	279	5941	789	263	1171	4.9(10)-119	Escherichia coli	b0219	[pn:hypothetical protein] [gn:yafv]
CONTIG237	21517313_f1_1	280	5942	498	166	483	3.8(10)-46	Escherichia coli	b4365	[pn:hypothetical 27.0 kd protein in dnat-hold intergenic region]
CONTIG237	24705188_f2_10	281	5943	1149	383	478	1.3(10)-45	Bacillus subtilis	lieC	[pn:phosphotransferase system] [gn:celb]
CONTIG237	30557000_f2_11	282	5944	213	71	93	0.00079	Borrelia burgdorferi	AE000792	[dc:borrelia burgdorferi plasmid cp26, complete plasmid sequence.] [pn:pts system, cellobiose-specific iic component] [gn:bbb04] [int:similar to gb]
CONTIG237	24431568_f3_14	283	5945	690	230	494	2.7(10)-47	Escherichia coli	b4366	[pn:hypothetical 25.6 kd protein in dnat-hold intergenic region] [gn:yjir]
CONTIG237	14237692_c1_17	284	5946	801	267	964	4.2(10)-97	Escherichia coli	b4367	[pn:hypothetical 30.1 kd protein in dnat-hold intergenic region] [gn:yjis]

CONTIG237	22765961_c1_20	285	5947	492	164	335	1.8(10)-30	Bacillus subtilis	ywhH	[pn:hypothetical protein]
CONTIG238	2382277_f3_9	286	5948	1005	335	1289	1.5(10)-131	Escherichia coli	b3862	[pn:hypothetical 36.3 kd protein in pola 5''' region] [gn:yihg]
CONTIG238	21488165_f3_12	287	5949	555	185	552	1.8(10)-53	Escherichia coli	b3857	[pn:molybdopterin-guanine dinucleotide biosynthesis protein a] [gn:moba]
CONTIG238	2034766_c1_13	288	5950	300	100	442	8.6(10)-42	Escherichia coli	b3858	[pn:hypothetical 10.3 kd protein in moba 3''' region] [gn:yihd]
CONTIG238	25603875_c1_14	289	5951	1002	334	1428	2.7(10)-146	Escherichia coli	b3859	[pn:hypothetical 38.1 kd protein in dsba 5''' region] [gn:yihe]
CONTIG238	12614200_c1_15	290	5952	651	217	867	8.0(10)-87	Escherichia coli	b3860	[pn:dsba] [gn:dsba]
CONTIG239	13063513_f1_3	291	5953	264	88	339	7.0(10)-31	Escherichia coli	b1203	[pn:hypothetical gtp-binding protein in pth 3''' region] [gn:yehf]
CONTIG239	4948290_f1_6	292	5954	249	83	154	1.3(10)-10	Escherichia coli	b1203	[pn:hypothetical gtp-binding protein in pth 3''' region] [gn:yehf]
CONTIG239	4948291_f2_7	293	5955	306	102	186	3.7(10)-14	Escherichia coli	b1203	[pn:hypothetical gtp-binding protein in pth 3''' region] [gn:yehf]
CONTIG239	3395628_c1_19	294	5956	1332	444	253	2.2(10)-28	Escherichia coli	b0703	[pn:hypothetical protein]
CONTIG239	5273307_c2_22	295	5957	804	268	126	6.4(10)-8	coliphage T4	P13309	hypothetical 17.5 kd protein in tk-vs intergenic region.
CONTIG240	26753130_c1_15	296	5958	204	68	298	1.6(10)-26	Escherichia coli	b2696	[pn:csra] [gn:csra]
CONTIG240	35554527_c2_16	297	5959	267	89	218	8.1(10)-17	Escherichia coli	b2697	[pn:alanyl-trna synthetase] [gn:alas]
CONTIG240	36611683_c3_17	298	5960	2121	707	2566	7.2(10)-267	Escherichia coli	b2697	[pn:alanyl-trna synthetase] [gn:alas]
CONTIG241	3224078_f1_2	299	5961	897	299	135	8.0(10)-9	Escherichia coli	b2358	[pn:hypothetical protein] [gn:yfdo]
CONTIG241	6367327_f1_3	300	5962	657	219	157	1.3(10)-11	Escherichia coli	b1361	[pn:hypothetical protein]
CONTIG241	4900300_f2_4	301	5963	417	139	350	4.9(10)-32	Escherichia coli	b1358	[pn:hypothetical protein]
CONTIG241	36207628_f2_6	302	5964	378	126	127	2.1(10)-8	Synechocystis sp.	S74697	[PN:hypothetical protein sll1193] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]

CONTIG241	35745317_c1_14	303	5965	615	205	117	0.00012	Helicobacter pylori	HP0966	[pn:conserved hypothetical protein]
CONTIG242	4491678_f2_5	304	5966	726	242	1200	4.0(10)-122	Escherichia coli	b4401	[pn:aerobic respiration control protein arca] [gn:arca]
CONTIG242	10954577_c2_15	305	5967	687	229	834	2.5(10)-83	Escherichia coli	b4403	[pn:hypothetical 25.3 kd protein in arca-thrl intergenic region] [gn:last]
CONTIG242	4098393_c3_16	306	5968	480	160	698	6.4(10)-69	Escherichia coli	b4397	[pn:crea protein] [gn:crea]
CONTIG243	245337_c1_13	307	5969	864	288	249	2.3(10)-21	Bacteriophage 186	U32222	or:bacteriophage 186 le:181 re:711 di:direct nt:orf38; similar to bacteriophage p2 i protein, probable tail fibre protein (gph).
CONTIG243	23714843_c3_20	308	5970	840	280	163	1.7(10)-9	Bacteriophage P2	P26700	
CONTIG244	16658141_f1_2	309	5971	357	119	502	3.7(10)-48	Escherichia coli	b4195	[pn:hypothetical phosphotransferase enzyme ii] [gn:ptxa]
CONTIG244	24617338_f1_3	310	5972	663	221	1063	1.3(10)-107	Escherichia coli	b4196	[pn:hypothetical 23.6 kd protein in audb-rpsf intergenic region] [gn:yjfv]
CONTIG244	4197943_f1_4	311	5973	870	290	1382	2.1(10)-141	Escherichia coli	b4197	[pn:hypothetical 32.0 kd protein in audb-rpsf intergenic region]
CONTIG244	22120707_f2_5	312	5974	654	218	897	5.2(10)-90	Escherichia coli	b4193	[pn:hypothetical 52.9 kd protein in audb-rpsf intergenic region] [gn:yjfs]
CONTIG244	5156693_f2_6	313	5975	318	106	421	1.5(10)-39	Escherichia coli	b4194	[pn:hypothetical 10.9 kd protein in audb-rpsf intergenic region] [gn:yjft]
CONTIG244	4473818_f2_7	314	5976	186	62	188	7.0(10)-15	Escherichia coli	b4195	[pn:hypothetical phosphotransferase enzyme ii] [gn:ptxa]
CONTIG244	24870965_f2_11	315	5977	570	190	706	9.1(10)-70	Escherichia coli	b4198	[pn:hypothetical protein] [gn:sgae]
CONTIG245	31377187_f2_6	316	5978	708	236	107	0.00058	Escherichia coli	b4366	[pn:hypothetical 25.6 kd protein in dnat-hold intergenic region] [gn:yjir]
CONTIG245	198377_f3_9	317	5979	762	254	107	0.0023	Escherichia coli	b0457	[pn:hypothetical protein] [gn:ylab]
CONTIG245	25583543_c2_16	318	5980	186	62	220	2.8(10)-18	Escherichia coli	b3661	[pn:lipoprotein-28 precursor] [gn:nlpa]
CONTIG245	1270761_c2_17	319	5981	555	185	750	2.0(10)-74	Escherichia coli	b3661	[pn:lipoprotein-28 precursor] [gn:nlpa]
CONTIG246	35722707_f1_4	320	5982	240	80	168	9.4(10)-13	Zea mays	S58640	hypothetical protein 137 - maize chloroplast
CONTIG246	31910000_c1_15	321	5983	237	79	351	3.7(10)-32	Escherichia coli	b3319	[pn:50s ribosomal subunit protein 14] [gn:rpld]

CONTIG246	22847717_c1_17	322	5984	819	273	1094	7.0(10)-111	Escherichia coli	b3314	[pn:30s ribosomal subunit protein s3] [gn:rpse]
CONTIG246	3213568_c1_18	323	5985	423	141	675	1.8(10)-66	Escherichia coli	b3313	[pn:50s ribosomal subunit protein l16] [gn:rplp]
CONTIG246	34627178_c2_19	324	5986	843	281	1349	6.7(10)-138	Escherichia coli	b3317	[pn:50s ribosomal subunit protein l2] [gn:rplb]
CONTIG246	5289213_c2_20	325	5987	342	114	469	1.2(10)-44	Escherichia coli	b3315	[pn:50s ribosomal subunit protein l22] [gn:rplv]
CONTIG246	25500038_c2_22	326	5988	270	90	325	2.2(10)-29	Escherichia coli	b3311	[pn:30s ribosomal subunit protein s17] [gn:rpss]
CONTIG246	35282943_c3_23	327	5989	315	105	209	4.2(10)-17	Escherichia coli	b3318	[pn:50s ribosomal subunit protein l23] [gn:rplw]
CONTIG246	32134658_c3_26	328	5990	282	94	441	1.1(10)-41	Escherichia coli	b3316	[pn:30s ribosomal subunit protein s19] [gn:rpss]
CONTIG246	6064788_c3_27	329	5991	204	68	210	3.2(10)-17	Escherichia coli	b3312	[pn:50s ribosomal subunit protein l29] [gn:rpnc]
CONTIG247	3125207_f1_1	330	5992	1308	436	1735	8.3(10)-179	Escherichia coli	b1309	[pn:hypothetical protein]
CONTIG247	20593891_f1_2	331	5993	375	125	292	3.5(10)-25	Escherichia coli	b1309	[pn:hypothetical protein]
CONTIG247	24227265_f2_9	332	5994	1326	442	1595	5.7(10)-164	Escherichia coli	b1310	[pn:hypothetical protein]
CONTIG247	15630213_f2_10	333	5995	903	301	1055	9.5(10)-107	Escherichia coli	b1311	[pn:hypothetical protein]
CONTIG247	16835032_f3_15	334	5996	645	215	917	4.0(10)-92	Escherichia coli	b1312	[pn:hypothetical protein]
CONTIG248	17003167_f1_1	335	5997	459	153	607	2.7(10)-59	Escherichia coli	b2210	[pn:hypothetical 60.2 kd protein in eco-alkb intergenic region] [gn:yojh]
CONTIG248	125915_f1_2	336	5998	372	124	221	2.2(10)-18	Escherichia coli	b1332	[pn:hypothetical protein]
CONTIG248	35650802_f1_7	337	5999	410	137	516	1.2(10)-49	Escherichia coli	b2186	[pn:hypothetical 37.8 kd protein in rply-prol intergenic region] [gn:yejk]
CONTIG248	16506555_c1_17	338	6000	1875	625	2506	1.7(10)-260	Escherichia coli	b2188	[pn:hypothetical 67.3 kd protein in rply-prol intergenic region]
CONTIG248	4976561_c2_22	339	6001	519	173	632	6.4(10)-62	Escherichia coli	b2209	[pn:tin precursor] [gn:eco]
CONTIG248	22369000_c3_24	340	6002	231	77	319	9.4(10)-29	Escherichia coli	b2187	[pn:hypothetical 8.3 kd protein in rply-prol intergenic region] [gn:yejl]

CONTIG249	25507783_f1_2	341	6003	1458	486	2340	6.5(10)-243	Escherichia coli	S70165	,
CONTIG249	35807766_f2_4	342	6004	732	244	963	5.2(10)-97	Escherichia coli	S70163	,
CONTIG249	546888_f2_5	343	6005	711	237	620	1.2(10)-60	Escherichia coli	b0571	[pn:hypothetical protein] [gn:yla]
CONTIG249	10563465_f3_9	344	6006	413	138	102	9.3(10)-6	Escherichia coli	b2861	[pn:insertion element is2 hypothetical 13.4 kd protein]
CONTIG250	12277217_c1_14	345	6007	1230	410	937	3.0(10)-94	Escherichia coli	b2349	[pn:putative prophage sf6-like integrase in argw 3'''region] [gn:yfdb]
CONTIG250	35552032_c2_15	346	6008	1227	409	1710	3.7(10)-176	Escherichia coli	b0243	[pn:gamma-glutamyl phosphate reductase] [gn:proa]
CONTIG251	34417067_c1_12	347	6009	399	133	631	8.0(10)-62	Escherichia coli	b3306	[pn:30s ribosomal subunit protein s8] [gn:rpsh]
CONTIG251	34198580_c1_13	348	6010	546	182	850	5.0(10)-85	Escherichia coli	b3305	[pn:50s ribosomal subunit protein l6] [gn:rplf]
CONTIG251	4020268_c1_14	349	6011	363	121	434	6.0(10)-41	Escherichia coli	b3304	[pn:50s ribosomal subunit protein l18] [gn:rplr]
CONTIG251	23572211_c1_18	350	6012	927	309	1047	6.7(10)-106	Escherichia coli	b3300	[pn:preprotein translocase secy subunit] [gn:secy]
CONTIG251	5267592_c3_22	351	6013	510	170	829	8.5(10)-83	Escherichia coli	b3303	[pn:30s ribosomal subunit protein s5] [gn:rpse]
CONTIG251	16832200_c3_23	352	6014	186	62	283	6.0(10)-25	Escherichia coli	b3302	[pn:50s ribosomal subunit protein l30] [gn:rpmd]
CONTIG251	259713_c3_24	353	6015	438	146	398	4.0(10)-37	Escherichia coli	b3301	[pn:50s ribosomal subunit protein l15] [gn:rplp]
CONTIG252	4698250_c1_32	354	6016	273	91	215	9.8(10)-18	Escherichia coli	b1346	[pn:hypothetical protein]
CONTIG252	11744091_c3_43	355	6017	1389	463	306	1.1(10)-24	Escherichia coli	b1350	[pn:exodeoxyribonuclease viii] [gn:rece]
CONTIG252	2845092_c3_45	356	6018	1392	464	1150	8.1(10)-117	Escherichia coli	b1345	[pn:hypothetical protein]
CONTIG253	29503136_f1_1	357	6019	522	174	338	9.0(10)-31	Escherichia coli	b3981	[pn:preprotein translocase secy subunit] [gn:sece]
CONTIG253	1035760_f2_3	358	6020	1221	407	1578	3.6(10)-162	Escherichia coli	b3339	[pn:elongation factor tu] [gn:tufa]
CONTIG253	5281893_f3_7	359	6021	555	185	927	3.5(10)-93	Escherichia coli	b3982	[pn:transcription antitermination protein nusg] [gn:nusg]

CONTIG254	3416407_f1_8	360	6022	309	103	365	1.2(10)-33	Escherichia coli	b2609	[pn:30s ribosomal subunit protein s16] [gn:rsp]
CONTIG254	7144130_f1_9	361	6023	555	185	812	5.4(10)-81	Escherichia coli	b2608	[pn:hypothetical 21.0 kd protein in trnd-rpsp intergenic region]
CONTIG254	22789178_f2_10	362	6024	441	147	622	7.2(10)-61	Escherichia coli	b2614	[pn:heat shock protein] [gn:grpel]
CONTIG254	12268766_f2_12	363	6025	1389	463	1971	8.1(10)-204	Escherichia coli	b2610	[pn:signal recognition particle protein] [gn:ffh]
CONTIG254	26366082_f2_14	364	6026	786	262	1233	1.3(10)-125	Escherichia coli	b2607	[pn:guanine-7methyltransferase] [gn:trmd]
CONTIG254	16304761_c1_27	365	6027	888	296	1070	2.5(10)-108	Escherichia coli	b2611	[pn:hypothetical protein]
CONTIG254	1385936_c2_37	366	6028	1302	434	934	6.2(10)-94	Escherichia coli	b2613	[pn:hypothetical protein in grpe 3''' region] [gn:yfjd]
CONTIG255	30328941_f2_6	367	6029	1095	365	1120	1.2(10)-113	Escherichia coli	b1620	[pn:repressor protein] [gn:mali]
CONTIG255	19922527_c1_11	368	6030	693	231	794	4.2(10)-79	Escherichia coli	b1621	[pn:pts system, maltose and glucose-specific ii abc component] [gn:malx]
CONTIG255	13674218_c1_12	369	6031	603	201	785	3.8(10)-78	Escherichia coli	b1622	[pn:maly protein] [gn:maly]
CONTIG255	1036625_c2_15	370	6032	993	331	1307	1.8(10)-133	Escherichia coli	b1621	[pn:pts system, maltose and glucose-specific ii abc component] [gn:malx]
CONTIG256	33725701_f1_2	371	6033	1035	345	1335	2.0(10)-136	Escherichia coli	b1235	[pn:hmr protein] [gn:hmr]
CONTIG256	1299183_f2_4	372	6034	954	318	1218	5.0(10)-124	Escherichia coli	b1234	[pn:hypothetical 34.4 kd protein in hmr-puru intergenic region]
CONTIG256	32126890_f2_6	373	6035	840	280	950	1.3(10)-95	Escherichia coli	b1236	[pn:glucose-1-phosphate uridylyltransferase] [gn:gal]
CONTIG256	14572040_c1_15	374	6036	891	297	1318	1.3(10)-134	Escherichia coli	b1232	[pn:formyltetrahydrofolate deformylase] [gn:puru]
CONTIG256	31416_c2_18	375	6037	495	165	542	2.2(10)-52	Escherichia coli	b1233	[pn:hypothetical 17.0 kd protein in hmr-puru intergenic region] [gn:ychj]
CONTIG257	32145043_f2_3	376	6038	222	74	235	7.5(10)-20	synthetic construct	M15619	or:artificial sequence le:29 re:>232 di:direct sr:c.coli (strain se5000) synthetic dna, clone pkl1 nt:orf16-lacZ fusion protein
CONTIG257	12781963_c3_15	377	6039	189	63	101	1.2(10)-5	Homo sapiens	A44803	pgl protein - human (fragment)
CONTIG258	22438128_f2_4	378	6040	645	215	846	1.3(10)-84	Escherichia coli	b3740	[pn:glucose inhibited division protein] [gn:gldb]

CONTIG258	24277186_f2_5	379	6041	411	137	600	1.6(10)-58	Escherichia coli	b3738	[pn:atp synthase f0 subunit a] [gn:atpb]
CONTIG258	13147637_f3_6	380	6042	1947	649	2757	4.2(10)-287	Escherichia coli	b3741	[pn:glucose inhibited division protein] [gn:gida]
CONTIG258	2071915_f3_7	381	6043	456	152	436	3.7(10)-41	Escherichia coli	b3739	[pn:atp synthase subunit] [gn:atpi]
CONTIG259	881516_f2_5	382	6044	768	256	441	1.1(10)-41	Escherichia coli	b2110	[pn:hypothetical 26.6 kd fimbrial chaperone in mrp 5'''region] [gn:yche]
CONTIG259	3007955_f2_6	383	6045	2508	836	1320	7.9(10)-135	Escherichia coli	b2109	[pn:hypothetical outer membrane usher protein in mrp 5'''region] [gn:yehb]
CONTIG259	3948925_f2_7	384	6046	1080	360	147	9.5(10)-8	Escherichia coli	b2108	[pn:hypothetical 36.9 kd protein in mrp 5'''region precursor] [gn:yeha]
CONTIG259	87513_c3_25	385	6047	498	166	176	1.3(10)-13	Escherichia coli	b2217	[pn:regulator of capsule synthesis b component] [gn:rcsb]
CONTIG260	16848787_f1_1	386	6048	1545	515	2236	6.7(10)-232	Escherichia coli	b2411	[pn:dna ase] [gn:lig]
CONTIG260	4114465_f3_11	387	6049	603	201	865	1.3(10)-86	Escherichia coli	b2411	[pn:dna ase] [gn:lig]
CONTIG260	5257752_f3_14	388	6050	951	317	1146	2.2(10)-116	Escherichia coli	b2409	[pn:hypothetical protein]
CONTIG260	1188966_c1_19	389	6051	1020	340	1320	7.9(10)-135	Escherichia coli	b2410	[pn:hypothetical 36.4 kd protein in xapb-lig intergenic region] [gn:yfeh]
CONTIG261	35816301_f1_1	390	6052	1587	529	1699	5.4(10)-175	Escherichia coli	b2176	[pn:hypothetical protein] [gn:rtn]
CONTIG261	21676375_f1_2	391	6053	1881	627	2470	1.1(10)-256	Escherichia coli	b2177	[pn:hypothetical protein in bcr 5'''region] [gn:yeja]
CONTIG261	5197318_f1_3	392	6054	834	278	1164	2.7(10)-118	Escherichia coli	b2178	[pn:hypothetical 40.4 kd protein in bcr 5'''region] [gn:yejb]
CONTIG261	35781511_f3_6	393	6055	294	98	394	1.1(10)-36	Escherichia coli	b2175	[pn:hypothetical protein] [gn:spr]
CONTIG262	13930381_c2_20	394	6056	1512	504	735	7.7(10)-73	Escherichia coli	b0139	[pn:outer membrane usher protein htre precursor] [gn:htrc]
CONTIG262	32287800_c2_22	395	6057	600	200	97	0.00459	Escherichia coli	b2369	[pn:putative positive transcription regulator evga] [gn:evga]
CONTIG262	22460963_c3_24	396	6058	1209	403	454	3.1(10)-42	Escherichia coli	b3144	[pn:hypothetical outer membrane usher protein in agal-mtr intergenic region] [gn:yraj]

CONTIG262	5286713_c3_25	397	6059	1161	387	107	0.016	Saccharomyces cerevisiae	YOL155C	[pn:similarity to glucan 1,4-alpha-glucosidase mal5p]
CONTIG263	5119186_f1_3	398	6060	1214	405	98	0.23	Saccharomyces cerevisiae	YCR089W	[pn:required for efficient mating]
CONTIG263	21641312_f2_4	399	6061	903	301	1471	7.9(10)-151	Serratia marcescens	U62007	[gn:fig2] rep protein,,rep hi2b,putative rep protein,, similar to inchi plasmid r27 traе protein.
CONTIG263	3164077_f2_5	400	6062	789	263	121	5.7(10)-6	Salmonella typhimurium	P12057	
CONTIG264	34386086_f1_2	401	6063	642	214	873	1.8(10)-87	Escherichia coli	b2302	[pn:hypothetical protein] [gn:yfcg]
CONTIG264	12239405_f1_3	402	6064	444	148	560	2.7(10)-54	Escherichia coli	b2303	[pn:hypothetical protein] [gn:folx]
CONTIG264	14503385_f1_4	403	6065	513	171	178	8.1(10)-14	Bacillus subtilis	yjeK	[pn:hypothetical protein]
CONTIG264	16286633_f2_10	404	6066	927	309	1223	1.5(10)-124	Escherichia coli	b2304	[pn:hypothetical protein]
CONTIG264	12001891_c1_24	405	6067	504	168	548	5.0(10)-53	Escherichia coli	b2301	[pn:hypothetical protein] [gn:yfcf]
CONTIG264	24634813_c2_25	406	6068	720	240	1065	8.3(10)-108	Escherichia coli	b2306	[pn:histidine transport atp-binding protein hisp] [gn:hisp]
CONTIG265	3145261_f1_1	407	6069	1050	350	1257	3.7(10)-128	Escherichia coli	b2810	[pn:hypothetical protein]
CONTIG265	16258266_f1_2	408	6070	501	167	574	8.9(10)-56	Escherichia coli	b2811	[pn:hypothetical protein] [gn:ygdK]
CONTIG265	32708250_f2_6	409	6071	210	70	301	7.5(10)-27	Escherichia coli	b2810	[pn:hypothetical protein]
CONTIG265	15136718_c2_20	410	6072	1134	378	1789	1.6(10)-184	Escherichia coli	b2813	[pn:membrane-bound lytic murein transglycosylase a precursor]
CONTIG265	10968768_c2_21	411	6073	813	271	1292	7.2(10)-132	Escherichia coli	b2812	[gn:mlta] [pn:hypothetical protein] [gn:ygdI]
CONTIG265	26756450_c3_29	412	6074	207	69	237	4.5(10)-20	Escherichia coli	b2809	[pn:hypothetical protein]
CONTIG266	30078286_f1_6	413	6075	462	154	452	7.5(10)-43	Escherichia coli	b2171	[pn:hypothetical 30.9 kd protein in frub 5'''region] [gn:yeip]
CONTIG266	16453125_f3_24	414	6076	1272	424	1593	9.3(10)-164	Escherichia coli	b2170	[pn:hypothetical 42.7 kd protein in frub 5'''region] [gn:yeio]
CONTIG266	25521057_c2_35	415	6077	996	332	1477	1.8(10)-151	Escherichia coli	b2168	[pn:l-phosphofructokinase] [gn:fruk]

CONTIG266	5195383_c3_42	416	6078	1167	389	1476	2.2(10)-151	Escherichia coli	b2169	[pn:pts system, fructose-specific iia/fpr component]
CONTIG266	14453287_c3_43	417	6079	1755	585	2135	3.3(10)-221	Escherichia coli	b2167	[pn:pts system, fructose-specific iibc component] [gn:frua]
CONTIG267	36570837_f1_2	418	6080	2496	832	3364	0	Escherichia coli	b3863	[pn:dna polymerase i] [gn:pola]
CONTIG267	24644037_f1_4	419	6081	258	86	116	3.0(10)-7	Escherichia coli	b3866	[pn:hypothetical 19.1 kd protein in pola-hemm intergenic region]
CONTIG267	11890640_f3_12	420	6082	471	157	650	1.1(10)-63	Escherichia coli	b3863	[pn:dna polymerase i] [gn:pola]
CONTIG267	5260155_c1_16	421	6083	663	221	878	5.4(10)-88	Escherichia coli	b3865	[pn:hypothetical protein] [gn:yih]
CONTIG268	5324009_c1_15	422	6084	650	216	795	3.3(10)-79	Escherichia coli	b2572	[pn:sigma-e factor negative regulatory protein] [gn:rsea]
CONTIG268	20109425_c1_18	423	6085	1632	544	2419	2.7(10)-251	Escherichia coli	b2569	[pn:gtp-binding protein lepa] [gn:lepa]
CONTIG268	29979502_c2_22	424	6086	492	164	513	2.6(10)-49	Escherichia coli	b2570	[pn:sigma-e factor regulatory protein rsec] [gn:rsec]
CONTIG268	24317933_c3_23	425	6087	1023	341	1294	4.5(10)-132	Escherichia coli	b2571	[pn:sigma-e factor regulatory protein rseb precursor] [gn:rseb]
CONTIG269	2428216_f2_5	426	6088	243	81	94	0.0015	Archaeoglobus fulgidus	H69378	[pn:purine ntpase homolog]
CONTIG269	10269038_c2_22	427	6089	816	272	915	6.5(10)-92	Escherichia coli	b0570	[pn:hypothetical protein] [gn:ybez]
CONTIG269	30111081_c2_23	428	6090	444	148	123	5.5(10)-8	Synechocystis sp.	S77018	[PN:hypothetical protein] [OR:Synechocystis sp] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG269	12620775_c3_27	429	6091	702	234	342	3.3(10)-31	Escherichia coli	S70162	.
CONTIG27	6511700_f2_2	430	6092	396	132	192	2.5(10)-14	Haemophilus influenzae	HI0539	[pn:urease alpha subunit] [gn:urea]
CONTIG270	14313817_f1_4	431	6093	768	256	727	5.5(10)-72	Shigella flexneri	P07044	mercuric resistance operon regulatory protein
CONTIG270	31284383_f1_5	432	6094	351	117	553	1.5(10)-53	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn:tnpa gn:tnpa le:10303 re:11307 di:complement
CONTIG270	31523431_f2_8	433	6095	3222	1074	4832	0	Escherichia coli	P03008	transposase for transposon tn3.

CONTIG270	32204791_c1_14	434	6096	399	133	628	1.7(10)-61	Enterobacteria ceae	S07447	[pn:hypothetical protein, 13.1k]
CONTIG270	1057266_c1_18	435	6097	438	146	122	4.7(10)-7	Streptomyces fradiae	P20188	hypothetical 44.4 kd protein in transposon tn4556.
CONTIG270	22550252_c1_19	436	6098	639	213	684	2.0(10)-67	Escherichia coli	P03011	transposon tn3 resolvase.
CONTIG270	25522168_c2_20	437	6099	297	99	165	2.0(10)-12	Shigella flexneri	P04337	hypothetical mercuric resistance protein merc.
CONTIG271	16820950_f1_1	438	6100	702	234	1040	3.7(10)-105	Escherichia coli	b0437	[pn:atp-dependent clp protease proteolytic subunit] [gn:clpp]
CONTIG271	183188_f2_3	439	6101	1332	444	1904	1.0(10)-196	Escherichia coli	b0438	[pn:atp-dependent clp protease atp- binding subunit clpx] [gn:clpx]
CONTIG271	2500431_f3_7	440	6102	1695	565	2578	3.8(10)-268	Escherichia coli	b0439	[pn:lon protease] [gn:lon]
CONTIG271	35736527_c1_10	441	6103	225	75	99	4.0(10)-5	Bacillus subtilis	Z75208	or:bacillus subtilis pn:hypothetical protein gn:ysoc le:80592 re:81206 di:complement nt:unknown function; putative
CONTIG271	11067152_c1_11	442	6104	192	64	112	1.3(10)-6	Bacillus subtilis	Z75208	or bacillus subtilis pn:hypothetical protein gn:ysoc le:80592 re:81206 di:complement nt:unknown function; putative
CONTIG272	36595388_f1_4	443	6105	483	161	113	6.2(10)-7	Escherichia coli	b1031	[pn:hypothetical protein] [gn:ycdv]
CONTIG272	16526588_f2_7	444	6106	1119	373	1440	1.5(10)-147	Escherichia coli	b1020	[pn:phoh protein] [gn:phoh]
CONTIG272	36620786_f2_8	445	6107	186	62	117	2.3(10)-7	Escherichia coli	b1031	[pn:hypothetical protein] [gn:ycdv]
CONTIG272	16853317_f3_9	446	6108	270	90	310	8.4(10)-28	Escherichia coli	b1017	[pn:hypothetical protein]
CONTIG272	13851425_f3_10	447	6109	1155	385	1589	2.5(10)-163	Escherichia coli	b1018	[pn:hypothetical protein]
CONTIG272	25978458_f3_11	448	6110	1287	429	1830	7.0(10)-189	Escherichia coli	b1019	[pn:hypothetical protein in phoh 5'''region] [gn:ycdb]
CONTIG272	3251026_f3_13	449	6111	312	104	106	3.5(10)-6	Escherichia coli	b1031	[pn:hypothetical protein] [gn:ycdv]
CONTIG273	5370841_f1_1	450	6112	1809	603	2802	7.0(10)-292	Escherichia coli	b0680	[pn:glutaminyl-trna synthetase] [gn:glns]

CONTIG273	13931505_f1_2	451	6113	615	205	948	2.1(10)-95	Escherichia coli	b0681	[pn:hypothetical protein]
CONTIG273	267062_f3_12	452	6114	2001	667	2384	1.3(10)-247	Escherichia coli	b0679	[pn:pts system, n-acetylglucosamine-specific iiabc component] [gn:nage]
CONTIG273	26659787_c3_23	453	6115	861	287	90	0.024	Homo sapiens	l53641	mucin - human (fragment)
CONTIG274	35752258_f2_2	454	6116	1101	367	1209	4.5(10)-123	Escherichia coli	b0356	[pn:alcohol--acetaldehyde dehydrogenase] [gn:adhc]
CONTIG274	20490962_f3_5	455	6117	312	104	243	1.1(10)-20	Escherichia coli	b0357	[pn:hypothetical protein]
CONTIG274	32594790_f3_8	456	6118	312	104	331	5.0(10)-30	Haemophilus influenzae	H10185	[pn:putative alcohol dehydrogenase class iii] [gn:adhc]
CONTIG274	24234380_f3_9	457	6119	1551	517	1357	9.5(10)-139	Escherichia coli	b1421	[pn:methyl-accepting chemotaxis protein iii] [gn:trg]
CONTIG274	4837_c2_18	458	6120	501	167	419	2.3(10)-39	Escherichia coli	b1931	[pn:yedg] [gn:yedk]
CONTIG274	31532686_c2_19	459	6121	333	111	486	1.8(10)-46	Escherichia coli	b1931	[pn:yedg] [gn:yedk]
CONTIG275	9892787_f1_1	460	6122	429	143	582	1.3(10)-56	Escherichia coli	b0240	[pn:curlin genes transcriptional activator] [gn:crf]
CONTIG275	31355201_f2_4	461	6123	507	169	731	2.1(10)-72	Escherichia coli	b0239	[pn:hypothetical protein in gpt-crl intergenic region] [gn:yafa]
CONTIG275	866576_f3_10	462	6124	1143	381	1784	5.4(10)-184	Escherichia coli	b0242	[pn:glutamate 5-kinase] [gn:prob]
CONTIG275	3906666_c1_13	463	6125	1080	360	1533	2.1(10)-157	Escherichia coli	b0241	[pn:outer membrane pore protein c precursor] [gn:phoe]
CONTIG276	20604691_f1_2	464	6126	732	244	856	1.2(10)-85	Escherichia coli	b0192	[pn:copper homeostasis protein precursor] [gn:cuf]
CONTIG276	9961630_f2_8	465	6127	453	151	492	4.4(10)-47	Escherichia coli	b0191	[pn:hypothetical protein in acca-cuff intergenic region] [gn:yac]
CONTIG276	34648525_f3_14	466	6128	564	188	842	3.5(10)-84	Escherichia coli	b0190	[pn:hypothetical protein in acca-cuff intergenic region] [gn:yaeq]
CONTIG276	24725817_c1_20	467	6129	183	61	290	1.1(10)-25	Escherichia coli	b0196	[pn:resf protein] [gn:resf]
CONTIG276	16100083_c1_21	468	6130	294	98	93	8.5(10)-5	Escherichia coli	C47040	orf3 3' to resf - escherichia coli
CONTIG276	907_c1_22	469	6131	1785	595	2738	4.2(10)-285	Escherichia coli	b0194	[pn:polyl-trna synthetase] [gn:pros]
CONTIG276	3236528_c2_30	470	6132	225	75	202	2.2(10)-16	Escherichia coli	P52099	hypothetical 7.2 kd protein in mesj-cuff intergenic region.

CONTIG276	26066886_c3_31	471	6133	720	240	1037	7.7(10)-105	Escherichia coli	b0195	[pn:hypothetical 26.4 kd protein in pros-rsf intergenic region]
CONTIG277	29886588_c1_14	472	6134	441	147	730	2.6(10)-72	Serratia marcescens	U59129	or:serratia marcescens pn:htdf gn:htdf le:29 re:454 di:direct
CONTIG277	26255000_c2_16	473	6135	3678	1226	92	0.68	Anas platyrhynchos	U27213	or:anas platyrhynchos pn:igm heavy chain, constant region domains one, gn:mu le:<1 re:1350 di:direct sr:domestic duck nt:presumed antibody; immunoglobulin heavy chain
CONTIG277	3937825_c3_17	474	6136	480	160	755	5.9(10)-75	Plasmid R478	A55209	h transfer determinant a - plasmid r478
CONTIG277	32687777_c3_18	475	6137	597	199	904	9.5(10)-91	Serratia marcescens	U59129	or:serratia marcescens pn:htdk gn:htdk lc:463 re:996 di:direct
CONTIG278	1362586_f1_4	476	6138	519	173	249	2.3(10)-21	Vibrio cholerae	S81006	or:vibrio cholerae pn:hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nt:28 kda secreted hydrophilic protein; this sequence
CONTIG278	3333152_c2_17	477	6139	1284	428	1901	2.1(10)-196	Escherichia coli	b1184	[pn:umuc protein] [gn:umuc]
CONTIG278	21759555_c3_18	478	6140	474	158	568	3.7(10)-55	Escherichia coli	b1183	[pn:umud protein] [gn:umud]
CONTIG279	995266_c1_16	479	6141	948	316	122	2.7(10)-6	Methanococcus jannaschii	MJ1494	[pn:aaa superfamily atpase, similar to fts]
CONTIG279	2145887_c2_23	480	6142	522	174	604	5.9(10)-59	Escherichia coli	A1224995	[dc:escherichia coli ecorii restriction endonuclease gene.] [pn:restriction endonuclease] [gn:ecorii]
CONTIG28	476581_f1_1	481	6143	243	81	173	2.6(10)-12	Escherichia coli	b4065	[pn:hypothetical 60.5 kd protein in soxr-acs intergenic region] [gn:yjee]
CONTIG28	29728382_f2_2	482	6144	315	105	133	5.2(10)-8	Escherichia coli	b4065	[pn:hypothetical 60.5 kd protein in soxr-acs intergenic region] [gn:yjee]
CONTIG280	23609515_f3_13	483	6145	294	98	419	2.3(10)-39	Enterobacter agglomerans	A38965	hypothetical protein a (insertion sequence is1222) -enterobacter agglomerans

CONTIG280	36211006_c1_14	484	6146	2109	703	107	0.028	Legionella pneumophila	AF026534	[de:legionella pneumophila dot region ii, cita, doto, dotn, dote, dotf, dotg, doth, doti, dotj, dotk, dotl, and dotm genes, complete cds.] [pn:dotl] [gn:dotl] [nt:similar to trbe from the inci plasmid r64.]
CONTIG280	14538317_c2_15	485	6147	2613	871	104	0.03799	Listeria monocytogenes	M80351	or:listeria monocytogenes pn:p60-related protein le:1 re:1437 di:direct sr:listeria monocytogenes (serovar 1/2a mackness) dna
CONTIG281	21567780_f2_8	486	6148	768	256	755	5 9(10)-75	Escherichia coli	b4190	[pn:hypothetical 27 6 kd protein in aidb-rpsf intergenic region] [gn:yjfp]
CONTIG281	26681526_c1_13	487	6149	759	253	1187	9.8(10)-121	Escherichia coli	b4191	[pn:hypothetical transcriptional regulator in aidb-rpsf intergenic region] [gn:yjfq]
CONTIG281	4392281_c1_15	488	6150	231	77	95	0.00025	Nannocystis exedens	U66220	or:nannocystis exedens pn:unknown le:<1 re:872 di:complement nt orf1
CONTIG281	23609702_c2_16	489	6151	447	149	408	3.5(10)-38	Escherichia coli	b4189	[pn:hypothetical 16.0 kd protein in aidb-rpsf intergenic region] [gn:yjfo]
CONTIG281	32501253_c3_23	490	6152	333	111	309	1.1(10)-27	Escherichia coli	b4188	[pn:hypothetical 11.0 kd protein in aidb-rpsf intergenic region] [gn:yjfn]
CONTIG282	17080463_f2_12	491	6153	1182	394	1562	1.8(10)-160	Escherichia coli	b4322	[pn:mannonate hydratase] [gn:uxua]
CONTIG282	20752305_c1_18	492	6154	1482	494	2008	9.8(10)-208	Escherichia coli	b2172	[pn:hypothetical 54.0 kd protein in fruk 5'''region] [gn:yeiq]
CONTIG282	13719178_c1_19	493	6155	1026	342	1336	1.6(10)-136	Escherichia coli	b2173	[pn:hypothetical 36.1 kd protein in frub-rtn intergenic region] [gn:yeir]
CONTIG282	895125_c1_20	494	6156	735	245	744	8.5(10)-74	Escherichia coli	b2174	[pn:hypothetical protein]
CONTIG283	32551313_f1_1	495	6157	369	123	362	2.6(10)-33	Escherichia coli	b3228	[pn:stringent starvation protein b] [gn:sspb]
CONTIG283	23850927_f1_3	496	6158	2436	812	1534	1.7(10)-157	Escherichia coli	b3216	[pn:hypothetical outer membrane usher protein in gltf-nant intergenic region] [gn:yhcd]
CONTIG283	4875010_f2_6	497	6159	816	272	565	8.0(10)-55	Escherichia coli	b3215	[pn:hypothetical 25.3 kd fimbrial chapcrone in gltf-nant intergenic region] [gn:yhca]
CONTIG283	24415941_f3_8	498	6160	681	227	242	1.3(10)-20	Escherichia coli	b3219	[pn:hypothetical protein] [gn:yhcf]

CONTIG283	24415936_f3_10	499	6161	282	94	160	6.5(10)-12	Escherichia coli	b3219	[pn.hypothetical protein] [gn.yhcf]
CONTIG284	14081275_f1_1	500	6162	228	76	115	2.2(10)-6	Escherichia coli	b1514	[pn.hypothetical protein]
CONTIG284	23464702_f1_2	501	6163	978	326	771	1.2(10)-76	Escherichia coli	b1515	[pn.hypothetical protein]
CONTIG284	22945418_f1_6	502	6164	978	326	1134	4.0(10)-115	Escherichia coli	b1517	[pn.hypothetical protein] [gn.yneb]
CONTIG284	16130028_f2_8	503	6165	1056	352	1315	2.7(10)-134	Escherichia coli	b1516	[pn.hypothetical protein]
CONTIG284	31845937_f3_13	504	6166	543	181	353	2.2(10)-32	Escherichia coli	b1518	[pn.hypothetical protein]
CONTIG285	23922002_f1_2	505	6167	1338	446	1837	1.3(10)-189	Escherichia coli	b1423	[pn.hypothetical protein]
CONTIG285	31753501_c3_22	506	6168	960	320	1315	2.7(10)-134	Escherichia coli	b1422	[pn.hypothetical protein]
CONTIG286	7207808_f2_9	507	6169	1038	346	1460	1.2(10)-149	Escherichia coli	b1097	[pn.hypothetical 38.2 kd protein in pabc-holb intergenic region] [gn.yceg]
CONTIG286	26303760_f2_11	508	6170	759	253	822	4.7(10)-82	Escherichia coli	b1099	[pn.dna polymerase iii, delta''' subunit] [gn.holb]
CONTIG286	84378_f3_12	509	6171	1299	433	1922	1.3(10)-198	Escherichia coli	b1095	[pn:3-oxoacyl-acyl-carrier-protein synthase ii] [gn:fabf]
CONTIG286	4019818_f3_13	510	6172	819	273	864	1.7(10)-86	Escherichia coli	b1096	[pn:4-amino-4-deoxychorismate lyase] [gn:pabc]
CONTIG286	33988967_f3_15	511	6173	660	220	904	9.5(10)-91	Escherichia coli	b1098	[pn:hypothetical protein in pabc-holb intergenic region] [gn:tmk]
CONTIG287	20525451_f1_1	512	6174	1008	336	1549	4.2(10)-159	Escherichia coli	b1779	[pn.glyceraldehyde 3-phosphate dehydrogenase a] [gn:gapa]
CONTIG287	29511057_f3_8	513	6175	900	300	1148	1.3(10)-116	Escherichia coli	b1780	[pn.hypothetical protein]
CONTIG287	36135312_f3_11	514	6176	1574	525	2554	1.3(10)-265	Escherichia coli	b1783	[pn.hypothetical protein]
CONTIG287	20125050_c2_19	515	6177	774	258	934	6.2(10)-94	Escherichia coli	b1782	[pn.hypothetical protein]
CONTIG288	206649_c1_21	516	6178	184	61	183	2.3(10)-14	Escherichia coli	b3179	[pn:cell division protein ftsj] [gn:ftsj]
CONTIG288	2187917_c1_23	517	6179	933	311	1346	1.3(10)-137	Escherichia coli	b3177	[pn.dihydropteroate synthase] [gn:folp]

CONTIG288	34038453_c2_25	518	6180	288	96	374	1.3(10)-34	Escherichia coli	b3179	[pn:cell division protein ftsj] [gn:ftsj]
CONTIG288	23495385_c2_26	519	6181	1959	653	2979	0	Escherichia coli	b3178	[pn:cell division protein ftsj] [gn:ftsj]
CONTIG288	6491462_c2_28	520	6182	1125	375	1407	4.7(10)-144	Escherichia coli	b3176	[pn:mrsa protein] [gn:mrsa]
CONTIG289	14338511_f3_21	521	6183	2178	726	522	3.1(10)-49	Achlya klebsiana	P41755	nad-specific glutamate dehydrogenase (ec 1.4.1.2) (nad-gdh).
CONTIG289	20183505_c1_25	522	6184	687	229	433	7.7(10)-41	Escherichia coli	b0019	[pn:na] [gn:nhaa]
CONTIG289	4877327_c2_27	523	6185	1914	638	2830	7.7(10)-295	Escherichia coli	b0014	[pn:dnak protein] [gn:dnak]
CONTIG289	13672255_c2_28	524	6186	1011	337	922	1.2(10)-92	Escherichia coli	b0019	[pn:na] [gn:nhaa]
CONTIG289	26658142_c2_30	525	6187	987	329	1437	3.2(10)-147	Escherichia coli	b0020	[pn:transcriptional activator protein nhar] [gn:nhar]
CONTIG289	24471958_c3_35	526	6188	1116	372	1243	3.0(10)-146	Escherichia coli	b0015	[pn:dnaj protein] [gn:dnaj]
CONTIG290	9896067_f1_4	527	6189	318	106	273	7.0(10)-24	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG290	23609515_f2_8	528	6190	294	98	419	2.3(10)-39	Enterobacter agglomerans	A38965	hypothetical protein a (insertion sequence is1222) -enterobacter agglomerans
CONTIG290	22905462_f3_15	529	6191	561	187	866	1.0(10)-86	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG290	24500893_c2_21	530	6192	2418	806	110	0.012	Escherichia coli	AF005044	[PN:TraN] [GN:traN] [DE:Escherichia coli plasmid R100-1 TraV (traV), TraR (traR), OrfG1 (orfG1), OrfH (orfH), OrfI (orfI), TraC (traC), TrbI (trbI), TraW (traW), TraU (traU), TrbC (trbC), TraN (traN), TrbE (trbE) and TraF (traF) genes, c
CONTIG290	32225050_c2_24	531	6193	1680	560	286	5.5(10)-22	Bacillus subtilis	yjcd	[pn:hypothetical protein]
CONTIG291	20370300_f2_10	532	6194	321	107	113	2.8(10)-6	Rhizobium sp.	P55426	hypothetical 34.2 kd protein y4ec.

CONTIG291	1050702_f3_13	533	6195	900	300	95	0.04	Bacillus subtilis	ripX	[pn:integrase/recombinase] [gn:ykqm]
CONTIG291	33879001_f3_17	534	6196	729	243	324	8.4(10)-28	Escherichia coli	P27190	dna primase trac (cc 2.7.7.-) (replication primase).
CONTIG291	16020063_c3_33	535	6197	192	64	259	2.1(10)-22	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn:tnpa gn:tnpa lc:13384 re:14388 di:direct
CONTIG292	4114091_f2_10	536	6198	480	160	439	1.8(10)-41	Escherichia coli	M16489	or:escherichia coli lc:627 re:1199 di:complement sr:escherichia coli dna nt:orf 4; putative
CONTIG292	24611566_c1_26	537	6199	450	150	644	3.3(10)-63	Escherichia coli	b0736	[pn:hypothetical 15.6 kd protein in cydb-tolq intergenic region] [gn:ybgc]
CONTIG292	802151_c1_28	538	6200	1128	376	211	2.8(10)-21	Escherichia coli	b0739	[pn:protein] [gn:tolq]
CONTIG292	1190692_c2_29	539	6201	1515	505	2417	4.5(10)-251	Escherichia coli	b0733	[pn:cytochrome d ubiquinol oxidase subunit i] [gn:cyda]
CONTIG292	21761538_c2_30	540	6202	1155	385	1632	6.7(10)-168	Escherichia coli	b0734	[pn:cytochrome d ubiquinol oxidase subunit ii] [gn:cydb]
CONTIG292	2867192_c3_38	541	6203	303	101	343	2.7(10)-31	Escherichia coli	b0735	[pn:10.9 kd protein in cydb-tolq intergenic region] [gn:ybgc]
CONTIG292	25509808_c3_39	542	6204	696	232	1068	4.0(10)-108	Escherichia coli	b0737	[pn:tolq protein] [gn:tolq]
CONTIG292	33728407_c3_40	543	6205	432	144	529	5.2(10)-51	Escherichia coli	b0738	[pn:tolr protein] [gn:tolr]
CONTIG293	20875925_f2_6	544	6206	903	301	1407	4.7(10)-144	Escherichia coli	b3073	[pn:probable ornithine aminotransferase] [gn:yggg]
CONTIG293	24728780_f3_14	545	6207	576	192	844	2.2(10)-84	Escherichia coli	b3073	[pn:probable ornithine aminotransferase] [gn:yggg]
CONTIG293	25509681_c1_20	546	6208	606	202	126	1.7(10)-7	Escherichia coli	b1434	[pn:hypothetical protein]
CONTIG294	10353302_f1_2	547	6209	414	138	421	1.5(10)-39	Escherichia coli	b0530	[pn:hypothetical protein] [gn:sfma]
CONTIG294	13947040_f1_3	548	6210	612	204	558	4.4(10)-54	Salmonella typhi	Q08456	fimbrin-like protein fimi.
CONTIG294	5963891_f1_5	549	6211	2586	862	2988	0	Escherichia coli	b0532	[pn:hypothetical protein] [gn:sfmd]
CONTIG294	25487750_f2_10	550	6212	738	246	660	6.9(10)-65	Escherichia coli	b0531	[pn:hypothetical protein] [gn:sfmc]

CONTIG294	26845900_f2_14	551	6213	1104	368	1037	7.7(10)-105	Escherichia coli	b0533	[pn:hypothetical protein] [gn:sfmh]
CONTIG294	391957_f3_17	552	6214	240	80	104	8.5(10)-6	Escherichia coli	b0530	[pn:hypothetical protein] [gn:sfma]
CONTIG294	30338206_f3_23	553	6215	498	166	333	3.1(10)-30	Escherichia coli	b0534	[pn:hypothetical fimbrial-like protein in fimz 5''' region] [gn:ybeg]
CONTIG294	32426319_c1_25	554	6216	503	167	156	1.8(10)-11	Salmonella typhimurium	P26318	fimbriae y protein.
CONTIG294	10417711_c1_37	555	6217	276	92	249	2.3(10)-21	Escherichia coli	b0529	[pn:methylenetetrahydrofolate dehydrogenase] [gn:fold]
CONTIG294	12697187_c3_44	556	6218	636	212	687	9.4(10)-68	Escherichia coli	b0535	[pn:fimbriae z protein] [gn:fimz]
CONTIG295	24647536_f1_6	557	6219	733	251	428	2.6(10)-40	Bacteriophage P21	P36693	terminase large subunit (gp2) (fragments).
CONTIG295	3960443_f1_7	558	6220	333	111	139	1.1(10)-9	Bacteriophage lambda	P03712	head decoration protein (gpd) (major capsid protein d)
CONTIG295	11207801_f2_16	559	6221	540	180	114	6.7(10)-7	Bacteriophage lambda	J02459	or:bacteriophage lambda le 5132 re:5737 di:direct sr lambda wild-type and lambda strain ci857s7 nt:nu3 (capsid assembly_201)
CONTIG295	9970952_f2_17	560	6222	1035	345	972	5.9(10)-98	Bacteriophage lambda	P03713	major head protein (gpe) (major coat protein).
CONTIG295	36135213_f2_18	561	6223	444	148	100	1.5(10)-5	Bacteriophage lambda	P03709	dna packaging protein fi.
CONTIG296	6281375_f2_2	562	6224	990	330	701	3.1(10)-69	Haemophilus influenzae	HI1144	[pn:udp-3-0-acyl n-acetylglucosamine deacetylase] [gn:lpxc]
CONTIG296	4942010_f2_3	563	6225	453	151	266	3.8(10)-23	Haemophilus influenzae	HI0293	[pn:mercury resistance homolog]
CONTIG296	978425_f2_4	564	6226	933	311	711	6.9(10)-70	Escherichia coli	b0462	[pn:acriflavin resistance protein b] [gn:acrb]
CONTIG296	4145218_f3_5	565	6227	3639	1213	282	1.6(10)-34	Bacillus subtilis	yoaE	[pn:hypothetical protein]
CONTIG296	13797188_f3_6	566	6228	1299	433	505	1.8(10)-48	Escherichia coli	b0463	[pn:acriflavin resistance protein a precursor] [gn:acra]
CONTIG297	30347307_f2_10	567	6229	546	182	180	5.9(10)-14	Escherichia coli	b3558	[pn:insertion element is150 hypothetical 33.3 kd protein] [gn:yi5b]
CONTIG297	12948567_f3_13	568	6230	291	97	391	2.2(10)-36	Escherichia coli	I41306	hypothetical protein (argf-lacz region) - escherichia coli

CONTIG297	1448266_c2_17	569	6231	2382	794	91	0.34	Candida albicans	P43060	phosphoribosylamidoimidazole-succinocarboxamide synthase (ec 6.3.2.6) (saicar synthetase).
CONTIG298	5971942_f1_1	570	6232	279	93	269	1.8(10)-23	Escherichia coli	b1648	[pn: hypothetical protein]
CONTIG298	2348136_f1_2	571	6233	921	307	1273	7.5(10)-130	Escherichia coli	b1647	[pn: hypothetical protein]
CONTIG298	2603262_f1_3	572	6234	573	191	789	1.5(10)-78	Escherichia coli	b1646	[pn: copper-zinc superoxide dismutase] [gn: sode]
CONTIG298	884512_c1_23	573	6235	282	94	295	3.2(10)-26	Escherichia coli	b1643	[pn: hypothetical protein]
CONTIG298	25907180_c2_31	574	6236	2100	700	2323	4.0(10)-241	Escherichia coli	b1645	[pn: hypothetical protein]
CONTIG298	12634512_c3_35	575	6237	945	315	1096	4.2(10)-111	Escherichia coli	b1644	[pn: hypothetical protein]
CONTIG299	4151412_f1_1	576	6238	1200	400	152	2.8(10)-8	Bacteriophage P1	P06956	recombinase cre.
CONTIG299	10006261_c3_21	577	6239	1032	344	98	0.056	Saccharomyces cerevisiae	YGR155W	[pn: cystathionine beta-synthase] [gn: cys4]
CONTIG3	4863125_c3_6	578	6240	606	202	473	4.5(10)-45	Escherichia coli	b0698	[pn: potassium-transporting atpase, a chain] [gn: kdpA]
CONTIG30	29728277_f1_1	579	6241	303	101	229	9.4(10)-19	Escherichia coli	b1053	[pn: hypothetical 43.9 kd protein in msyB-hrb intergenic region] [gn: ycee]
CONTIG300	5163340_f1_2	580	6242	438	146	493	3.3(10)-47	Erwinia carotovora subsp. carotovora	JC4727	mob protein a - erwinia carotovora subsp. carotovora a cis-acting locus, orit and trans-acting locus, mob are involved in mobilization of pec3, a non-self-transmissible multiple-copy plasmid. the mob consists of five proteins.
CONTIG300	14866452_f3_5	581	6243	432	144	546	8.3(10)-53	Erwinia carotovora subsp. carotovora	JC4729	mob protein c - erwinia carotovora subsp. carotovora a cis-acting locus, orit and trans-acting locus, mob are involved in mobilization of pec3, a non-self-transmissible multiple-copy plasmid. the mob consists of five proteins.

CONTIG301	31755158_fl_1	582	6244	993	331	1496	1.8(10)-153	Escherichia coli	b3974	[pn:pantothenate kinase] [gn:coaa]
CONTIG301	33475302_c1_29	583	6245	1185	395	1621	1.0(10)-166	Escherichia coli	b3543	[pn:dipeptide transport system permease protein dppb] [gn:dppb]
CONTIG301	4332343_c1_30	584	6246	912	304	1144	3.5(10)-116	Escherichia coli	b3542	[pn:dipeptide transport system permease protein dppc] [gn:dppc]
CONTIG301	17011415_c1_32	585	6247	1032	344	1665	2.2(10)-171	Escherichia coli	b3540	[pn:dipeptide transport atp-binding protein dppf] [gn:dppf]
CONTIG301	20167543_c2_35	586	6248	228	76	392	1.7(10)-36	Escherichia coli	b3544	[pn:periplasmic dipeptide transport protein precursor] [gn:dppa]
CONTIG301	34564667_c2_37	587	6249	1002	334	1402	1.6(10)-143	Escherichia coli	b3541	[pn:dipeptide transport atp-binding protein dppd] [gn:dppd]
CONTIG302	13753811_fl_3	588	6250	1221	407	1664	2.7(10)-171	Escherichia coli	b2844	[pn:hypothetical protein]
CONTIG302	6445812_fl_4	589	6251	717	239	136	1.5(10)-7	Escherichia coli	b4311	[pn:hypothetical 28.3 kd protein in feci-fimb intergenic region]
CONTIG302	4461517_f2_6	590	6252	327	109	137	6.4(10)-9	Escherichia coli	b0208	[pn:hypothetical transcriptional regulator in rrnh-dnir intergenic region] [gn:yafc]
CONTIG302	3176081_f2_7	591	6253	555	185	91	0.041	Haemophilus influenzae	HI0681	[pn:transcriptional activator protein] [gn:ilvy]
CONTIG302	2078535_c3_37	592	6254	276	92	338	9.0(10)-31	Escherichia coli	b2845	[pn:hypothetical protein]
CONTIG303	894181_fl_1	593	6255	1428	476	834	2.5(10)-83	Escherichia coli	b1525	[pn:hypothetical protein]
CONTIG303	32689752_c1_13	594	6256	1863	621	2460	1.2(10)-255	Salmonella enterica	X99719	or:salmonella enterica le:<142 re:1998 di.direct nt:similarity with helicase; orf1
CONTIG303	25986000_c3_29	595	6257	567	189	356	1.1(10)-32	Escherichia coli	b2250	[pn:hypothetical protein]
CONTIG304	22656568_f3_8	596	6258	222	74	359	5.4(10)-33	Escherichia coli	b1823	[pn:cold shock-like protein cspe] [gn:cspe]
CONTIG304	1308402_f3_9	597	6259	1779	593	1863	2.2(10)-192	Escherichia coli	b0084	[pn:penicillin-binding protein 3 precursor] [gn:fts]
CONTIG304	9879466_f3_10	598	6260	855	285	1136	2.5(10)-115	Escherichia coli	b1822	[pn:hypothetical 30.4 kd protein in manz-cspe intergenic region] [gn:yebh]
CONTIG304	12531889_c1_13	599	6261	425	141	561	2.1(10)-54	Escherichia coli	b1819	[pn:pts system, mannose-specific iid component] [gn:manz]

CONTIG304	14110327_c1_14	600	6262	459	153	602	9.5(10)-59	Escherichia coli	b1820	[pn: hypothetical protein]
CONTIG304	31770643_c3_26	601	6263	774	258	832	4.0(10)-83	Escherichia coli	b1821	[pn: hypothetical protein]
CONTIG305	1424025_f1_1	602	6264	204	68	101	0.00029	Porphyromonas gingivalis	P46071	protease prth (ec 3.4.22.-).
CONTIG305	34085002_f3_7	603	6265	3627	1209	560	5.2(10)-51	Acinetobacter calcoaceticus	AF011339	[PN: unknown] [DE: Acinetobacter calcoaceticus unknown protein gene, partial cds.] [LE: <1] [RE: 2753] [DI: direct]
CONTIG305	6101512_c2_16	604	6266	570	190	172	3.5(10)-13	Escherichia coli	b2846	[pn: hypothetical protein]
CONTIG305	24254687_c2_17	605	6267	1806	602	310	8.5(10)-25	Escherichia coli	X86087	or: escherichia coli gn.ehec-hlyb le: 3628 re.5748 di: direct
CONTIG306	15750937_f1_1	606	6268	990	330	1061	2.2(10)-107	Escherichia coli	b2100	[pn: hypothetical protein]
CONTIG306	26351577_f2_7	607	6269	1005	335	1345	1.8(10)-137	Escherichia coli	b2099	[pn: hypothetical protein]
CONTIG306	29718840_f3_15	608	6270	1236	412	1733	1.3(10)-178	Escherichia coli	b2098	[pn: hypothetical protein]
CONTIG306	11885284_c1_20	609	6271	896	298	1152	5.0(10)-117	Escherichia coli	b2103	[pn: hypothetical protein] [gn: thid]
CONTIG306	29850408_c1_21	610	6272	789	263	1085	6.2(10)-110	Escherichia coli	b2101	[pn: hypothetical protein]
CONTIG307	4332807_f1_2	611	6273	1629	543	2360	4.9(10)-245	Escherichia coli	b2574	[pn: l-aspartate oxidase] [gn: nadb]
CONTIG307	5978412_f3_12	612	6274	1332	444	1704	1.6(10)-175	Escherichia coli	b2576	[pn: atp-dependent rna helicase srmb] [gn: srmb]
CONTIG307	22449093_c1_14	613	6275	396	132	599	2.0(10)-58	Escherichia coli	b2579	[pn: hypothetical 14.3 kd protein in srmb-ung intergenic region]
CONTIG307	32531250_c2_28	614	6276	1089	363	969	1.2(10)-97	Escherichia coli	b2575	[pn: hypothetical protein in nadb-srmb intergenic region] [gn: yfic]
CONTIG307	9817892_c3_36	615	6277	414	138	602	9.5(10)-59	Escherichia coli	b2573	[pn: rna polymerase sigma-e factor] [gn: rpoel]
CONTIG308	4306635_f2_9	616	6278	915	305	1404	9.9(10)-144	Escherichia coli	b2843	[pn: 5-keto-4-deoxyuronate isomerase] [gn: kdui]
CONTIG308	4491568_f2_10	617	6279	771	257	1202	2.5(10)-122	Escherichia coli	b2842	[pn: 2-deoxy-d-gluconate 3-dehydrogenase] [gn: kdud]

CONTIG308	3203441_f2_11	618	6280	1557	519	1989	1.0(10)-205	Escherichia coli	b2841	[pn:l-arabinose isomerase] [gn:arae]
CONTIG308	20038125_c3_30	619	6281	741	247	958	1.8(10)-96	Erwinia chrysanthemi	P21258	oligogalacturonate lyase (ec 4.2.2.6).
CONTIG309	25802285_f2_15	620	6282	861	287	696	1.1(10)-68	Mycobacterium tuberculosis	Z95121	unknown..mtey20b1.07c.mtey20b1.07c. len
CONTIG309	15834716_f2_24	621	6283	930	310	978	1.3(10)-98	Escherichia coli	b1473	[pn:yddg]
CONTIG309	23443818_f2_25	622	6284	531	177	606	3.6(10)-59	Escherichia coli	b0553	[pn:outer membrane porin protein nmpe precursor] [gn:nmpe]
CONTIG309	4817250_c1_37	623	6285	282	94	284	9.0(10)-24	Escherichia coli	b1474	[pn:alpha subunit of formate dehydrogenase n] [gn:fdng]
CONTIG309	17083292_c1_38	624	6286	333	111	465	3.6(10)-43	Escherichia coli	b1474	[pn:alpha subunit of formate dehydrogenase n] [gn:fdng]
CONTIG309	14555411_c1_39	625	6287	2460	820	3784	0	Escherichia coli	b1474	[pn:alpha subunit of formate dehydrogenase n] [gn:fdng]
CONTIG309	13784625_c1_42	626	6288	717	239	803	4.7(10)-80	Escherichia coli	b1476	[pn:gamma subunit of formate dehydrogenase n] [gn:fdng]
CONTIG309	7054750_c2_52	627	6289	270	90	253	1.3(10)-21	Escherichia coli	b0396	[pn:araj protein precursor] [gn:araj]
CONTIG309	26604202_c3_57	628	6290	885	295	1459	1.5(10)-149	Escherichia coli	b1475	[pn:beta subunit of formate dehydrogenase n] [gn:fdnh]
CONTIG31	29877090_c1_7	629	6291	297	99	122	7.0(10)-8	unidentified	X06035	or:unidentified le.107 re:>319 di:direct nt:laci gene product (71 aa)
CONTIG31	32605456_c2_8	630	6292	453	151	226	6.7(10)-19	Haemophilus influenzae	HI0522	[pn:sp]
CONTIG311	21776426_f3_19	631	6293	483	161	233	1.2(10)-19	Haemophilus influenzae	HI1623	[pn:mercury resistance regulatory protein]
CONTIG311	4494003_c1_26	632	6294	468	156	276	3.3(10)-24	Escherichia coli	b0487	[pn:hypothetical protein] [gn:ybbi]
CONTIG311	3959387_c1_27	633	6295	243	81	151	5.9(10)-11	Escherichia coli	b1531	[pn:multiple antibiotic resistance protein] [gn:maral]
CONTIG311	3986268_c2_28	634	6296	1641	547	778	2.1(10)-77	Bacillus subtilis	yvgX	[pn:hypothetical protein]
CONTIG311	26069675_c2_30	635	6297	2556	852	1087	3.8(10)-110	Escherichia coli	b3469	[pn:hypothetical protein] [gn:yhhol]
CONTIG311	32714701_c3_31	636	6298	948	316	608	2.2(10)-59	Bacillus subtilis	yvgX	[pn:hypothetical protein]

CONTIG312	34551934_c2_38	637	6299	866	288	1314	3.3(10)-134	Escherichia coli	b1851	[pn:phosphogluconate dehydratase] [gn:edd]
CONTIG312	5082913_c2_39	638	6300	681	227	1022	3.0(10)-103	Escherichia coli	b1850	[pn:2-keto-3-deoxygluconate 6-p aldolase]
CONTIG312	10973301_c2_40	639	6301	2520	840	261	6.5(10)-19	Escherichia coli	AF044503	[de:escherichia coli strain ec11 unknown (498), hcp gene, complete cds;and thsg accessory genetic element vrg protein, core component anddsorf-g1 genes, complete cds.] [pn:vrg protein]
CONTIG313	2082812_f1_1	640	6302	1311	437	1695	1.3(10)-174	Escherichia coli	b1650	[pn:hypothetical protein] [gn:nema]
CONTIG313	2828405_f1_2	641	6303	435	145	661	5.4(10)-65	Escherichia coli	b1651	[pn:hypothetical protein] [gn:glol]
CONTIG313	5097838_f1_3	642	6304	669	223	887	6.0(10)-89	Escherichia coli	b1652	[pn:ribonuclease t] [gn:mt]
CONTIG313	5093876_f1_5	643	6305	849	283	749	2.5(10)-74	Escherichia coli	b1655	[pn:hypothetical protein] [gn:ydh]
CONTIG313	4589017_f2_10	644	6306	609	203	840	5.7(10)-84	Escherichia coli	b1649	[pn:hypothetical protein]
CONTIG313	13870968_f3_19	645	6307	1767	589	1323	3.7(10)-135	Escherichia coli	b4114	[pn:hypothetical 61.7 kd protein in bass-adiy intergenic region]
CONTIG313	6735627_f3_21	646	6308	822	274	862	2.7(10)-86	Escherichia coli	b1656	[pn:superoxide dismutase] [gn:sodb]
CONTIG313	20114567_c1_22	647	6309	414	138	374	1.3(10)-34	Escherichia coli	b1657	[pn:hypothetical protein]
CONTIG313	26354717_c3_44	648	6310	360	120	593	8.5(10)-58	Escherichia coli	b1654	[pn:hypothetical protein in lhr 5' region] [gn:ydh]
CONTIG313	35411430_c3_46	649	6311	633	211	90	0.066	Rhodobacter sphaeroides	A57140	motb protein homolog - rhodobacter sphaeroides
CONTIG314	4332768_c2_19	650	6312	231	77	224	1.1(10)-18	Escherichia coli	b3267	[pn:hypothetical 7.5 kd protein in acrf-rmd intergenic region]
CONTIG314	12269541_c3_20	651	6313	2973	991	3597	0	Escherichia coli	b3266	[pn:acrf] [gn:acrf]
CONTIG315	9786501_f1_11	652	6314	495	165	451	9.5(10)-43	Escherichia coli	b1668	[pn:hypothetical protein]
CONTIG315	26306432_c2_43	653	6315	318	106	185	1.5(10)-14	Escherichia coli	b3049	[pn:glycogen synthesis protein g[gs] [gn:g[gs]]

CONTIG315	1959386_c3_45	654	6316	522	174	250	1.8(10)-21	Escherichia coli	AF044503	[de:escherichia coli strain ec11 unknown (498), hcp gene, complete cds;and rhsg accessory genetic element vrg protein, core component anddsorf-g1 genes, complete cds.] [pn:unknown] [gn:498]
CONTIG315	2470468_c3_51	655	6317	438	146	174	2.2(10)-13	Escherichia coli	b1419	[pn:hypothetical protein] [gn:ydea]
CONTIG315	23729187_c3_52	656	6318	543	181	212	2.0(10)-17	Escherichia coli	b3686	[pn:hs1s] [gn:ibpb]
CONTIG316	36572802_f1_1	657	6319	669	223	998	1.0(10)-100	Escherichia coli	b1040	[pn:putative regulatory protein] [gn:csgd]
CONTIG316	14568878_f1_2	658	6320	450	150	569	3.0(10)-55	Escherichia coli	b1038	[pn:assembly /transport component in curli production] [gn:csgf]
CONTIG316	4881326_f2_11	659	6321	450	150	555	9.1(10)-54	Escherichia coli	b1039	[pn:assembly /transport component in curli production] [gn:csgc]
CONTIG316	24022000_f3_19	660	6322	867	289	1323	3.7(10)-135	Escherichia coli	b1037	[pn:assembly /transport component in curli production] [gn:csgg]
CONTIG316	24407841_c1_34	661	6323	567	189	808	1.3(10)-80	Escherichia coli	b1035	[pn:hypothetical protein] [gn:ycdy]
CONTIG316	22351626_c1_35	662	6324	579	193	720	3.0(10)-71	Escherichia coli	b1036	[pn:hypothetical protein] [gn:ycdz]
CONTIG316	22781591_c2_37	663	6325	801	267	277	2.6(10)-24	Haemophilus influenzae	H11364	[pn:hypothetical protein]
CONTIG316	35984376_c2_38	664	6326	435	145	249	2.3(10)-21	Escherichia coli	b1031	[pn:hypothetical protein] [gn:ycdv]
CONTIG316	14882337_c3_47	665	6327	951	317	1285	4.0(10)-131	Escherichia coli	b1033	[pn:hypothetical protein] [gn:ycdw]
CONTIG316	475201_c3_48	666	6328	774	258	1079	2.7(10)-109	Escherichia coli	b1034	[pn:hypothetical protein] [gn:ycdx]
CONTIG317	23937778_f2_8	667	6329	1527	509	591	1.3(10)-57	Escherichia coli	b2155	[pn:colicin i receptor precursor] [gn:cira]
CONTIG317	781555_f2_15	668	6330	1104	368	1339	7.7(10)-137	Escherichia coli	b2158	[pn:hypothetical 36.9 kd protein in lysp-nfo intergenic region] [gn:yeih]
CONTIG317	7281308_f3_23	669	6331	873	291	1163	3.3(10)-118	Escherichia coli	b2159	[pn:endonuclease iv] [gn:nfo]

CONTIG317	22691558_c1_26	670	6332	873	291	1169	7.9(10)-119	Escherichia coli	b2157	[pn:hypothetical transcriptional regulator in lysp-nfo intergenic region] [gn:yeie]
CONTIG317	3922542_c3_41	671	6333	1557	519	2396	7.5(10)-249	Escherichia coli	b2156	[pn:lysine-specific permease] [gn:lysp]
CONTIG318	23722842_f1_4	672	6334	609	203	856	1.2(10)-85	Serratia marcescens	U60283	or:serratia marcescens pn:restriction methylase gn:trag1 le:84 re:1775 di:direct nt:putative restriction methylase
CONTIG318	4351033_f2_9	673	6335	1173	391	1857	9.8(10)-192	Serratia marcescens	U60283	or:serratia marcescens pn:restriction methylase gn:trag1 le:84 re:1775 di:direct nt:putative restriction methylase
CONTIG318	30273558_f3_14	674	6336	1188	396	101	0.012	Pseudomonas putida	P31857	hypothetical 32.4 kd protein in gidb-unc1 intergenic region
CONTIG318	10172502_c2_28	675	6337	858	286	424	7.0(10)-40	Haemophilus influenzae	HI0209	[pn:dna adenine methylase] [gn:dam]
CONTIG319	14486288_c1_28	676	6338	597	199	116	1.8(10)-5	Escherichia coli	b0535	[pn:fimbriae z protein] [gn:fimz]
CONTIG319	24648952_c1_29	677	6339	7962	2654	1058	3.7(10)-128	Escherichia coli	b1509	[pn:hypothetical protein]
CONTIG320	25492191_f1_3	678	6340	1248	416	1489	9.6(10)-153	Escherichia coli	b2907	[pn:ubih protein] [gn:ubih]
CONTIG320	14850443_f1_4	679	6341	1215	405	1730	2.7(10)-178	Escherichia coli	b2906	[pn:visc protein] [gn:visc]
CONTIG320	2596033_f1_6	680	6342	426	142	630	1.0(10)-61	Escherichia coli	b2904	[pn:glycine cleavage system h protein] [gn:gcvh]
CONTIG320	1291416_f2_7	681	6343	1206	402	1832	4.4(10)-189	Escherichia coli	b2908	[pn:proline aminopeptidase ii] [gn:pepp]
CONTIG320	1289712_f2_9	682	6344	1170	390	1730	2.7(10)-178	Escherichia coli	b2905	[pn:aminomethyltransferase] [gn:gvt]
CONTIG321	24666092_f2_17	683	6345	1035	345	1509	7.4(10)-155	Escherichia coli	b2151	[pn:mgl repressor and galactose ultrainduction factor] [gn:gals]
CONTIG321	9770002_f3_20	684	6346	1179	393	262	6.7(10)-22	Escherichia coli	b4332	[pn:hypothetical 41.4 kd protein in iada-mcd intergenic region] [gn:yij]
CONTIG321	19743927_f3_21	685	6347	759	253	883	1.6(10)-88	Escherichia coli	b2153	[pn:gtp cyclohydrolase i] [gn:fole]
CONTIG321	17067305_f3_22	686	6348	1176	392	1277	2.7(10)-130	Escherichia coli	b2152	[pn:hypothetical 43.4 kd protein in gals-fole intergenic region] [gn:yeib]

CONTIG321	15712632_f3_23	687	6349	966	322	1479	1.1(10)-151	Escherichia coli	b2150	[pn:d-galactose-binding periplasmic protein precursor] [gn:mglb]
CONTIG321	4143937_c1_29	688	6350	879	293	1253	9.9(10)-128	Escherichia coli	b2154	[pn:hypothetical 31.3 kd protein in fole-cira intergenic region] [gn:yeig]
CONTIG321	7078550_c2_37	689	6351	663	221	95	0.01099	Synechococcus PCC7942	U59236	or:synechococcus pcc7942 pn:unknown le:3661 re:4344 di:complement nt:orf227
CONTIG321	5963902_c2_41	690	6352	666	222	230	2.7(10)-18	Escherichia coli	b2155	[pn:colicin i receptor precursor] [gn:cira]
CONTIG322	26855467_f2_9	691	6353	612	204	715	1.0(10)-70	Escherichia coli	b1857	[pn:31.1 kd protein in msbb-ruvb intergenic region] [gn:yebl]
CONTIG322	25664816_f2_10	692	6354	1335	445	1985	2.7(10)-205	Escherichia coli	b1856	[pn:hypothetical 46.7 kd protein in msbb-ruvb intergenic region] [gn:yebl]
CONTIG322	6535437_f2_11	693	6355	216	72	161	1.6(10)-11	Escherichia coli	b1855	[pn:msbb protein] [gn:msbb]
CONTIG322	13797676_f2_12	694	6356	858	286	1320	7.9(10)-135	Escherichia coli	b1855	[pn:msbb protein] [gn:msbb]
CONTIG322	26734465_f2_14	695	6357	771	257	892	1.8(10)-89	Escherichia coli	b1852	[pn:glucose 6-phosphate 1 dehydrogenase] [gn:zwf]
CONTIG322	80333_f3_27	696	6358	759	253	1123	5.9(10)-114	Escherichia coli	b1852	[pn:glucose 6-phosphate 1 dehydrogenase] [gn:zwf]
CONTIG322	24245760_c2_39	697	6359	942	314	1296	2.7(10)-132	Escherichia coli	b1853	[pn:hypothetical 32.0 kd protein in pyka-zwf intergenic region] [gn:yebl]
CONTIG322	13945816_c2_40	698	6360	1554	518	2232	1.8(10)-231	Escherichia coli	b1854	[pn:pyruvate kinase a] [gn:pyka]
CONTIG323	16823587_f3_8	699	6361	240	80	196	1.0(10)-15	Escherichia coli	b2809	[pn:hypothetical protein]
CONTIG323	10651717_c1_11	700	6362	498	166	760	1.7(10)-75	Plasmid pSW200	L42525	or:plasmid psw200 gn:mobb le:2345 re:2830 di:direct sr:plasmid psw200 dna
CONTIG323	26681536_c1_12	701	6363	213	71	270	1.5(10)-23	Plasmid pSW200	L42525	or:plasmid psw200 gn:mobb le:2834 re:3049 di:direct sr:plasmid psw200 dna
CONTIG323	5130252_c3_15	702	6364	336	112	455	3.6(10)-43	Plasmid pSW200	L42525	or:plasmid psw200 gn:moba le:1657 re:3156 di:direct sr:plasmid psw200 dna

CONTIG323	24783153_c3_16	703	6365	708	236	967	2.0(10)-97	Plasmid pSW200	L42525	or:plasmid psw200 gn:moba lc:1657 re:3156 di:direct sr:plasmid psw200 dna
CONTIG324	24088337_f2_4	704	6366	3273	1091	276	1.5(10)-23	Escherichia coli	b1350	[pn:exodeoxyribonuclease viii] [gn:rece]
CONTIG324	3914843_f2_5	705	6367	1095	365	259	4.7(10)-44	Escherichia coli	JN0845	enterohemolysin 1 - escherichia coli
CONTIG324	22744032_f2_6	706	6368	216	72	244	8.3(10)-21	Escherichia coli	b1346	[pn:hypothetical protein]
CONTIG324	16143775_f3_8	707	6369	210	70	196	1.0(10)-15	Salmonella typhimurium	AF001386	[dc:salmonella typhimurium prophage-like element gifsy-1, partial sequence.] [nt:orf-3, similar to orf sequence of e coli ""rac""]
CONTIG324	23697218_f3_19	708	6370	1251	417	1525	1.5(10)-156	Escherichia coli	b1345	[pn:hypothetical protein]
CONTIG325	16298292_f1_4	709	6371	252	84	223	1.3(10)-18	Escherichia coli	b3184	[pn:hypothetical 35.0 kd protein in dacb-rpma intergenic region] [gn:yhbce]
CONTIG325	34588378_f1_5	710	6372	1191	397	1569	3.2(10)-161	Escherichia coli	b3183	[pn:hypothetical 43.3 kd gtp-binding protein in dacb-rpma intergenic region] [gn:yhbz]
CONTIG325	16437552_f2_13	711	6373	366	122	522	2.8(10)-50	Escherichia coli	b3186	[pn:50s ribosomal subunit protein t21] [gn:rplu]
CONTIG325	9777178_f2_14	712	6374	843	281	1077	4.4(10)-109	Escherichia coli	b3184	[pn:hypothetical 35.0 kd protein in dacb-rpma intergenic region] [gn:yhbce]
CONTIG325	16587811_f2_22	713	6375	480	160	670	6.0(10)-66	Escherichia coli	b3181	[pn:grea]
CONTIG325	23616702_f3_23	714	6376	258	86	418	3.0(10)-39	Escherichia coli	b3185	[pn:50s ribosomal subunit protein t27] [gn:rpsa]
CONTIG325	21666317_c1_35	715	6377	1095	365	736	6.0(10)-73	Escherichia coli	b4112	[pn:sensor protein bass/pmrh] [gn:bass]
CONTIG325	31437785_c2_39	716	6378	375	125	461	8.4(10)-44	Escherichia coli	b3180	[pn:hypothetical 10.8 kd protein in ftsj-grea intergenic region] [gn:yhby]
CONTIG325	24651051_c2_42	717	6379	669	223	530	4.0(10)-51	Escherichia coli	b4113	[pn:transcriptional regulatory protein basr/pmrh] [gn:basr]
CONTIG325	3948541_c3_51	718	6380	1443	481	2243	1.2(10)-232	Escherichia coli	b3182	[pn:d-alanyl-l-d-alanine carboxypeptidase, fraction b] [gn:"]

CONTIG326	10994040_c1_37	719	6381	696	232	128	2.7(10)-17	Mycoplasma sp.	P43641	modification methylase muni (ec 2.1.1.72) (adenine-specific methyltransferase muni) (m.muni).
CONTIG326	32664142_c1_38	720	6382	768	256	503	3.0(10)-48	Escherichia coli	b1560	[pn:hypothetical protein]
CONTIG326	23708141_c2_45	721	6383	531	177	130	1.0(10)-8	Escherichia coli	b1147	[pn:hypothetical protein]
CONTIG326	2151943_c2_47	722	6384	570	190	184	1.8(10)-14	Escherichia coli	b2357	[pn:hypothetical protein] [gn:yfdn]
CONTIG326	24422952_c2_49	723	6385	417	139	210	3.2(10)-17	Escherichia coli	b0550	[pn:hypothetical protein] [gn:rus]
CONTIG326	32070417_c2_50	724	6386	456	152	279	1.6(10)-24	Escherichia coli	b0551	[pn:hypothetical protein] [gn:ybcq]
CONTIG326	4416592_c3_57	725	6387	936	312	136	5.2(10)-7	Bacteriophage SPP1	S43811	gene 38 protein - phage spp1
CONTIG326	35657508_c3_58	726	6388	375	125	178	8.1(10)-14	Escherichia coli	b4043	[pn:lexa] [gn:lexa]
CONTIG326	12298415_c3_60	727	6389	216	72	329	8.1(10)-30	Escherichia coli	b1560	[pn:hypothetical protein]
CONTIG327	22369627_f1_1	728	6390	1446	482	765	5.0(10)-76	Ralstonia solanacearum	A36929	virulence regulatory protein vsrb - pseudomonas solanacearum
CONTIG327	30746031_f1_3	729	6391	1386	462	1149	1.0(10)-116	Escherichia coli	b4052	[pn:replicative dna helicase] [gn:dnab]
CONTIG327	24072317_f3_15	730	6392	888	296	136	5.2(10)-7	Bacillus subtilis	soj	[pn:hypothetical protein]
CONTIG327	12511376_f3_16	731	6393	1725	575	95	0.11	Agrobacterium rhizogenes	P05683	possible replication protein b.
CONTIG327	33798336_f3_19	732	6394	804	268	91	0.02999	Hyphomicrobium sp.	Y08074	[de:hyphomicrobium sp. mxaf gene, partial, strain b 69.] [pn:methanol dehydrogenase] [gn:mxaf] [nt:alpha-subunit]
CONTIG328	32505382_f1_5	733	6395	855	285	884	1.3(10)-88	Escherichia coli	b1226	[pn:respiratory nitrate reductase I delta chain] [gn:nari]
CONTIG328	36049181_f2_9	734	6396	1557	519	2592	1.3(10)-269	Escherichia coli	b1225	[pn:respiratory nitrate reductase I beta chain] [gn:narh]
CONTIG328	4771955_f3_12	735	6397	3840	1280	6414	0	Escherichia coli	b1224	[pn:respiratory nitrate reductase I alpha chain] [gn:narg]
CONTIG328	16527216_f3_17	736	6398	273	91	360	4.2(10)-33	Escherichia coli	b1227	[pn:respiratory nitrate reductase I gamma chain] [gn:nari]

CONTIG329	2863535_f1_3	737	6399	897	299	252	1.2(10)-21	Haemophilus influenzae	HI0359	[pn:gb]
CONTIG329	2214012_f1_4	738	6400	633	211	753	9.5(10)-75	Escherichia coli	b2700	[pn:hypothetical 17.6 kd protein in mltb-reca intergenic region] [gn:ygad]
CONTIG329	33595376_f1_7	739	6401	588	196	931	1.3(10)-93	Escherichia coli	b2697	[pn:alanyl-tRNA synthetase] [gn:alas]
CONTIG329	6034638_f2_9	740	6402	759	253	327	1.3(10)-29	Bacillus subtilis	yigB	[pn:hypothetical protein]
CONTIG329	1442277_f2_11	741	6403	516	172	746	5.2(10)-74	Escherichia coli	b2698	[pn:regulatory protein recx] [gn:oraa]
CONTIG329	16307256_f3_15	742	6404	912	304	409	2.7(10)-38	Haemophilus influenzae	HI0362	[pn:adhesin b precursor] [gn:fima]
CONTIG329	15679167_f3_16	743	6405	1095	365	1601	1.3(10)-164	Escherichia coli	b2699	[pn:reca protein] [gn:reca]
CONTIG33	36343781_f1_2	744	6406	240	80	213	2.3(10)-17	Escherichia coli	b1486	[pn:hypothetical protein]
CONTIG330	23439000_c2_40	745	6407	330	110	119	1.5(10)-7	Haemophilus influenzae	HI1250	[pn:hypothetical protein]
CONTIG330	5105068_c2_43	746	6408	1260	420	325	2.2(10)-29	Proteus vulgaris	S04739	site-specific dna-methyltransferase (cytosine-specific) (ec2.1.1.73) pvuii - proteus vulgaris
CONTIG331	4027290_c1_32	747	6409	816	272	102	0 0085	Treponema denticola	U84257	or:treponema denticola pn:methyl-accepting chemotaxis protein b gn:dmbc le:1 re:>1107 di:direct
CONTIG331	14652281_c2_34	748	6410	585	195	152	4.7(10)-11	Haemophilus influenzae	HI1418	[pn:hypothetical protein]
CONTIG331	392502_c2_38	749	6411	1881	627	1007	1.2(10)-101	Bacteriophage P4	P10277	putative p4-specific dna primase (ec 2.7.7.-)
CONTIG331	20491562_c3_40	750	6412	393	131	104	5.7(10)-6	Escherichia coli	b2624	[pn:prophage cp4-57 regulatory protein alpa] [gn:alpa]
CONTIG332	23993956_f1_1	751	6413	975	325	1387	6.2(10)-142	Escherichia coli	b0025	[pn:hypothetical 34.6 kd protein in rpst-iles intergenic region] [gn:yaac]
CONTIG332	23464537_f1_2	752	6414	2862	954	4572	0	Escherichia coli	b0026	[pn:isoleucyl-tRNA synthetase] [gn:iles]
CONTIG332	5209791_f2_10	753	6415	549	183	638	1.5(10)-62	Escherichia coli	b0028	[pn:probable fkb-type 16 kd peptidyl-prolyl cis- trans isomerase]
CONTIG332	5098753_f3_15	754	6416	510	170	739	2.8(10)-73	Escherichia coli	b0027	[pn:lipoprotein signal peptidase] [gn:lspl]

CONTIG332	34614462_f3_16	755	6417	987	329	1496	1.8(10)-153	Escherichia coli	b0029	[pn:lytb protein] [gn:lytb]
CONTIG333	23556562_f1_4	756	6418	384	128	397	5.0(10)-37	Escherichia coli	b4168	[pn:hypothetical 16.9 kd protein in psd-amib intergenic region] [gn:yjee]
CONTIG333	32625456_f1_5	757	6419	1368	456	1651	6.5(10)-170	Escherichia coli	b4169	[pn:n-acetylmutamoyl-L-alanine amidase precursor] [gn:amib]
CONTIG333	4307943_f1_6	758	6420	1818	606	2103	8.4(10)-218	Escherichia coli	b4170	[pn:dna mismatch repair protein mutI] [gn:mutI]
CONTIG333	33414068_f1_8	759	6421	324	108	340	5.5(10)-31	Escherichia coli	b4172	[pn:host factor-i] [gn:hfq]
CONTIG333	21907291_f3_23	760	6422	1692	564	2008	9.8(10)-208	Escherichia coli	b4167	[pn:hypothetical 54.7 kd protein in psd-amib intergenic region] [gn:yjee]
CONTIG333	11022125_f3_24	761	6423	225	75	295	3.2(10)-26	Escherichia coli	b4168	[pn:hypothetical 16.9 kd protein in psd-amib intergenic region] [gn:yjee]
CONTIG333	25509662_f3_26	762	6424	954	318	1439	1.8(10)-147	Escherichia coli	b4171	[pn:trna delta-2-isopentenylpyrophosphate] [gn:miaa]
CONTIG333	32033567_f3_27	763	6425	372	124	586	4.7(10)-57	Escherichia coli	b4173	[pn:gtp-binding protein hflx] [gn:hflx]
CONTIG333	12928592_c3_67	764	6426	1251	417	1857	9.8(10)-192	Escherichia coli	b4166	[pn:hypothetical 43.1 kd protein in psd-amib intergenic region] [gn:yjee]
CONTIG334	35362692_f2_8	765	6427	273	91	449	1.6(10)-42	Escherichia coli	b0954	[pn:d-3-hydroxydecanoyl-acyl carrier-protein] [gn:fabA]
CONTIG334	6283552_f2_16	766	6428	450	150	117	6.4(10)-7	Pseudomonas aeruginosa	JQ0133	[hypothetical 26.4k protein - pseudomonas aeruginosa]
CONTIG334	660278_f3_29	767	6429	315	105	113	1.6(10)-6	Haemophilus influenzae	H11343	[pn:nitrogen fixation protein] [gn:nifs]
CONTIG334	25634630_c1_39	768	6430	1257	419	1795	3.7(10)-185	Escherichia coli	b0950	[pn:pqia] [gn:pqia]
CONTIG334	2463131_c2_43	769	6431	231	77	111	1.2(10)-5	Escherichia coli	b0951	[pn:pqib] [gn:pqib]
CONTIG334	14661713_c2_44	770	6432	579	193	688	7.4(10)-68	Escherichia coli	b0952	[pn:hypothetical protein]
CONTIG334	21541091_c3_45	771	6433	2025	675	3149	0	Escherichia coli	b0948	[pn:hypothetical protein] [gn:ycby]
CONTIG334	4688202_c3_46	772	6434	1908	636	2661	6.2(10)-277	Escherichia coli	b0949	[pn:hypothetical protein] [gn:ycbh]
CONTIG334	34039693_c3_50	773	6435	1656	552	2259	2.5(10)-234	Escherichia coli	b0951	[pn:pqib] [gn:pqib]

CONTIG335	156328_c1_33	774	6436	399	133	91	0.0008	Escherichia coli	b2354	[pn:hypothetical protein]
CONTIG335	4100463_c1_34	775	6437	1074	358	160	3.3(10)-9	unclassified	JC4865	contractile tail sheath protein - pseudomonas aeruginosaphage ps17
CONTIG335	31427007_c2_38	776	6438	582	194	199	1.7(10)-15	unclassified	JC4865	contractile tail sheath protein - pseudomonas aeruginosaphage ps17
CONTIG335	23471062_c2_39	777	6439	525	175	146	2.0(10)-10	no gb taxonomy match	JC5192	,
CONTIG335	6020968_c2_41	778	6440	1539	513	98	0.22	Archaeoglobus fulgidus	E69444	[pn:chromosome segregation protein (smc1) homolog]
CONTIG335	4040875_c3_49	779	6441	219	73	137	1.8(10)-9	Bacteriophage P2	P51772	tail protein x (gpx).
CONTIG335	34431916_c3_52	780	6442	309	103	147	4.4(10)-9	Escherichia coli	b1372	[pn:hypothetical protein]
CONTIG336	3959462_f1_2	781	6443	906	302	1083	1.0(10)-109	Escherichia coli	b4211	[pn:hypothetical 29.7 kD protein in rplI-cpD intergenic region] [gn:ytfG]
CONTIG336	34647781_f1_3	782	6444	843	281	272	9.0(10)-24	Bacillus subtilis	ybfI	[pn:hypothetical protein]
CONTIG336	26604652_f1_4	783	6445	984	328	1215	1.1(10)-123	Escherichia coli	b4210	[pn:hypothetical 35.5 kD protein in rplI-cpD intergenic region] [gn:ytfF]
CONTIG336	19616637_f2_14	784	6446	699	233	1036	9.8(10)-105	Escherichia coli	b4209	[pn:hypothetical protein] [gn:ytfE]
CONTIG336	34037501_c1_33	785	6447	417	139	550	3.1(10)-53	Escherichia coli	b4212	[pn:hypothetical protein] [gn:ytfH]
CONTIG336	32214687_c2_35	786	6448	1662	554	1202	2.5(10)-122	Escherichia coli	b4355	[pn:methyl-accepting chemotaxis protein i] [gn:tsr]
CONTIG337	22864163_f1_1	787	6449	720	240	1125	3.6(10)-114	Escherichia coli	b2565	[pn:dna repair protein reco] [gn:reco]
CONTIG337	12539057_f1_2	788	6450	753	251	1131	8.4(10)-115	Escherichia coli	b2564	[pn:pyridoxal phosphate biosynthetic protein pdxJ] [gn:pdxJ]
CONTIG337	24627067_f2_11	789	6451	435	145	699	5.0(10)-69	Escherichia coli	b2566	[pn:gtp-binding protein] [gn:era]
CONTIG337	19687915_f2_17	790	6452	936	312	815	2.6(10)-81	Escherichia coli	b2428	[pn:hypothetical protein] [gn:yfeU]
CONTIG337	3916713_f2_18	791	6453	1374	458	702	2.3(10)-69	Bacillus subtilis	ybbF	[pn:hypothetical protein]
CONTIG337	33728143_f2_19	792	6454	639	213	774	5.7(10)-77	Escherichia coli	b2560	[pn:hypothetical 21.9 kD protein in purI-dpJ intergenic region] [gn:yfHb]

CONTIG337	20720005_f2_20	793	6455	564	188	687	9.4(10)-68	Escherichia coli	b2559	[pn:hypothetical 20.0 kd protein in purl-dpj intergenic region] [gn:yfhc]
CONTIG337	32120791_f3_25	794	6456	543	181	611	1.1(10)-59	Escherichia coli	b2563	[pn:dpj protein] [gn:acps]
CONTIG337	7133415_c1_36	795	6457	288	96	95	0.00058	Mycobacterium leprae	Z70722	[de:mycobacterium leprae cosmid b1770.] [pn:probable phosphoprotein phosphatase] [gn:ppp] [nt.mlb1770.13c, ppp; putative phosphoprotein]
CONTIG337	15631650_c1_39	796	6458	891	297	1094	7.0(10)-111	Escherichia coli	b2561	[pn:hypothetical protein in purl-dpj intergenic region] [gn:yfhh]
CONTIG337	34425883_c2_44	797	6459	819	273	977	1.8(10)-98	Escherichia coli	b2558	[pn:hypothetical 53.2 kd protein in purl-dpj intergenic region] [gn:yfhf]
CONTIG337	15813833_c3_61	798	6460	306	102	468	1.5(10)-44	Escherichia coli	b2562	[pn:hypothetical protein] [gn:yfhf]
CONTIG338	26301586_f2_11	799	6461	1548	516	2212	2.3(10)-229	Escherichia coli	b2011	[pn:exodeoxyribonuclease i] [gn:sbeb]
CONTIG338	30663417_c1_29	800	6462	1167	389	1330	6.9(10)-136	Escherichia coli	b2008	[pn:hypothetical 40.0 kd protein in cobu-sbeb intergenic region] [gn:yeec]
CONTIG338	627287_c1_30	801	6463	384	128	589	2.2(10)-57	Escherichia coli	b2007	[pn:hypothetical protein]
CONTIG338	3145787_c2_31	802	6464	930	310	1209	4.5(10)-123	Escherichia coli	b2015	[pn:hypothetical protein]
CONTIG338	4120381_c2_34	803	6465	1182	394	1718	5.2(10)-177	Escherichia coli	b2010	[pn:yeec] [gn:yeec]
CONTIG338	14492842_c3_39	804	6466	1371	457	2127	2.3(10)-220	Escherichia coli	b2014	[pn:hypothetical 49.8 kd transport protein in sbcb 3'''region] [gn:yeef]
CONTIG338	29695755_c3_45	805	6467	525	175	569	3.0(10)-55	Escherichia coli	b2009	[pn:hypothetical 18.1 kd protein in phse 5'''region] [gn:sbmc]
CONTIG339	22073430_f2_23	806	6468	195	65	218	4.7(10)-18	Escherichia coli	D90862	or:escherichia coli gn:cvpa lc:13907 re:14203 di:direct sr:escherichia coli (stram:k12) dna, clone_lib:kohara lambda minise nt:similar to [pir accession number a04446]
CONTIG339	1445258_c1_28	807	6469	819	273	778	2.1(10)-77	Escherichia coli	b2313	[pn:colicin v production protein] [gn:cvpa]
CONTIG339	30353282_c1_29	808	6470	1551	517	2388	5.2(10)-248	Escherichia coli	b2312	[pn:amidophosphoribosyltransferase] [gn:purf]

CONTIG339	12244766_c1_32	809	6471	759	253	951	1.0(10)-95	Escherichia coli	b2308	[pn:histidine transport system permease protein hisq] [gn:hisq]
CONTIG339	36042669_c2_33	810	6472	464	154	404	9.1(10)-38	Escherichia coli	b2314	[pn:dedd protein] [gn:dedd]
CONTIG339	9766650_c2_41	811	6473	987	329	1107	2.8(10)-112	Escherichia coli	b2310	[pn:lysine-arginine-ornithine-binding periplasmic protein precursor] [gn:argt]
CONTIG339	24705382_c3_47	812	6474	216	72	141	6.7(10)-10	Escherichia coli	D90862	or:escherichia coli gn:cypa le:13892 re:14173 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [swissprot accession number p03820];
CONTIG339	22391387_c3_49	813	6475	612	204	864	1.7(10)-86	Escherichia coli	b2311	[pn:3-octaprenyl-4-hydroxybenzoate carboxy-lyase] [gn:ubix]
CONTIG339	1174038_c3_51	814	6476	804	268	1160	7.0(10)-118	Escherichia coli	b2309	[pn:histidine-binding periplasmic protein hisj] [gn:hisj]
CONTIG339	25431631_c3_52	815	6477	717	239	1070	2.5(10)-108	Escherichia coli	b2307	[pn:histidine transport system permease protein hism] [gn:hism]
CONTIG340	34004425_f2_9	816	6478	927	309	1467	2.1(10)-150	Escherichia coli	b1344	[pn:hypothetical protein] [gn:ydao]
CONTIG340	24320165_c1_32	817	6479	1164	388	572	1.5(10)-55	Escherichia coli	b1885	[pn:methyl-accepting chemotaxis protein iv] [gn:tap]
CONTIG340	36221037_c1_33	818	6480	999	333	1494	2.8(10)-153	Escherichia coli	b1342	[pn:hypothetical protein]
CONTIG340	867076_c2_38	819	6481	1401	467	2143	4.9(10)-222	Escherichia coli	b1343	[pn:atp-dependent rna helicase dbpa] [gn:dbpa]
CONTIG340	1959386_c3_40	820	6482	522	174	250	1.8(10)-21	Escherichia coli	AF044503	[de:escherichia coli strain ec11 unknown (498), hcp gene, complete cds;and rhsg accessory genetic element vrg protein, core component anddsorf-g1 genes, complete cds] [pn:unknown] [gn:498]
CONTIG341	5992932_f1_3	821	6483	657	219	967	2.0(10)-97	Escherichia coli	b1662	[pn:riboflavin synthase alpha chain] [gn:ribe]
CONTIG341	33854677_f1_7	822	6484	1332	444	1429	2.2(10)-146	Escherichia coli	b1659	[pn:hypothetical transcriptional regulator in cfa- purr intergenic region] [gn:ydhb]

CONTIG341	35673775_f2_17	823	6485	837	279	1176	1.3(10)-119	Escherichia coli	b1657	[pn:hypothetical protein]
CONTIG341	33630193_c1_33	824	6486	327	109	93	0.00031	Corynebacterium glutamicum	U85507	or:corynebacterium glutamicum pn:unknown gn:orf6 le:3532 re:4290 di:complement
CONTIG341	23992051_c1_45	825	6487	1395	465	1790	1.2(10)-184	Escherichia coli	b1663	[pn:hypothetical protein in ribe 5 ^m region] [gn:ydhc]
CONTIG341	16834386_c2_48	826	6488	1032	344	1704	1.6(10)-175	Escherichia coli	b1658	[pn:purine nucleotide synthesis repressor] [gn:purr]
CONTIG341	12988952_c2_51	827	6489	1290	430	1494	2.8(10)-153	Escherichia coli	b1660	[pn:hypothetical 43.4 kd protein in purr-cfa intergenic region] [gn:ydhc]
CONTIG341	36120180_c3_63	828	6490	1173	391	1810	9.4(10)-187	Escherichia coli	b1661	[pn:cyclopropane-fatty-acyl- phospholipid synthase] [gn:cfa]
CONTIG342	17036458_f1_6	829	6491	1091	364	343	1.8(10)-30	Escherichia coli	P22520	colicin v secretion atp-binding protein cvab.
CONTIG342	2926577_f2_7	830	6492	624	208	241	1.7(10)-20	Escherichia coli	b0293	[pn:hypothetical 20.1 kd protein in intf-each intergenic region precursor] [gn:yagz]
CONTIG342	4564068_f2_8	831	6493	687	229	439	1.8(10)-41	Escherichia coli	b0292	[pn:hypothetical 24.5 kd protein in intf-each intergenic region precursor] [gn:yagy]
CONTIG342	7067568_f2_9	832	6494	2601	867	1162	4.4(10)-118	Escherichia coli	b0291	[pn:hypothetical 91.2 kd protein in intf-each intergenic region precursor] [gn:yagx]
CONTIG342	35806508_f3_11	833	6495	828	276	127	3.7(10)-6	Escherichia coli	b1608	[pn:rsta] [gn:rsta]
CONTIG342	32135053_f3_15	834	6496	1740	580	138	5.0(10)-6	Escherichia coli	b0290	[pn:hypothetical 60.0 kd protein in intf-each intergenic region] [gn:yagw]
CONTIG342	14879055_f3_16	835	6497	660	220	319	9.4(10)-29	Escherichia coli	b0289	[pn:hypothetical 28.2 kd protein in intf-each intergenic region] [gn:ada]
CONTIG343	5182963_f1_3	836	6498	1071	357	1273	7.5(10)-130	Escherichia coli	b2213	[pn:ada regulatory protein] [gn:ada]
CONTIG343	10940625_f1_5	837	6499	1668	556	2187	1.1(10)-226	Escherichia coli	b2211	[pn:hypothetical abc transporter in eco-alkb intergenic region] [gn:yoi]
CONTIG343	7130050_f2_10	838	6500	1035	345	1454	5.0(10)-149	Escherichia coli	b2215	[pn:outer membrane protein c precursor] [gn:ompc]
CONTIG343	4119056_f2_11	839	6501	393	131	288	1.8(10)-25	Escherichia coli	b2214	[pn:hypothetical 38.5 kd protein in ada-ompc intergenic region]

CONTIG343	36572037_f2_12	840	6502	618	206	897	5.2(10)-90	Escherichia coli	b2214	[pn: hypothetical 38.5 kd protein in ada-ompC intergenic region]
CONTIG343	12679793_f3_24	841	6503	672	224	843	2.7(10)-84	Escherichia coli	b2212	[pn: alkB protein] [gn: alkB]
CONTIG343	7119075_f3_28	842	6504	1440	480	322	4.5(10)-29	Bacillus subtilis	ykoK	[pn: hypothetical protein]
CONTIG343	16491667_f3_29	843	6505	204	68	93	0.0018	Caenorhabditis elegans	Z81518	[de: caenorhabditis elegans cosmid f28d9, complete sequence] [pn: f28d9 a] [nt: protein predicted using genefinder; preliminary]
CONTIG343	10400826_f3_30	844	6506	977	326	1363	2.2(10)-139	Escherichia coli	b2210	[pn: hypothetical 60.2 kd protein in eco-alkB intergenic region] [gn: yojh]
CONTIG343	23446927_c1_31	845	6507	1401	467	705	1.2(10)-69	Bacillus subtilis	ybaR	[pn: hypothetical protein]
CONTIG344	4197127_f1_12	846	6508	606	202	578	3.3(10)-56	Escherichia coli	b1304	[pn: phage shock protein a] [gn: pspa]
CONTIG344	4551958_f1_13	847	6509	255	85	342	3.3(10)-31	Escherichia coli	b1305	[pn: phage shock protein b] [gn: pspb]
CONTIG344	23463300_f3_26	848	6510	615	205	137	1.8(10)-9	Escherichia coli	b0464	[pn: potential acraB operon repressor] [gn: acrr]
CONTIG344	21601437_f3_37	849	6511	294	98	344	2.1(10)-31	Escherichia coli	b1304	[pn: phage shock protein a] [gn: pspa]
CONTIG344	14713512_f3_38	850	6512	429	143	401	1.8(10)-37	Escherichia coli	b1306	[pn: phage shock protein c] [gn: pspc]
CONTIG344	19649088_f3_39	851	6513	237	79	287	2.2(10)-25	Escherichia coli	b1307	[pn: phage shock protein d] [gn: pspd]
CONTIG344	23494193_c2_53	852	6514	996	332	1387	6.2(10)-142	Escherichia coli	b1303	[pn: hypothetical protein in pspa 5' region] [gn: pspF]
CONTIG344	34102188_c2_55	853	6515	990	330	1302	6.4(10)-133	Escherichia coli	b1293	[pn: peptide transport system permease protein sapB] [gn: sapB]
CONTIG344	32704131_c2_58	854	6516	1041	347	1550	3.2(10)-159	Escherichia coli	b1291	[pn: peptide transport system aip-binding protein sapD] [gn: sapD]
CONTIG344	10392093_c3_68	855	6517	1761	587	2401	2.2(10)-249	Escherichia coli	b1294	[pn: peptide transport periplasmic protein sapa precursor] [gn: sapa]
CONTIG344	24881542_c3_69	856	6518	906	302	1169	7.9(10)-119	Escherichia coli	b1292	[pn: peptide transport system permease protein sapC] [gn: sapC]
CONTIG344	26448807_c3_70	857	6519	825	275	1289	1.5(10)-131	Escherichia coli	b1290	[pn: peptide transport system aip-binding protein sapF] [gn: sapF]

CONTIG345	33617808_f2_11	858	6520	435	145	329	8.1(10)-30	Escherichia coli	b1856	[pn:hypothetical 46.7 kd protein in msbb-ruvb intergenic region] [gn:yebea]
CONTIG345	16303831_c2_48	859	6521	1341	447	1384	1.3(10)-141	Escherichia coli	b0574	[pn:hypothetical protein] [gn:yled]
CONTIG345	24629011_c2_53	860	6522	2496	832	1315	2.7(10)-134	Bacillus subtilis	yvgX	[pn:hypothetical protein]
CONTIG345	1219468_c3_55	861	6523	573	191	584	7.7(10)-57	Escherichia coli	b0572	[pn:hypothetical protein] [gn:ylcb]
CONTIG345	4688752_c3_56	862	6524	381	127	253	9.1(10)-22	Escherichia coli	b0573	[pn:hypothetical protein] [gn:ylcc]
CONTIG345	21520677_c3_58	863	6525	3177	1059	4318	0	Escherichia coli	b0575	[pn:hypothetical protein in phev 5''' region] [gn:ybde]
CONTIG346	878876_f1_1	864	6526	402	134	518	7.7(10)-50	Escherichia coli	b2582	[pn:hypothetical protein in the ung 3''' region] [gn:yfig]
CONTIG346	32617793_f1_3	865	6527	2715	905	3772	0	Escherichia coli	b2584	[pn:hypothetical protein] [gn:yfiq]
CONTIG346	29782832_f2_8	866	6528	783	261	999	8.1(10)-101	Escherichia coli	b2583	[pn:hypothetical protein] [gn:yfip]
CONTIG346	24807932_f2_14	867	6529	1377	459	1923	1.0(10)-198	Escherichia coli	b2585	[pn:cdp-diacylglycerol-serine o-phosphatidyltransferase] [gn:pssa]
CONTIG346	19972900_f3_26	868	6530	423	141	417	3.8(10)-39	Escherichia coli	b2586	[pn:hypothetical 9.9 kd protein in pss-kgtp intergenic region] [gn:yfim]
CONTIG346	50066_c3_52	869	6531	1377	459	1610	1.5(10)-165	Escherichia coli	b2587	[pn:alpha-ketoglutarate permease] [gn:kgtp]
CONTIG347	6658593_f1_1	870	6532	441	147	479	1.0(10)-45	Escherichia coli	AJ224995	[de:escherichia coli ecorii restriction endonuclease gene.] [pn:restriction endonuclease] [gn:ecorii]
CONTIG347	10605292_f1_5	871	6533	1557	519	124	3.2(10)-8	Bacillus subtilis	yerF	[pn:hypothetical protein]
CONTIG347	20722933_f1_6	872	6534	1644	548	93	1.0(10)0	Caenorhabditis elegans	U33058	or:caenorhabditis elegans pn:unc-89 gn:unc-89 le:join(4920 re:4969,5656 di:direct nt giant ig superfamily member located in the middle
CONTIG347	2133550_f3_21	873	6535	1404	468	1121	9.6(10)-114	Pseudomonas alcaligenes	U77945	[de:pseudomonas alcaligenes maturase-related protein gene, completecds.] [pn:maturase-related protein]

CONTIG347	24729507_c2_50	874	6536	204	68	116	1.5(10)-6	Anabaena PCC7120	AF047044	[de:anabaena pcc7120 insertion sequence is1594 putative transposase, complete cds.] [pn:putative transposase] [nt:tnp1594]
CONTIG347	12319757_c2_51	875	6537	1596	532	1528	7.2(10)-157	Escherichia coli	b1961	[pn:dna-cytosine methyltransferase] [gn:dcml]
CONTIG347	35597962_c3_58	876	6538	306	102	176	3.2(10)-13	Pseudomonas atlantica	A32816	hypothetical protein, 33k (insertion sequence is492) -pseudomonas atlantica
CONTIG348	25422808_f1_1	877	6539	1383	461	2037	8.3(10)-211	Escherichia coli	b0211	[pn:regulatory protein dnr and hypothetical yafg] [gn:mltd]
CONTIG348	3393955_f1_6	878	6540	306	102	108	6.7(10)-6	Corynebacterium glutamicum	U85507	or corynebacterium glutamicum pn:unknown gn:orf6 le 3532 re:4290 di:complement
CONTIG348	26687512_f1_7	879	6541	927	309	1370	4.0(10)-140	Escherichia coli	b0208	[pn:hypothetical transcriptional regulator in rnh- dnr intergenic region] [gn:yafc]
CONTIG348	16047027_f2_12	880	6542	192	64	212	2.0(10)-17	Escherichia coli	b0212	[pn:hypothetical protein] [gn:glob]
CONTIG348	24884441_c1_24	881	6543	819	273	1204	1.5(10)-122	Escherichia coli	b0207	[pn:hypothetical 29.4 kd protein in aspu-dnr intergenic region]
CONTIG348	12148381_c1_29	882	6544	873	291	1288	1.8(10)-131	Escherichia coli	b0209	[pn:hypothetical protein in aspu-dnr intergenic region] [gn:yafd]
CONTIG348	6926692_c2_34	883	6545	1191	397	1054	1.2(10)-106	Bacillus subtilis	ytdD	[pn:hypothetical protein]
CONTIG348	24098587_c3_41	884	6546	786	262	771	1.2(10)-76	Escherichia coli	b0210	[pn:hypothetical 23.0 kd protein in aspu-dnr intergenic region]
CONTIG349	31489806_f1_10	885	6547	1011	337	782	8.0(10)-78	Escherichia coli	b1899	[pn:hypothetical protein]
CONTIG349	2907256_f1_11	886	6548	914	305	702	2.3(10)-69	Escherichia coli	b1897	[pn:trehalose phosphatase] [gn:otsb]
CONTIG349	35397937_f2_12	887	6549	420	140	307	1.7(10)-27	Escherichia coli	P52092	hypothetical 9.1 kd protein in araf- fln intergenic region.
CONTIG349	4886041_f2_15	888	6550	609	203	194	1.6(10)-15	Escherichia coli	b0424	[pn:thij protein] [gn:thij]
CONTIG349	32301093_f2_17	889	6551	1554	518	2320	8.5(10)-241	Escherichia coli	b1900	[pn:l-arabinose transport apb-binding protein arag] [gn:arag]

CONTIG349	22123378_f3_22	890	6552	1041	347	1573	1.2(10)-161	Escherichia coli	b1901	[pn:l-arabinose-binding periplasmic protein precursor] [gn:araF]
CONTIG349	34069716_c1_39	891	6553	540	180	539	4.5(10)-52	Escherichia coli	b1902	[pn:ferritin-like protein] [gn:yecI]
CONTIG349	4574191_c1_40	892	6554	1356	452	1123	5.9(10)-114	Escherichia coli	b4123	[pn:anaerobic c4-dicarboxylate transporter dcub] [gn:dcub]
CONTIG349	24880458_c2_56	893	6555	1266	422	713	1.7(10)-70	Escherichia coli	b3754	[pn:hypothetical 51.5 kd protein in rbsr-rsc intergenic region] [gn:yieO]
CONTIG349	32441526_c3_70	894	6556	240	80	171	4.5(10)-13	Escherichia coli	b1903	[pn:hypothetical protein]
CONTIG350	31913255_f2_14	895	6557	636	212	946	3.3(10)-95	Escherichia coli	b2186	[pn:hypothetical 37.8 kd protein in rply-prol intergenic region] [gn:yecK]
CONTIG350	4298562_f2_20	896	6558	717	239	1101	1.3(10)-111	Escherichia coli	b2183	[pn:hypothetical 25.9 kd protein in bcr-rply intergenic region] [gn:yecJ]
CONTIG350	24823252_f2_21	897	6559	1215	405	1519	6.5(10)-156	Escherichia coli	b2182	[pn:bicyclicomycin resistance protein] [gn:bcr]
CONTIG350	15632767_f2_22	898	6560	372	124	460	1.1(10)-43	Escherichia coli	b2181	[pn:hypothetical 12.5 kd protein in bcr 5''' region] [gn:yecG]
CONTIG350	26602187_c1_45	899	6561	399	133	94	0.00339	Listeria innocua	Q01836	protein p60 precursor (invasion-associated protein).
CONTIG350	26439076_c1_47	900	6562	1776	592	2642	6.4(10)-275	Escherichia coli	b2184	[pn:hypothetical 66.4 kd protein in rsua-rply intergenic region] [gn:yecH]
CONTIG350	5103968_c2_51	901	6563	1035	345	1250	2.1(10)-127	Escherichia coli	b2179	[pn:hypothetical 38.1 kd protein in bcr 5''' region] [gn:yecE]
CONTIG350	682093_c3_56	902	6564	906	302	1310	9.0(10)-134	Escherichia coli	b2178	[pn:hypothetical 40.4 kd protein in bcr 5''' region] [gn:yecB]
CONTIG350	16803125_c3_58	903	6565	1644	548	1921	1.6(10)-198	Escherichia coli	b2180	[pn:hypothetical abc transporter in bcr 5''' region] [gn:yecF]
CONTIG350	25885842_c3_64	904	6566	480	160	117	2.3(10)-7	Escherichia coli	S24805	hypothetical protein fwd1566 - escherichia coli
CONTIG350	14504807_c3_65	905	6567	363	121	172	3.5(10)-13	Escherichia coli	P28247	very hypothetical 19.2 kd protein in bcr 3' region.
CONTIG350	20500018_c3_68	906	6568	309	103	343	2.7(10)-31	Escherichia coli	b2185	[pn:50s ribosomal protein l25] [gn:rplY]
CONTIG351	4015938_f1_1	907	6569	1488	496	1348	8.5(10)-138	Bacillus subtilis	ybaR	[pn:hypothetical protein]

CONTIG351	36219711_f1_2	908	6570	846	282	1339	7.7(10)-137	Yersinia enterocolitica	Y13308	[PN:hypothetical protein] [DE:Yersinia enterocolitica plasmid DNA fragment, strain 15673.] [NT:ORF2] [LE:3722] [RE:4588] [DI:complement]
CONTIG351	30275251_f2_16	909	6571	726	242	1028	6.9(10)-104	Yersinia enterocolitica	U58366	or:yersinia enterocolitica pn:arsh gn:arsh le:3823 re:4521 di:direct nt:required for arsenic resistance
CONTIG351	9947125_f3_29	910	6572	1536	512	536	9.5(10)-52	Escherichia coli	b3558	[pn:insertion element is150 hypothetical 33.3 kd protein] [gn:yi5b]
CONTIG351	10979628_c1_32	911	6573	1443	481	942	9.0(10)-95	Rhizobium sp.	P55373	putative transposase y4bf,
CONTIG351	1282876_c2_43	912	6574	465	155	105	4.5(10)-6	Escherichia coli	P19770	insertion element is150 hypothetical 14 kd protein (orf).
CONTIG351	22350087_c2_48	913	6575	375	125	385	9.5(10)-36	Escherichia coli	b3501	[pn:arsenical resistance operon arsefg repressor] [gn:arsf]
CONTIG351	1964202_c2_49	914	6576	1302	434	1649	1.1(10)-169	Escherichia coli	b3502	[pn:arsenical pump membrane protein] [gn:arsb]
CONTIG351	4110263_c2_50	915	6577	435	145	659	8.8(10)-65	Escherichia coli	b3503	[pn:arsenate reductase] [gn:arsc]
CONTIG352	30475831_f1_4	916	6578	624	208	90	0.51	Rattus norvegicus	S54307	myosin heavy chain - rat
CONTIG352	5156338_f1_6	917	6579	486	162	101	9.4(10)-5	Mycobacterium tuberculosis	Z95586	unknown,,micy336.26,micy336.26, len
CONTIG352	35329530_f2_11	918	6580	1326	442	532	2.5(10)-51	Bacteriophage HK97	P49859	portal protein (gp3).
CONTIG352	33694458_f3_14	919	6581	408	136	153	3.6(10)-11	Bacteriophage phi-105	L35561	or:bacteriophage phi-105 pn:holin le:796 re:1170 di:direct sr:bacteriophage phi-105 dna nt:orf2; potential dual start motif; putative
CONTIG352	31922905_f3_15	920	6582	1770	590	611	1.1(10)-59	Escherichia coli	b1149	[pn:hypothetical protein]
CONTIG352	3230287_f3_17	921	6583	876	292	108	0.00035	Haemophilus influenzae	H10714	[pn:atp-dependent clp protease proteolytic component] [gn:clpp]
CONTIG353	5352308_f1_3	922	6584	1251	417	1489	9.6(10)-153	Haemophilus influenzae	H10166	[pn:nitrogen fixation protein] [gn:rmf]
CONTIG353	4900311_f1_5	923	6585	1227	409	1512	3.6(10)-155	Haemophilus influenzae	H10171	[pn:phenolhydroxylase component]

CONTIG353	23600408_f1_11	924	6586	489	163	608	2.2(10)-59	Haemophilus influenzae	H10674	[pn:xanthine guanine phosphoribosyl transferase gpt] [gn:ht0692]
CONTIG353	31257276_f2_12	925	6587	1449	483	1348	8.5(10)-138	Haemophilus influenzae	H10164	[pn:nadh]
CONTIG353	886265_f2_14	926	6588	879	293	617	2.5(10)-60	Haemophilus influenzae	H10167	[pn.hypothetical protein]
CONTIG353	4015843_f2_19	927	6589	1068	356	1529	5.5(10)-157	Escherichia coli	b0231	[pn.hypothetical protein dinp] [gn:dinp]
CONTIG353	25525302_f3_25	928	6590	642	214	586	4.7(10)-57	Haemophilus influenzae	H10168	[pn:nadh]
CONTIG353	16835331_f3_26	929	6591	603	201	672	3.7(10)-66	Haemophilus influenzae	HIN_166	[pn:nadh] [gn:ht0170]
CONTIG353	3402000_f3_27	930	6592	216	72	102	9.3(10)-6	Haemophilus influenzae	H10173	[pn.hypothetical protein]
CONTIG353	897881_c2_41	931	6593	558	186	857	9.0(10)-86	Escherichia coli	b0237	[pn:aminoacyl-histidine dipeptidase precursor] [gn:pepd]
CONTIG353	5283561_c2_42	932	6594	942	314	1379	4.4(10)-141	Escherichia coli	b0237	[pn:aminoacyl-histidine dipeptidase precursor] [gn:pepd]
CONTIG354	32426885_f1_1	933	6595	1701	567	2515	1.8(10)-261	Escherichia coli	b0779	[pn:excision nuclease abc subunit b] [gn:uvrb]
CONTIG354	5113562_f1_5	934	6596	252	84	310	8.4(10)-28	Escherichia coli	b0784	[pn:molybdopterin converting factor, subunit 1] [gn:moad]
CONTIG354	26442752_f1_11	935	6597	444	148	374	1.3(10)-34	Escherichia coli	b0791	[pn.hypothetical protein]
CONTIG354	29941531_f2_18	936	6598	513	171	694	1.7(10)-68	Escherichia coli	b0785	[pn:molybdopterin converting factor, subunit 2] [gn:moae]
CONTIG354	5192562_f3_31	937	6599	1212	404	1473	4.7(10)-151	Escherichia coli	b0781	[pn:molybdenum cofactor biosynthesis protein a] [gn:moaa]
CONTIG354	33208555_f3_32	938	6600	537	179	816	2.0(10)-81	Escherichia coli	b0782	[pn:molybdenum cofactor biosynthesis protein b] [gn:moab]
CONTIG354	22353383_f3_33	939	6601	489	163	768	2.5(10)-76	Escherichia coli	b0783	[pn:molybdenum cofactor biosynthesis protein c] [gn:moac]
CONTIG354	31853402_f3_35	940	6602	711	237	998	1.0(10)-100	Escherichia coli	b0786	[pn.hypothetical protein]
CONTIG354	36582349_c1_45	941	6603	1297	432	1608	2.3(10)-165	Escherichia coli	b0792	[pn.hypothetical protein]
CONTIG354	15907653_c1_48	942	6604	1155	385	1314	3.3(10)-134	Escherichia coli	b0788	[pn.hypothetical protein]

CONTIG354	4194068_c1_54	943	6605	918	306	974	3.7(10)-98	Escherichia coli	b0780	[pn.hypothetical protein]
CONTIG354	24878930_c2_61	944	6606	306	102	454	4.5(10)-43	Escherichia coli	b0790	[pn.hypothetical protein]
CONTIG354	32048331_c2_62	945	6607	1344	448	1686	1.3(10)-173	Escherichia coli	b0789	[pn.hypothetical protein]
CONTIG354	34018807_c3_74	946	6608	717	239	721	2.3(10)-71	Escherichia coli	b0790	[pn.hypothetical protein]
CONTIG355	6350712_f1_4	947	6609	717	239	1055	9.5(10)-107	Escherichia coli	b3651	[pn.spou protein] [gn.spou]
CONTIG355	36134652_f1_5	948	6610	2085	695	3169	0	Escherichia coli	b3652	[pn.dna recombinase] [gn.reg]
CONTIG355	644762_f1_8	949	6611	1425	475	1955	4.0(10)-202	Escherichia coli	b3654	[pn.hypothetical 48.9 kd protein in glts 3'''region] [gn.yice]
CONTIG355	21488907_f2_14	950	6612	330	110	347	1.0(10)-31	Escherichia coli	b3649	[pn.dna-directed rna polymerase omega chain] [gn.rpoz]
CONTIG355	6016411_f2_24	951	6613	1728	576	2085	6.7(10)-216	Escherichia coli	b3655	[pn.hypothetical 62.3 kd protein in glts-selc intergenic region] [gn.yich]
CONTIG355	11223782_f3_26	952	6614	2130	710	3369	0	Escherichia coli	b3650	[pn.diphosphate 3'''-pyrophosphohydrolase] [gn.spot]
CONTIG355	104836_c1_42	953	6615	1215	405	1441	1.2(10)-147	Escherichia coli	b3653	[pn.sodium/glutamate symport carrier protein] [gn.gls]
CONTIG355	24035758_c2_62	954	6616	585	195	632	6.4(10)-62	Escherichia coli	A30374	hypothetical 77k protein (spot 3' region) - escherichia coli
CONTIG356	23962828_f1_8	955	6617	255	85	398	4.0(10)-37	Escherichia coli	b3610	[pn.glutaredoxin 3] [gn.grxc]
CONTIG356	21532290_f1_9	956	6618	1086	362	1613	7.0(10)-166	Escherichia coli	b3608	[pn.l-glycerol 3-phosphate dehydrogenase] [gn.gpsa]
CONTIG356	13066577_f1_10	957	6619	876	292	1374	1.5(10)-140	Escherichia coli	b3607	[pn.serine acetyltransferase] [gn.cyse]
CONTIG356	31515805_f2_15	958	6620	459	153	626	2.7(10)-61	Escherichia coli	b3611	[pn.hypothetical 15.6 kd protein in secb-tdh intergenic region] [gn.yibn]
CONTIG356	602133_f2_16	959	6621	504	168	736	6.0(10)-73	Escherichia coli	b3609	[pn.protein-export protein secb] [gn.sec]
CONTIG356	31773430_c1_32	960	6622	519	173	345	1.6(10)-31	Escherichia coli	P20343	very hypothetical cysx protein.
CONTIG356	24348137_c2_46	961	6623	1587	529	2409	3.2(10)-250	Escherichia coli	b3612	[pn.putative 2,3-bisphosphoglycerate independent phosphoglycerate] [gn.yitbo]

CONTIG356	4393955_c2_47	962	6624	1293	431	1601	1.3(10)-164	Escherichia coli	b3613	[pn:hypothetical 47.5 kd protein in secb-ldh intergenic region] [gn:yibp]
CONTIG356	21509378_c2_48	963	6625	966	322	1034	1.6(10)-104	Escherichia coli	b3614	[pn:hypothetical 30.7 kd protein in secb-ldh intergenic region] [gn:yibq]
CONTIG356	25562927_c3_51	964	6626	417	139	523	2.2(10)-50	Escherichia coli	P15041	very hypothetical 17.7 kd protein in secb region.
CONTIG357	33777166_f1_3	965	6627	606	202	717	6.2(10)-71	Escherichia coli	b2136	[pn:hypothetical 21.4 kd protein in pbpg-cdd intergenic region] [gn:yohd]
CONTIG357	23595075_f1_10	966	6628	432	144	404	9.1(10)-38	Escherichia coli	b2141	[pn:hypothetical 14.6 kd protein in pbpg-cdd intergenic region]
CONTIG357	22048902_f2_25	967	6629	360	120	126	6.0(10)-8	Escherichia coli	U00007	or:escherichia coli pn:yohk le-43789 re:44535 di:direct sr:escherichia coli k12 bbb2600
CONTIG357	4348418_f2_26	968	6630	894	298	1234	1.0(10)-125	Escherichia coli	b2143	[pn:cytidine deaminase] [gn:cdd]
CONTIG357	36580143_f3_41	969	6631	720	240	784	5.0(10)-78	Escherichia coli	b2142	[pn:hypothetical 24.5 kd protein in pbpg-cdd intergenic region] [gn:yohk]
CONTIG357	20989806_f3_42	970	6632	765	255	1098	2.6(10)-111	Escherichia coli	b2144	[pn:sana protein] [gn:sana]
CONTIG357	13804192_c1_50	971	6633	978	326	1378	5.5(10)-141	Escherichia coli	b2140	[pn:hypothetical 35.2 kd protein in pbpg-cdd intergenic region]
CONTIG357	33625277_c1_56	972	6634	537	179	399	3.1(10)-37	Escherichia coli	b2134	[pn:penicillin-binding protein 7 precursor] [gn:pbpg]
CONTIG357	9960917_c2_65	973	6635	930	310	1038	6.0(10)-105	Escherichia coli	b2137	[pn:hypothetical oxidoreductase in pbpg-cdd intergenic region]
CONTIG357	29820255_c2_67	974	6636	645	215	899	3.2(10)-90	Escherichia coli	b2135	[pn:hypothetical 22.4 kd protein in pbpg-cdd intergenic region] [gn:yohc]
CONTIG357	34547640_c2_68	975	6637	267	89	349	6.2(10)-32	Escherichia coli	b2134	[pn:penicillin-binding protein 7 precursor] [gn:pbpg]
CONTIG357	6532628_c3_76	976	6638	1431	477	1491	6.0(10)-153	Escherichia coli	b2138	[pn:hypothetical 43.3 kd protein in pbpg-cdd intergenic region] [gn:yohg]
CONTIG358	35257828_f1_2	977	6639	2559	853	3835	0	Escherichia coli	b1049	[pn:periplasmic glucans biosynthesis protein mdoh] [gn:mdoh]
CONTIG358	4506967_f1_3	978	6640	237	79	333	3.1(10)-30	Escherichia coli	b1050	[pn:hypothetical protein in mdoh-msyb intergenic region] [gn:yock]

CONTIG358	30476516_f2_17	979	6641	1137	379	1610	1.5(10)-165	Escherichia coli	b1055	[pn: hypothetical 40.0 kd protein in hrb 5 ^{'''} region] [gn:ycea]
CONTIG358	23472503_f3_22	980	6642	1614	538	2500	7.2(10)-260	Escherichia coli	b1048	[pn: periplasmic glucans biosynthesis protein mdog precursor] [gn:mdog]
CONTIG358	632292_c1_35	981	6643	621	207	788	1.8(10)-78	Escherichia coli	b1056	[pn: hypothetical 18.7 kd protein in hrb 5 ^{'''} region] [gn:ycei]
CONTIG358	15112506_c2_56	982	6644	957	319	1353	2.5(10)-138	Escherichia coli	b1054	[pn: membrane protein affecting cell division, growth and high temperature survival] [gn:hrb]
CONTIG358	19688586_c2_57	983	6645	1290	430	1516	1.3(10)-155	Escherichia coli	b1053	[pn: hypothetical 43.9 kd protein in msyb-hrb intergenic region] [gn:ycee]
CONTIG358	11132918_c2_65	984	6646	471	157	714	1.3(10)-70	Escherichia coli	b1047	[pn: hypothetical protein]
CONTIG358	32632692_c3_66	985	6647	309	103	392	1.7(10)-36	Escherichia coli	b1059	[pn: hypothetical protein] [gn: sola]
CONTIG358	788387_c3_67	986	6648	651	217	655	2.2(10)-64	Escherichia coli	b1057	[pn: hypothetical protein]
CONTIG358	1985430_c3_73	987	6649	423	141	608	2.2(10)-59	Escherichia coli	b1051	[pn: acidic protein msyb, multicopy suppressor of secy] [gn:msyb]
CONTIG358	11892042_c3_74	988	6650	273	91	90	0.00063	Mycobacterium tuberculosis	Q10700	hypothetical 26.0 kd protein cy49.31c.
CONTIG359	23704667_f1_3	989	6651	1299	433	1955	4.0(10)-202	Escherichia coli	b3780	[pn: rhb] [gn: rhb]
CONTIG359	3157813_f1_4	990	6652	1491	497	1952	8.4(10)-202	Escherichia coli	b3779	[pn: guanosine pentaphosphatase] [gn: gppa]
CONTIG359	36110330_f1_8	991	6653	277	93	344	2.1(10)-31	Escherichia coli	b3775	[pn: peptidyl-prolyl cis-trans isomerase c] [gn: ppic]
CONTIG359	15812950_c1_32	992	6654	405	135	595	5.2(10)-58	Escherichia coli	b3781	[pn: thioredoxin] [gn: trxa]
CONTIG359	32453180_c2_37	993	6655	2031	677	3208	0	Escherichia coli	b3778	[pn: atp-dependent dna helicase rep] [gn: rep]
CONTIG359	4382713_c2_41	994	6656	498	166	643	4.2(10)-63	Escherichia coli	b3784	[pn: putative undecaprenyl-phosphate alpha-n-acetylglucosaminyltransferase] [gn: rfe]
CONTIG359	26599182_c3_44	995	6657	1338	446	2038	6.5(10)-211	Escherichia coli	b3783	[pn: transcription termination factor] [gn: rho]

CONTIG36	7089053_c3_5	996	6658	525	175	891	2.2(10)-89	Escherichia coli	b2580	[pn:uracil-dna glycosylase] [gn:ung]
CONTIG360	6522187_f1_2	997	6659	885	295	949	1.6(10)-95	Klebsiella pneumoniae	AF040380	[de:klebsiella pneumoniae ribosomal protein 111 methyltransferase(prma) gene, partial cds; carbonic anhydrase (cah) and yhdg homologues, complete cds; and small dna binding protein f'] [pn:carbonic anhydrase] [gn:cah]
CONTIG360	4741568_f1_9	998	6660	1149	383	1396	7.0(10)-143	Escherichia coli	b3265	[pn:acrf] [gn:acrf]
CONTIG360	6292163_f2_10	999	6661	1275	425	2007	1.3(10)-207	Escherichia coli	b3256	[pn:biotin carboxylase] [gn:accc]
CONTIG360	30163283_f2_11	1000	6662	291	97	200	3.7(10)-16	Escherichia coli	b3257	[pn:hypothetical 9.1 kd protein in accc-panf intergenic region] [gn:yhdg]
CONTIG360	34569061_f2_14	1001	6663	900	300	1313	4.4(10)-134	Escherichia coli	b3259	[pn:ribosomal protein 111 methyltransferase] [gn:prma]
CONTIG360	33797942_f2_17	1002	6664	312	104	401	1.8(10)-37	Haemophilus influenzae	H10980	[pn:factor-for-inversion stimulation protein] [gn:fis]
CONTIG360	2908507_f2_19	1003	6665	2253	751	809	1.3(10)-94	Bacillus subtilis	ykoW	[pn:hypothetical protein]
CONTIG360	3991262_f3_22	1004	6666	1488	496	1914	9.0(10)-198	Escherichia coli	b3258	[pn:sodium/pantothenate symporter] [gn:panf]
CONTIG360	4556526_f3_25	1005	6667	969	323	1585	6.5(10)-163	Escherichia coli	b3260	[pn:hypothetical 35.9 kd protein in pmra-fis intergenic region] [gn:yhdg]
CONTIG360	26036410_f3_31	1006	6668	233	78	145	6.5(10)-9	Escherichia coli	b3266	[pn:acrf] [gn:acrf]
CONTIG360	16834836_c3_58	1007	6669	654	218	555	9.1(10)-54	Escherichia coli	b3264	[pn:potential acrf/enved operon repressor] [gn:envr]
CONTIG361	16853457_f1_1	1008	6670	918	306	1425	5.9(10)-146	Escherichia coli	b0750	[pn:quinolate synthetase a protein] [gn:nada]
CONTIG361	14457650_f2_13	1009	6671	789	263	881	2.6(10)-88	Escherichia coli	b0751	[pn:pnuc protein] [gn:pnuc]
CONTIG361	33876317_f2_17	1010	6672	1077	359	1703	2.1(10)-175	Escherichia coli	b0754	[pn:phospho-2-dehydro-3-deoxyheptone aldolase]
CONTIG361	34241057_c1_38	1011	6673	1113	371	1434	6.5(10)-147	Escherichia coli	b0756	[pn:aldose 1-epimerase] [gn:galm]

CONTIG361	11995900_c1_42	1012	6674	447	149	149	9.6(10)-11	Escherichia coli	b0753	[pn:hypothetical protein] [gn:ybgs]
CONTIG361	25980277_c1_43	1013	6675	954	318	930	1.7(10)-93	Escherichia coli	b0752	[pn:hypothetical protein] [gn:ybgr]
CONTIG361	877066_c2_47	1014	6676	1182	394	1686	1.3(10)-173	Escherichia coli	b0757	[pn:galactokinase] [gn:galk]
CONTIG361	23572188_c2_50	1015	6677	756	252	1120	1.2(10)-113	Escherichia coli	b0755	[pn:phosphoglycerate mutase 1] [gn:gpmA]
CONTIG361	36541291_c3_57	1016	6678	1218	406	1734	1.1(10)-178	Escherichia coli	b0759	[pn:udp-glucose 4-epimerase] [gn:gale]
CONTIG361	4343818_c3_58	1017	6679	1056	352	1772	1.0(10)-182	Escherichia coli	b0758	[pn:galactose-1-phosphate uridylyltransferase] [gn:galt]
CONTIG362	20177211_f1_1	1018	6680	696	232	798	1.6(10)-79	Escherichia coli	b0489	[pn:hypothetical protein] [gn:ybbk]
CONTIG362	1054782_f1_5	1019	6681	858	286	824	2.8(10)-82	Escherichia coli	b0482	[pn:hypothetical protein] [gn:ybap]
CONTIG362	12913181_f1_6	1020	6682	579	193	666	1.6(10)-65	Escherichia coli	b0481	[pn:hypothetical protein] [gn:ybak]
CONTIG362	2283_f2_13	1021	6683	2640	880	3509	0	Escherichia coli	b0484	[pn:hypothetical protein] [gn:ybar]
CONTIG362	25431562_f3_20	1022	6684	456	152	449	1.6(10)-42	Escherichia coli	b0488	[pn:hypothetical protein] [gn:ybbj]
CONTIG362	6456561_f3_27	1023	6685	1026	342	1248	3.3(10)-127	Escherichia coli	b0479	[pn:fosmidomycin resistance protein] [gn:fsr]
CONTIG362	4735278_c1_29	1024	6686	1698	566	2631	9.4(10)-274	Escherichia coli	b0480	[pn:udp-sugar hydrolase precursor] [gn:ushA]
CONTIG362	21659407_c3_62	1025	6687	444	148	603	7.5(10)-59	Escherichia coli	b0487	[pn:hypothetical protein] [gn:ybbi]
CONTIG362	672192_c3_66	1026	6688	207	69	113	6.7(10)-6	Escherichia coli	b0544	[pn:hypothetical protein] [gn:ybek]
CONTIG363	21666540_f1_5	1027	6689	735	245	1128	1.8(10)-114	Transposon Tn1525	M12900	or:transposon tn1525 gn:p12 le:996 re:>1721 di:direct sr:transposon tn1525 dna nt:putative
CONTIG363	4085387_f3_19	1028	6690	228	76	96	0.00018	Thiobacillus ferrooxidans	AF032884	[de:thiobacillus ferrooxidans n-acetylglucosamine-1-phosphateuridylyltransferase (glmu) gene, partial cds; glucosamine synthase(glms)"] [pn:transposition complex] [gn:tnsa]

CONTIG363	2928432_f3_25	1029	6691	861	287	1457	2.3(10)-149	Cloning vector pKF296	D63840	or:cloning vector pki296 pn:aminoglucoside phosphotransferase in supe host gn:apg3 lc:322 re:1137 di:complement sr:cloning vector pki296 dna nt:cag for gln at the
CONTIG363	21666540_f3_26	1030	6692	786	262	1128	1.8(10)-114	Transposon Tn1525	M12900	or:transposon tn1525 gn:p12 lc:996 re:>1721 di:direct sr:transposon tn1525 dna nt:putative
CONTIG363	6439528_f3_31	1031	6693	255	85	345	1.6(10)-31	Escherichia coli	I77547	hypothetical protein 2 (insertion sequence is903) -escherichia coli
CONTIG363	4772550_c1_32	1032	6694	1665	555	1066	6.5(10)-108	Escherichia coli	b4114	[pn:hypothetical 61.7 kd protein in bass-adiy intergenic region]
CONTIG363	11891882_c1_35	1033	6695	738	246	1268	2.6(10)-129	Salmonella ordonez	S34451	hypothetical protein (insertion sequence is261) - salmonellaordonez plasmid pip173
CONTIG363	25558159_c2_40	1034	6696	821	273	1387	6.2(10)-142	Escherichia coli	X02527	or:escherichia coli lc:199 re 1122 di:direct nt:orf1 (aa 1-307)
CONTIG363	11891882_c2_45	1035	6697	738	246	1268	2.6(10)-129	Salmonella ordonez	S34451	hypothetical protein (insertion sequence is261) - salmonellaordonez plasmid pip173
CONTIG363	2397500_c2_47	1036	6698	999	333	1492	4.7(10)-153	Yersinia pestis	AF053946	[de:yersinia pestis plasmid pcd1, complete plasmid sequence.] [pn:transposase (tn1000) homolog] [gn:tnpa]
CONTIG363	12553761_c3_49	1037	6699	2148	716	2685	1.8(10)-279	Escherichia coli	i56963	transposase (transposons) - escherichia coli
CONTIG364	4979758_f1_7	1038	6700	591	197	571	1.8(10)-55	Escherichia coli	b0622	[pn:hypothetical protein in cspe 5'''region] [gn:ybeg]
CONTIG364	25882937_f1_12	1039	6701	2715	905	1008	9.0(10)-102	Methanobacter ium thermoautotro phicum	MTH1516	[pn:cation-transporting p-atpase pac]
CONTIG364	2350761_f2_26	1040	6702	540	180	370	3.7(10)-34	Escherichia coli	b0607	[pn:hypothetical protein] [gn:ybdq]
CONTIG364	14260803_f3_46	1041	6703	713	238	928	2.7(10)-93	Escherichia coli	b1990	[pn:31.6 kd protein in cobt 3'''region precursor] [gn:erfk]
CONTIG364	19689037_c1_55	1042	6704	1110	370	186	7.7(10)-12	Escherichia coli	b2074	[pn:hypothetical protein]

CONTIG364	16103578_c2_70	1043	6705	477	159	169	7.4(10)-13	Saccharomyces cerevisiae	X85757	or:saccharomyces cerevisiae pn:unknown gn:internal orf g1669 le:6964 re:7365 di:direct sr:baker's yeast
CONTIG364	33632800_c2_77	1044	6706	1344	448	1931	1.3(10)-199	Escherichia coli	b1981	[pn:hypothetical protein] [gn:shia]
CONTIG364	4027332_c3_85	1045	6707	3075	1025	633	2.5(10)-59	Haemophilus influenzae	HI0895	[pn:acriflavine resistance protein] [gn:acrb]
CONTIG364	32523467_c3_88	1046	6708	1551	517	2201	3.5(10)-228	Escherichia coli	b1982	[pn:amp nucleosidase] [gn:amn]
CONTIG365	24237891_f1_12	1047	6709	538	180	509	6.9(10)-49	Escherichia coli	b3939	[pn:cystathionine gamma-synthase] [gn:metb]
CONTIG365	7110281_f2_15	1048	6710	312	104	106	3.5(10)-6	Helicobacter pylori	AC000108	or:helicobacter pylori pn:orf2 le:155 re:595 di:complement nt:orf2 - probable transmembrane regions @ aa 18-36;
CONTIG365	4391268_f2_24	1049	6711	222	74	345	1.6(10)-31	Escherichia coli	b3936	[pn:50s ribosomal protein l31] [gn:rpmel]
CONTIG365	15738762_f2_25	1050	6712	765	255	345	1.6(10)-31	Salmonella typhimurium	P43022	hypothetical 15.6 kd protein in rhat 5' region.
CONTIG365	24266301_c1_46	1051	6713	1080	360	1477	1.8(10)-151	Escherichia coli	b3934	[pn:transcriptional repressor eytr] [gn:eytr]
CONTIG365	31885957_c1_48	1052	6714	459	153	124	1.6(10)-7	Escherichia coli	L06547	or:escherichia coli pn:suppressor protein gn:msga le:92 re:961 di:direct sr:escherichia coli (strain [pn:heat shock protein hslv] [gn:hslv]
CONTIG365	2246056_c1_49	1053	6715	546	182	757	3.6(10)-75	Escherichia coli	b3932	[pn:heat shock protein hslv] [gn:hslv]
CONTIG365	4400693_c1_50	1054	6716	1074	358	1692	3.0(10)-174	Escherichia coli	b3931	[pn:heat shock protein hslu] [gn:hslu]
CONTIG365	32656378_c2_53	1055	6717	2325	775	3256	0	Escherichia coli	b3935	[pn:primosomal protein replication factor] [gn:pria]
CONTIG365	4313842_c3_57	1056	6718	327	109	518	7.7(10)-50	Escherichia coli	b3938	[pn:metf aporepressor] [gn:metj]
CONTIG365	23635316_c3_63	1057	6719	996	332	421	2.0(10)-81	Escherichia coli	b3933	[pn:cell division protein ftsn] [gn:ftsn]
CONTIG366	25676576_f1_4	1058	6720	2142	714	2255	6.5(10)-234	Escherichia coli	b0661	[pn:hypothetical protein] [gn:y1ea]
CONTIG366	34414182_f1_5	1059	6721	474	158	593	8.5(10)-58	Escherichia coli	b0659	[pn:hypothetical protein] [gn:ybey]

CONTIG366	25503555_f1_6	1060	6722	963	321	1269	2.0(10)-129	Escherichia coli	b0658	[pn:hypothetical protein]
CONTIG366	33703178_f2_14	1061	6723	1227	409	1648	1.3(10)-169	Escherichia coli	b0660	[pn:hypothetical protein]
CONTIG366	4532311_f2_17	1062	6724	768	256	1032	2.6(10)-104	Escherichia coli	b0655	[pn:hypothetical protein in gltj 5'''region] [gn:ybej]
CONTIG366	15632327_f3_25	1063	6725	1539	513	2176	1.5(10)-225	Escherichia coli	b0657	[pn:apolipoprotein n-acyltransferase] [gn:nt]
CONTIG366	14897193_c1_35	1064	6726	1188	396	1499	8.5(10)-154	Escherichia coli	b0662	[pn:hypothetical protein]
CONTIG366	4586018_c1_36	1065	6727	297	99	232	1.6(10)-19	Escherichia coli	b0663	[pn:hypothetical protein]
CONTIG366	22678556_c1_37	1066	6728	246	82	139	1.1(10)-9	Escherichia coli	b0667	[pn:hypothetical protein]
CONTIG366	20510955_c2_48	1067	6729	246	82	169	7.4(10)-13	Escherichia coli	b0669	[pn:hypothetical protein]
CONTIG366	10400328_c3_58	1068	6730	378	126	149	9.6(10)-11	Escherichia coli	b0669	[pn:hypothetical protein]
CONTIG367	33828125_f1_9	1069	6731	588	196	736	6.0(10)-73	Escherichia coli	b1158	[pn:dna-invertase pin] [gn:pin]
CONTIG367	13800432_f2_20	1070	6732	501	167	567	4.9(10)-55	Escherichia coli	b1183	[pn:umud protein] [gn:umud]
CONTIG367	21878768_f3_24	1071	6733	531	177	829	8.5(10)-83	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is 1222) -enterobacter agglomerans
CONTIG367	17000680_f3_25	1072	6734	645	215	264	6.2(10)-23	Haemophilus influenzae	H11415	[pn:hypothetical protein]
CONTIG367	11468_f3_26	1073	6735	1023	341	115	0.00016	Bacillus subtilis	xtmA	[pn:pbsx defective prophage terminase] [gn:ykxf]
CONTIG367	859550_f3_30	1074	6736	1299	433	1893	1.5(10)-195	Escherichia coli	b1184	[pn:umuc protein] [gn:umuc]
CONTIG367	16813157_c2_45	1075	6737	360	120	277	2.6(10)-24	Escherichia coli	b1931	[pn:yedg] [gn:yedk]
CONTIG367	284787_c2_50	1076	6738	636	212	98	1.8(10)-5	coliphage T2	P07067	tail fiber protein gp37.
CONTIG367	9823576_c3_61	1077	6739	318	106	496	1.6(10)-47	Escherichia coli	b1931	[pn:yedg] [gn:yedk]
CONTIG368	4964080_c1_40	1078	6740	1146	382	1728	4.5(10)-178	Escherichia coli	b3786	[gn:rffe]

CONTIG368	12969003_c1_44	1079	6741	1266	422	1583	1.1(10)-162	Escherichia coli	b3792	[pn:hypothetical 45.0 kd protein in rffe-rftf intergenic region] [gn:yifj]
CONTIG368	1223875_c2_53	1080	6742	981	327	1423	9.5(10)-146	Escherichia coli	b3785	[pn:hypothetical protein] [gn:yifc]
CONTIG368	32695160_c2_56	1081	6743	696	232	620	1.2(10)-60	Escherichia coli	b3790	[pn:hypothetical 19.6 kd protein in rffe-rftf intergenic region] [gn:yifh]
CONTIG368	23886_c2_59	1082	6744	1425	475	1579	2.7(10)-162	Escherichia coli	b3793	[pn:4-alpha-l-fucosyltransferase] [gn:rftf]
CONTIG368	3949178_c2_60	1083	6745	753	251	1103	7.7(10)-112	Escherichia coli	b3794	[pn:probable udp-n-acetyl-d-mannosaminuronic acid transferase] [gn:rftm]
CONTIG368	31285313_c2_61	1084	6746	984	328	1153	3.8(10)-117	Escherichia coli	b3795	[pn:probable transport protein yifk] [gn:yifk]
CONTIG368	36413932_c3_64	1085	6747	1281	427	1871	3.2(10)-193	Escherichia coli	b3787	[pn:udp-mannac dehydrogenase] [gn:rftd]
CONTIG368	16927331_c3_66	1086	6748	1305	435	1799	1.3(10)-185	Escherichia coli	b3791	[pn:hypothetical 41.9 kd protein in rffe-rftf intergenic region] [gn:yifi]
CONTIG368	14880207_c3_70	1087	6749	1086	362	863	2.1(10)-86	Escherichia coli	b4405	[pn:hypothetical protein]
CONTIG369	12144586_f1_4	1088	6750	873	291	116	0.00024	Chlorella virus SC-1A	U65736	or:chlorella virus sc-1a pn.dna adenine methyltransferase gn:m.ovisi le:51 re:1169 di:direct
CONTIG369	14875251_c3_55	1089	6751	1095	365	1548	5.5(10)-159	Serratia marcescens	U62006	rep protein, rep h2a-putative rep protein; similar to f plasmid rep
CONTIG370	6413317_c1_37	1090	6752	819	273	166	1.0(10)-10	Methanococcus jannaschii	MJ1187	[pn:dinitrogenase reductase activating glycolhydrolase] [gn:drag]
CONTIG370	26056543_c1_42	1091	6753	4371	1457	354	4.4(10)-64	Escherichia coli	b3593	[pn:rha protein precursor] [gn:rha]
CONTIG370	6369787_c2_45	1092	6754	2283	761	656	1.8(10)-64	Escherichia coli	AF044503	[de:escherichia coli strain ccl1 unknown (498), hcp gene, complete cds;and rhsg accessory genetic element vgrg protein, core component anddsorf-g1 genes, complete cds] [pn:vgrg protein]
CONTIG371	4538312_f1_10	1093	6755	1071	357	606	3.6(10)-59	Escherichia coli	b0846	[pn:hypothetical protein]
CONTIG371	32531952_f3_34	1094	6756	738	246	1154	3.1(10)-117	Escherichia coli	b0839	[pn:penicillin-binding protein 6 precursor] [gn:dacc]

CONTIG371	4532942_f3_36	1095	6757	1242	414	1804	4.0(10)-186	Escherichia coli	b0842	[pn:hypothetical protein] [gn:cmr]
CONTIG371	4454693_c1_46	1096	6758	489	163	170	5.7(10)-13	Vibrio cholerae	S81006	or:vibrio cholerae pn:hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nt:28 kda secreted hydrophilic protein; this sequence
CONTIG371	1962837_c1_48	1097	6759	1293	431	1611	1.2(10)-165	Escherichia coli	b3502	[pn:arsenical pump membrane protein] [gn:arsb]
CONTIG371	4119678_c1_49	1098	6760	441	147	605	4.5(10)-59	Escherichia coli	b3503	[pn:arsenate reductase] [gn:arsc]
CONTIG371	10400802_c2_66	1099	6761	1377	459	1517	1.1(10)-155	Escherichia coli	b0845	[pn:hypothetical protein]
CONTIG371	36407965_c2_71	1100	6762	741	247	700	4.0(10)-69	Escherichia coli	b0841	[pn:hypothetical protein]
CONTIG371	21894191_c3_75	1101	6763	429	143	364	1.6(10)-33	Escherichia coli	b3501	[pn:arsenical resistance operon arsefg repressor] [gn:arsr]
CONTIG371	12896930_c3_78	1102	6764	885	295	987	1.5(10)-99	Escherichia coli	b0844	[pn:hypothetical protein]
CONTIG371	2472658_c3_82	1103	6765	801	267	1094	7.0(10)-111	Escherichia coli	b0840	[pn:deoxyribose operon repressor] [gn:deor]
CONTIG372	25500018_f1_2	1104	6766	408	136	636	2.3(10)-62	Escherichia coli	b3294	[pn:50s ribosomal subunit protein 117] [gn:rplq]
CONTIG372	15808568_f1_11	1105	6767	486	162	756	4.5(10)-75	Escherichia coli	b3284	[pn:smg protein] [gn:smg]
CONTIG372	15626037_f1_13	1106	6768	627	209	817	1.6(10)-81	Escherichia coli	b3282	[pn:hypothetical protein in aroC-smg intergenic region] [gn:yrdc]
CONTIG372	6676963_f2_14	1107	6769	366	122	570	2.3(10)-55	Escherichia coli	b3298	[pn:30s ribosomal subunit protein s13] [gn:rpsm]
CONTIG372	34119062_f2_15	1108	6770	624	208	1008	9.0(10)-102	Escherichia coli	b3296	[pn:30s ribosomal subunit protein s4] [gn:rpsd]
CONTIG372	13859837_f2_16	1109	6771	459	153	632	6.4(10)-62	Escherichia coli	b3292	[pn:hypothetical transcriptional regulator in mscL-rplq intergenic region] [gn:yhdm]
CONTIG372	36020676_f2_17	1110	6772	234	78	319	9.4(10)-29	Escherichia coli	P36675	hypothetical 8.1 kd protein in mscL-rplq intergenic region.
CONTIG372	6447956_f2_24	1111	6773	306	102	354	1.8(10)-32	Escherichia coli	b3281	[pn:shikimate dehydrogenase] [gn:aroE]
CONTIG372	24353427_f3_25	1112	6774	393	131	522	2.8(10)-50	Escherichia coli	b3297	[pn:30s ribosomal subunit protein s11] [gn:rpsk]

CONTIG372	26445160_f3_27	1113	6775	1008	336	1641	7.5(10)-169	Escherichia coli	b3295	[pn.rpoa] [gn.rpoa]
CONTIG372	26440705_f3_28	1114	6776	510	170	508	8.8(10)-49	Escherichia coli	b3293	[pn.hypothetical 13.9 kd protein in mscL-rplq intergenic region] [gn.yhdn]
CONTIG372	31735932_f3_38	1115	6777	1200	400	683	2.5(10)-67	Escherichia coli	b3286	[pn.hypothetical protein]
CONTIG372	15751342_f3_39	1116	6778	597	199	744	8.5(10)-74	Escherichia coli	b3283	[pn.hypothetical 18.6 kd protein in aroC-smg intergenic region]
CONTIG372	1228918_c1_45	1117	6779	1323	441	1963	5.7(10)-203	Escherichia coli	b3289	[pn.fimU] [gn.sun]
CONTIG372	25667180_c2_56	1118	6780	1410	470	2235	8.5(10)-232	Escherichia coli	b3290	[pn.trkA protein of the constitutive k+ transport system trk] [gn.trkA]
CONTIG372	29711432_c3_69	1119	6781	528	176	795	3.3(10)-79	Escherichia coli	b3287	[pn.n-formylmethionylaminoacyl-tRNA ornase] [gn.def]
CONTIG372	26660166_c3_70	1120	6782	972	324	1435	5.0(10)-147	Escherichia coli	b3288	[pn.methionyl-tRNA formyltransferase] [gn.fmt]
CONTIG372	23484430_c3_74	1121	6783	459	153	329	8.1(10)-30	Escherichia coli	b3291	[pn.large conductance mechanosensitive channel] [gn.mscL]
CONTIG373	3961086_f1_10	1122	6784	408	136	515	1.6(10)-49	Escherichia coli	b3148	[pn.hypothetical 14.8 kd protein in agai-mtr intergenic region] [gn.yraa]
CONTIG373	6361092_f1_11	1123	6785	600	200	974	3.7(10)-98	Escherichia coli	b3149	[pn.hypothetical 21.1 kd protein in agai-mtr intergenic region] [gn.yraa]
CONTIG373	4312943_f1_12	1124	6786	585	195	693	2.2(10)-68	Escherichia coli	b3150	[pn.hypothetical 20.0 kd protein in agai-mtr intergenic region] [gn.yrap]
CONTIG373	5371093_f2_15	1125	6787	1173	391	949	1.6(10)-95	Escherichia coli	b1621	[pn.pts system, maltose and glucosyl-specific ii abc component] [gn.malX]
CONTIG373	6464836_f2_16	1126	6788	1185	395	658	1.1(10)-64	Bacillus subtilis	patB	[pn.aminotransferase]
CONTIG373	23696933_f2_20	1127	6789	2169	723	1318	1.1(10)-251	Escherichia coli	b3147	[pn.hypothetical 72.8 kd protein in agai-mtr intergenic region]
CONTIG373	13864777_c1_39	1128	6790	885	295	1225	9.1(10)-125	Escherichia coli	b3146	[pn.hypothetical 31.3 kd protein in agai-mtr intergenic region] [gn.yraa]
CONTIG373	2376312_c2_42	1129	6791	339	113	395	8.3(10)-37	Escherichia coli	b3151	[pn.hypothetical 37.3 kd protein in agai-mtr intergenic region] [gn.yraa]
CONTIG374	5995468_f1_1	1130	6792	291	97	426	4.2(10)-40	Escherichia coli	b2606	[pn.50s ribosomal subunit protein 119] [gn.rplS]
CONTIG374	22854707_f1_16	1131	6793	996	332	1524	1.8(10)-156	Escherichia coli	b2594	[pn.fish suppressor protein sfhB] [gn.sfhB]

CONTIG374	6095760_f2_24	1132	6794	1134	378	1646	2.2(10)-169	Escherichia coli	b2601	[pn:phospho-2-dehydro-3-deoxyheptanate aldolase, tyrosensitive] [gn:arof]
CONTIG374	16125281_f2_33	1133	6795	387	129	103	4.5(10)-5	Escherichia coli	D90887	or:escherichia coli gn:yfii le:13236 re:14294 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [swissprot accession number p33643];
CONTIG374	33464032_f2_35	1134	6796	1554	518	2377	7.7(10)-247	Escherichia coli	b2592	[pn:clpb protein] [gn:clpb]
CONTIG374	3384667_f3_36	1135	6797	1599	533	214	1.3(10)-30	Pseudomonas aeruginosa	D28119	or:pseudomonas aeruginosa le:3035 re:4450 di:direct sr:pseudomonas aeruginosa, (strain pao1), dna, (clone ptn100) nt:putative
CONTIG374	29957332_f3_45	1136	6798	1161	387	1630	1.1(10)-167	Escherichia coli	b2600	[pn:chorismate mutase/prephenate dehydrogenase] [gn:tyra]
CONTIG374	6064015_f3_46	1137	6799	933	311	354	1.8(10)-32	Bacillus subtilis	yvrE	[pn:hypothetical protein]
CONTIG374	35413193_f3_50	1138	6800	750	250	1091	1.5(10)-110	Escherichia coli	b2593	[pn:hypothetical 26.3 kd protein in clpb 5'''region] [gn:yfih]
CONTIG374	36359756_f3_51	1139	6801	1077	359	1542	2.3(10)-158	Escherichia coli	b2592	[pn:clpb protein] [gn:clpb]
CONTIG374	29323783_c1_64	1140	6802	699	233	1092	1.1(10)-110	Escherichia coli	b2595	[pn:hypothetical protein]
CONTIG374	35605011_c1_65	1141	6803	396	132	542	2.2(10)-52	Escherichia coli	b2597	[pn:12.7 kd protein in sfhb-phel intergenic region] [gn:yfia]
CONTIG374	32145012_c2_93	1142	6804	429	143	328	1.0(10)-29	Escherichia coli	b2602	[pn:hypothetical protein in arof-rpls intergenic region] [gn:yfil]
CONTIG374	837807_c2_94	1143	6805	600	200	484	3.1(10)-46	Escherichia coli	b2603	[pn:hypothetical protein]
CONTIG374	26292262_c3_104	1144	6806	1179	393	1642	6.0(10)-169	Escherichia coli	b2599	[pn:chorismate mutase-p/prephenate dehydratase] [gn:phea]
CONTIG374	35728790_c3_112	1145	6807	1242	414	1260	1.8(10)-128	Escherichia coli	b2604	[pn:hypothetical protein in rpls 5'''region] [gn:yfin]
CONTIG374	25992337_c3_113	1146	6808	498	166	651	6.2(10)-64	Escherichia coli	b2605	[pn:hypothetical 17.2 kd protein in rpls 5'''region] [gn:yfib]

CONTIG375	3251076_f1_6	1147	6809	816	272	1019	6.2(10)-103	Escherichia coli	b0933	[pn:hypothetical abc transporter atp-binding protein in pepn-pyrd intergenic region] [gn:ycbe]
CONTIG375	13839807_f1_8	1148	6810	249	83	283	6.0(10)-25	Escherichia coli	b0931	[pn:nicotinate phosphoribosyltransferase] [gn:pncl]
CONTIG375	4413568_f2_12	1149	6811	585	195	812	5.4(10)-81	Escherichia coli	b0937	[pn:hypothetical protein] [gn:ycbp]
CONTIG375	4882842_f2_14	1150	6812	1158	386	1803	5.2(10)-186	Escherichia coli	b0935	[pn:hypothetical protein] [gn:ycbn]
CONTIG375	4410443_f2_15	1151	6813	801	267	1066	6.5(10)-108	Escherichia coli	b0934	[pn:hypothetical protein] [gn:ycbm]
CONTIG375	5362907_f3_27	1152	6814	1014	338	1333	3.2(10)-136	Escherichia coli	b0936	[pn:hypothetical protein]
CONTIG375	1292785_c1_50	1153	6815	306	102	410	2.1(10)-38	Escherichia coli	b0946	[pn:hypothetical protein]
CONTIG375	17070301_c3_60	1154	6816	2718	906	3941	0	Escherichia coli	b0932	[pn:aminopeptidase n] [gn:pepn]
CONTIG375	35641405_c3_69	1155	6817	1050	350	1608	2.3(10)-165	Escherichia coli	b0945	[pn:dihydroorotate dehydrogenase] [gn:pyrd]
CONTIG376	204126_f1_5	1156	6818	1404	468	1811	7.4(10)-187	Escherichia coli	b2509	[pn:exodeoxyribonuclease large subunit] [gn:xsea]
CONTIG376	16273437_f2_13	1157	6819	1107	369	1263	8.6(10)-129	Erwinia carotovora	Q99132	extracellular metalloprotease precursor (ec 3.4.24.-)
CONTIG376	31765664_c1_29	1158	6820	437	145	644	3.3(10)-63	Escherichia coli	b2511	[pn:hypothetical protein]
CONTIG376	6534456_c1_30	1159	6821	1599	533	429	4.2(10)-71	Bacillus subtilis	ycfF	[pn:hypothetical protein]
CONTIG376	11207056_c1_36	1160	6822	1491	497	1945	4.7(10)-201	Escherichia coli	b2508	[pn:inosine-5"-monophosphate dehydrogenase] [gn:guab]
CONTIG376	863205_c2_40	1161	6823	348	116	276	3.3(10)-24	Escherichia coli	b2510	[pn:hypothetical protein]
CONTIG376	24319441_c2_46	1162	6824	1686	562	2669	8.8(10)-278	Escherichia coli	b2507	[pn:gmp synthase] [gn:guaa]
CONTIG377	15704432_f1_8	1163	6825	510	170	685	1.5(10)-67	Escherichia coli	b0965	[pn:hypothetical protein]
CONTIG377	160378_f2_11	1164	6826	702	234	541	2.7(10)-52	Escherichia coli	b0959	[pn:hypothetical protein]
CONTIG377	10830131_f3_31	1165	6827	2076	692	2895	1.0(10)-301	Escherichia coli	b0962	[pn:helicase iv] [gn:heli]

CONTIG377	35585843_c1_40	1166	6828	759	253	786	3.1(10)-78	Escherichia coli	b0964	[pn:hypothetical protein]
CONTIG377	32616015_c1_42	1167	6829	255	85	99	5.2(10)-5	Paramecium bursaria	U42580	or:paramecium bursaria chlorella virus 1 gn:a316r le:158299 re:158976 di:direct nt:papk (17x); similar to pbcv-1 orf a41r, encoded
CONTIG377	34406561_c2_51	1168	6830	1197	399	1740	2.5(10)-179	Escherichia coli	b0967	[pn:hypothetical protein]
CONTIG377	23678515_c2_52	1169	6831	348	116	506	1.3(10)-48	Escherichia coli	b0966	[pn:hypothetical protein]
CONTIG377	32453218_c2_61	1170	6832	453	151	627	2.2(10)-61	Escherichia coli	b0961	[pn:hypothetical protein in held 5'" region] [gn:yccf]
CONTIG377	16150193_c2_62	1171	6833	2178	726	2662	4.9(10)-277	Escherichia coli	b0960	[pn:hypothetical protein]
CONTIG377	2533566_c3_67	1172	6834	483	161	714	1.3(10)-70	Escherichia coli	b0963	[pn:hypothetical 17.3 kd protein in held-sert intergenic region] [gn:yccg]
CONTIG378	5267193_f1_8	1173	6835	672	224	779	1.7(10)-77	Escherichia coli	b3552	[pn:hypothetical 22.2 kd lipoprotein in bise-cspa intergenic regi]
CONTIG378	32212756_f2_19	1174	6836	585	195	716	8.0(10)-71	Escherichia coli	b3549	[pn:3-methyladenine dna glycosylase i, constitutive] [gn:tag]
CONTIG378	35742087_f2_25	1175	6837	1170	390	573	1.1(10)-55	Bacillus subtilis	kdgR	[pn:transcriptional regulator]
CONTIG378	24009657_f2_27	1176	6838	942	314	762	1.1(10)-75	Bacillus subtilis	kdgK	[pn:2-keto-3-deoxygluconate kinase]
CONTIG378	20754033_f2_28	1177	6839	1338	446	336	1.5(10)-30	Escherichia coli	b3691	[pn:hypothetical 48.8 kd protein in ibpa-gyrb intergenic region]
CONTIG378	24218902_f2_29	1178	6840	1002	334	1353	2.5(10)-138	Escherichia coli	b3553	[pn:putative 2-hydroxyacid dehydrogenase in bise- cspa intergenic region] [gn:yiae]
CONTIG378	2128201_f3_30	1179	6841	507	169	92	0.028	Escherichia coli	b2321	[pn:div protein] [gn:div]
CONTIG378	16926562_f3_37	1180	6842	552	184	460	1.1(10)-43	Escherichia coli	b3550	[pn:hypothetical 17.1 kd protein in tag-bise intergenic region] [gn:yiae]
CONTIG378	10838453_c1_64	1181	6843	231	77	249	2.8(10)-20	Escherichia coli	b3551	[pn:biotin sulfoxide reductase] [gn:bise]
CONTIG378	12975261_c1_66	1182	6844	375	125	211	2.6(10)-17	Escherichia coli	b3548	[pn:hypothetical 26.0 kd protein in prok-tag intergenic region] [gn:yhiy]
CONTIG378	2110138_c2_69	1183	6845	324	108	283	6.0(10)-25	Escherichia coli	b3554	[pn:hypothetical 30.2 kd protein in bise-cspa intergenic region] [gn:yiaf]

CONTIG378	21503156_c2_70	1184	6846	294	98	354	1.8(10)-32	Escherichia coli	b3556	[pn:cold shock protein cspa]
CONTIG378	6726562_c2_80	1185	6847	534	178	265	3.7(10)-27	Escherichia coli	b3548	[pn:hypothetical 26.0 kd protein in prok-tag intergenic region] [gn:yhiy]
CONTIG378	36463138_c2_83	1186	6848	1287	429	1411	1.8(10)-144	Escherichia coli	b3546	[pn:64.9 kd protein in prok-tag intergenic region] [gn:yhiw]
CONTIG378	4769752_c3_96	1187	6849	2232	744	2986	0	Escherichia coli	b3551	[pn:biotin sulfoxide reductase] [gn:bisc]
CONTIG378	22659625_c3_102	1188	6850	1224	408	1401	2.1(10)-143	Escherichia coli	b3547	[pn:hypothetical 43.0 kd protein in prok-tag intergenic region] [gn:yhix]
CONTIG379	14580087_fl_8	1189	6851	1194	398	956	3.0(10)-96	Escherichia coli	b1163	[pn:hypothetical protein]
CONTIG379	6855218_c1_40	1190	6852	858	286	266	3.8(10)-23	Escherichia coli	b1559	[pn:hypothetical protein]
CONTIG379	35283591_c2_44	1191	6853	699	233	710	3.5(10)-70	Bacteriophage phi-80	P14814	replication protein 14.
CONTIG379	25628816_c2_45	1192	6854	312	104	129	1.3(10)-8	Bacillus subtilis	ydfG	[pn:hypothetical protein]
CONTIG379	9974138_c2_48	1193	6855	486	162	101	1.2(10)-5	Escherichia coli	b1651	[pn:hypothetical protein] [gn:gloa]
CONTIG379	23542083_c2_51	1194	6856	474	158	510	5.4(10)-49	Escherichia coli	b0550	[pn:hypothetical protein] [gn:rus]
CONTIG379	9896067_c2_53	1195	6857	894	298	1229	3.5(10)-125	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG379	35320333_c3_56	1196	6858	459	153	252	1.2(10)-21	Bacteriophage phi-80	P14820	regulatory protein cii.
CONTIG379	13086467_c3_57	1197	6859	990	330	1068	4.0(10)-108	Bacteriophage phi-80	P14815	replication protein 15.
CONTIG379	4145052_c3_64	1198	6860	267	89	157	1.3(10)-11	Escherichia coli	b1061	[pn:dna-damage-inducible protein i] [gn:dini]
CONTIG379	23609515_c3_68	1199	6861	294	98	419	2.3(10)-39	Enterobacter agglomerans	A38965	hypothetical protein a (insertion sequence is1222) -enterobacter agglomerans
CONTIG38	24714410_c3_7	1200	6862	783	261	1109	1.8(10)-112	Escherichia coli	b4371	[pn:hypothetical 37.6 kd protein in dna1-hold intergenic region] [gn:yji]
CONTIG380	12695760_fl_15	1201	6863	938	313	1475	3.0(10)-151	Escherichia coli	b2114	[pn:methionyl-tRNA synthetase] [gn:metg]

CONTIG380	3992202_f2_17	1202	6864	1101	367	136	4.7(10)-6	Haemophilus influenzae	U38617	or:haemophilus influenzae pn:hia gn:hia le:251 re:3547 di:direct sr:haemophilus influenzae strain=nontypeable strain 11
CONTIG380	35833441_f2_18	1203	6865	1401	467	1336	1.6(10)-136	Haemophilus influenzae	HI0949	[pn:gamma-aminobutyric acid transaminase]
CONTIG380	792331_f2_19	1204	6866	1485	495	1247	4.2(10)-127	Haemophilus influenzae	HIN_937	[pn:l-2,4-diaminobutyrate decarboxylase] [gn:hi0946]
CONTIG380	22112882_f2_28	1205	6867	399	133	318	1.2(10)-28	Escherichia coli	b2107	[pn:hypothetical protein]
CONTIG380	12932325_f3_42	1206	6868	492	164	154	2.8(10)-11	Escherichia coli	b3550	[pn:hypothetical 17.1 kd protein in tag-bisc intergenic region] [gn:yiaa]
CONTIG380	36042042_c1_54	1207	6869	2250	750	1965	3.5(10)-203	Escherichia coli	b0981	[pn:hypothetical protein in appa 3'''region] [gn:yccc]
CONTIG380	33463915_c1_61	1208	6870	504	168	475	2.7(10)-45	Escherichia coli	b2104	[pn:hypothetical protein] [gn:thim]
CONTIG380	24473131_c2_68	1209	6871	492	164	487	1.5(10)-46	Escherichia coli	b0982	[pn:hypothetical protein] [gn:yccy]
CONTIG380	21515768_c3_78	1210	6872	1140	380	1734	1.1(10)-178	Escherichia coli	b2113	[pn:mrp] [gn:mrp]
CONTIG380	24805387_c3_80	1211	6873	1203	401	1445	4.5(10)-148	Escherichia coli	b0983	[pn:hypothetical protein] [gn:yccz]
CONTIG381	25503383_f1_1	1212	6874	840	280	265	4.9(10)-23	Escherichia coli	b0300	[pn:hypothetical transcriptional regulator in each-beta intergenic region] [gn:ykga]
CONTIG381	4032952_f1_10	1213	6875	762	254	1010	5.5(10)-102	Escherichia coli	b1284	[pn:hypothetical protein]
CONTIG381	1306711_f2_14	1214	6876	243	81	300	9.6(10)-27	Escherichia coli	b4248	[pn:hypothetical 14.6 kd protein in pyrI-argI intergenic region] [gn:yjgh]
CONTIG381	14742013_f2_16	1215	6877	1002	334	596	7.9(10)-68	Escherichia coli	b1287	[pn:hypothetical protein]
CONTIG381	4103433_f3_20	1216	6878	813	271	1271	1.2(10)-129	Escherichia coli	b1288	[pn:enoyl-acyl-carrier-protein reductase nadh] [gn:fabI]
CONTIG381	1203412_f3_23	1217	6879	1941	647	3006	0	Escherichia coli	b1286	[pn:exoribonuclease ii] [gn:rmb]
CONTIG381	20181625_f3_24	1218	6880	2025	675	2702	2.7(10)-281	Escherichia coli	b1285	[pn:hypothetical protein] [gn:ycir]
CONTIG381	9954777_f3_27	1219	6881	243	81	156	1.8(10)-11	Escherichia coli	b1283	[pn:osmotically inducible lipoprotein b precursor] [gn:osmb]

CONTIG381	25503415_c1_29	1220	6882	351	117	405	7.2(10)-38	Escherichia coli	b1282	[pn:hypothetical 11.4 kd protein in pyrf-osmb intergenic region] [gn:ychi]
CONTIG381	34667968_c2_41	1221	6883	870	290	958	1.8(10)-96	Escherichia coli	b1281	[pn:orotidine-5"-p decarboxylase] [gn:pyrf]
CONTIG381	34505012_c2_54	1222	6884	1407	469	768	2.5(10)-76	Escherichia coli	b1025	[pn:hypothetical protein] [gn:ycdt]
CONTIG381	15742130_c3_58	1223	6885	915	305	390	2.7(10)-36	Xanthomonas campestris	Y09701	.,,rpf
CONTIG382	2361512_f1_3	1224	6886	1323	441	2095	5.9(10)-217	Escherichia coli	b0154	[pn:glutamate-1-semialdehyde 2,1-aminomutase] [gn:hemi]
CONTIG382	21650204_c1_36	1225	6887	587	195	810	8.6(10)-81	Escherichia coli	b0149	[pn:peptidoglycan synthetase] [gn:mrcb]
CONTIG382	9956407_c1_37	1226	6888	2334	778	1322	1.8(10)-253	Escherichia coli	b0150	[pn:ferrichrome-iron receptor precursor] [gn:fhua]
CONTIG382	15836458_c1_38	1227	6889	2142	714	2080	2.2(10)-215	Escherichia coli	b0153	[pn:ferrichrome transport protein fhuf precursor] [gn:fhuf]
CONTIG382	35785137_c1_41	1228	6890	825	275	675	1.8(10)-66	Escherichia coli	b0155	[pn:hypothetical protein in heml-pfs intergenic region] [gn:yadq]
CONTIG382	35285941_c2_46	1229	6891	975	325	1086	4.9(10)-110	Escherichia coli	b0152	[pn:ferrichrome-binding periplasmic protein precursor] [gn:fhud]
CONTIG382	21892677_c3_56	1230	6892	933	311	1265	5.2(10)-129	Escherichia coli	b0151	[pn:ferrichrome transport atp-binding protein fhuc] [gn:fhuc]
CONTIG383	35281502_f1_2	1231	6893	2499	833	3387	0	Escherichia coli	b4179	[pn:vacb protein] [gn:vacb]
CONTIG383	14082000_f1_3	1232	6894	795	265	1184	2.0(10)-120	Escherichia coli	b4180	[pn:hypothetical 26.6 kd protein in vacb-aidb intergenic region]
CONTIG383	16804581_f2_12	1233	6895	1392	464	2087	4.2(10)-216	Escherichia coli	b4177	[pn:adenylosuccinate synthetase] [gn:pura]
CONTIG383	29969426_f2_13	1234	6896	501	167	669	7.5(10)-66	Escherichia coli	b4178	[pn:hypothetical 15.6 kd protein in pura-vacb intergenic region] [gn:yjeb]
CONTIG383	21957031_f2_19	1235	6897	1695	565	2361	3.7(10)-245	Escherichia coli	b4187	[pn:aidb protein] [gn:aidb]
CONTIG383	4547906_f3_22	1236	6898	186	62	222	1.8(10)-18	Escherichia coli	b4176	[pn:hypothetical protein] [gn:yjet]
CONTIG383	4067692_c1_36	1237	6899	1383	461	545	1.1(10)-52	Escherichia coli	b1886	[pn:methyl-accepting chemotaxis protein ii] [gn:tar]

CONTIG383	23948293_c1_43	1238	6900	1347	449	154	1.0(10)-7	Shigella flexneri	P30851	vacB protein.
CONTIG383	31875013_c2_52	1239	6901	411	137	101	0.00011	Glucobacter suboxydans	O05543	[sp:o05543] [de:hypothetical protein in adhS 5' region (orf3) (fragment)]
CONTIG383	9922177_c3_70	1240	6902	1311	437	570	2.3(10)-55	Escherichia coli	b4111	[pn:proline/betaine transporter] [gn:prop]
CONTIG384	33413132_f2_31	1241	6903	732	244	757	3.6(10)-75	Escherichia coli	b1908	[pn:hypothetical 25.0 kd protein in tyrp-leuz intergenic region]
CONTIG384	19532255_f2_33	1242	6904	264	88	314	3.2(10)-28	Escherichia coli	b1906	[pn:hypothetical 7.3 kd protein in tyrp-rsga intergenic region]
CONTIG384	171887_f3_37	1243	6905	933	311	239	2.7(10)-20	Escherichia coli	b2808	[pn:regulatory protein for glycine cleavage pathway] [gn:gcva]
CONTIG384	32228407_c1_54	1244	6906	342	114	239	2.7(10)-20	Escherichia coli	b1904	[pn:hypothetical protein]
CONTIG384	24881642_c1_64	1245	6907	1293	431	702	2.3(10)-69	Escherichia coli	b3456	[pn:high-affinity branched-chain amino acid transport permease protein livm] [gn:livm]
CONTIG384	15051625_c2_69	1246	6908	1287	429	1480	8.8(10)-152	Escherichia coli	b1907	[pn:tyrosine-specific transport protein] [gn:tyrp]
CONTIG384	4424067_c2_74	1247	6909	996	332	808	1.3(10)-80	Escherichia coli	b3457	[pn:high-affinity branched-chain amino acid transport permease protein livh] [gn:livh]
CONTIG384	29455312_c2_76	1248	6910	765	255	662	4.2(10)-65	Escherichia coli	b3454	[pn:high-affinity branched-chain amino acid transport atp-binding] [gn:livf]
CONTIG384	19725927_c3_85	1249	6911	555	185	787	2.3(10)-78	Escherichia coli	b1905	[pn:ferritin-like protein] [gn:fm]
CONTIG384	32547515_c3_89	1250	6912	1281	427	765	5.0(10)-76	Escherichia coli	b3460	[pn:leu/ile/val-binding protein precursor] [gn:livj]
CONTIG384	16299092_c3_93	1251	6913	888	296	541	2.2(10)-72	Escherichia coli	b3455	[pn:high-affinity branched-chain amino acid transport atp-binding protein livg] [gn:livg]
CONTIG385	12150208_f1_1	1252	6914	885	295	1078	3.5(10)-109	Escherichia coli	b3424	[pn:glpG protein] [gn:glpG]
CONTIG385	5203167_f2_13	1253	6915	243	81	367	7.7(10)-34	Escherichia coli	b3425	[pn:protein] [gn:g/pe]
CONTIG385	786635_f2_14	1254	6916	903	301	1076	5.7(10)-109	Escherichia coli	b3423	[pn:glycerol-3-phosphate regulon repressor] [gn:g/pr]

CONTIG385	30507666_f3_29	1255	6917	2433	811	3553	0	Escherichia coli	b3417	[pn:maltodextrin phosphorylase] [gn:malp]
CONTIG385	5208443_f3_30	1256	6918	2091	697	3271	0	Escherichia coli	b3416	[pn:4-alpha-glucanotransferase] [gn:malq]
CONTIG385	22128751_c1_38	1257	6919	267	89	90	0.00044	Rattus norvegicus	P0474	acidic proline-rich protein precursor (clone prp33).
CONTIG385	16289550_c1_39	1258	6920	2760	920	3776	0	Escherichia coli	b3418	[pn:malt] [gn:malt]
CONTIG385	34629027_c3_53	1259	6921	189	63	193	1.1(10)-14	Escherichia coli	b3415	[pn:high-affinity gluconate transporter] [gn:gntt]
CONTIG386	22479712_f2_19	1260	6922	1053	351	931	1.3(10)-93	Escherichia coli	b0419	[pn:hypothetical protein] [gn:yajo]
CONTIG386	3017328_f2_26	1261	6923	1023	341	515	1.6(10)-49	Escherichia coli	b0900	[pn:hypothetical protein] [gn:ycan]
CONTIG386	13166067_f2_29	1262	6924	537	179	135	8.8(10)-9	Escherichia coli	b1967	[pn:hypothetical protein] [gn:yedu]
CONTIG386	4384828_f3_30	1263	6925	186	62	164	2.5(10)-12	Escherichia coli	I41306	hypothetical protein (argI-lacZ region) - escherichia coli
CONTIG386	32667087_f3_37	1264	6926	528	176	169	2.2(10)-12	Haemophilus influenzae	I410821	[pn:gals] [gn:galr]
CONTIG386	15861432_c2_67	1265	6927	1068	356	901	2.0(10)-90	Bacillus subtilis	ypgG	[pn:hypothetical protein]
CONTIG386	34589712_c2_80	1266	6928	453	151	97	0.01799	Methanococcus jannaschii	MJ1643	[pn:chromosome segregation protein]
CONTIG386	3942063_c3_82	1267	6929	909	303	301	7.5(10)-27	Escherichia coli	b0900	[pn:hypothetical protein] [gn:ycan]
CONTIG386	14925383_c3_86	1268	6930	1290	430	700	4.0(10)-69	Helicobacter pylori	HP1193	[pn:aldo-keto reductase, putative]
CONTIG386	11807803_c3_87	1269	6931	975	325	163	9.8(10)-10	Zymomonas mobilis	Q01578	gluconolactonase precursor (ec 3.1.1.17) (d-glucono-delta-lactone lactonohydrolase)
CONTIG387	36415791_f1_1	1270	6932	561	187	748	3.2(10)-74	Escherichia coli	b1181	[pn:hypothetical protein]
CONTIG387	10667163_f3_38	1271	6933	894	298	1177	1.1(10)-119	Escherichia coli	b1187	[pn:fatty acid--fatty acyl responsive dna-binding protein] [gn:fadr]
CONTIG387	29501675_f3_42	1272	6934	1335	445	2065	8.9(10)-214	Escherichia coli	b1189	[pn:d-amino acid dehydrogenase] [gn:dada]
CONTIG387	4816068_f3_43	1273	6935	1080	360	1507	1.2(10)-154	Escherichia coli	b1190	[pn:alanine racemase, catabolic precursor] [gn:dadx]

CONTIG387	34016706_f3_48	1274	6936	633	211	892	1.8(10)-89	Escherichia coli	b1193	[pn:hypothetical protein]
CONTIG387	33805281_c1_49	1275	6937	771	257	845	1.7(10)-84	Escherichia coli	b1194	[pn:hypothetical protein]
CONTIG387	21518877_c1_50	1276	6938	939	313	1176	1.3(10)-119	Escherichia coli	b1192	[pn:hypothetical protein]
CONTIG387	33673808_c1_64	1277	6939	552	184	716	8.0(10)-71	Escherichia coli	b1185	[pn:disulfide bond formation protein b] [gn:dsbb]
CONTIG387	23714768_c2_72	1278	6940	1752	584	2241	2.0(10)-232	Escherichia coli	b1191	[pn:hypothetical protein]
CONTIG387	2089212_c2_78	1279	6941	1581	527	2647	1.8(10)-275	Escherichia coli	b1188	[pn:hypothetical protein in fadr-dada intergenic region] [gn:ycgb]
CONTIG387	437640_c2_81	1280	6942	1620	540	1544	1.3(10)-158	Escherichia coli	b1186	[pn:regulator of intracellular ph] [gn:nhab]
CONTIG387	3986291_c3_95	1281	6943	375	125	226	4.0(10)-18	Escherichia coli	b1186	[pn:regulator of intracellular ph] [gn:nhab]
CONTIG387	13681887_c3_96	1282	6944	186	62	161	5.2(10)-12	Escherichia coli	M83655	or:escherichia coli lc:1764 re:1952 di:direct sr:escherichia coli (sub_strain w1333, strain k-12) dna nt:putative orf
CONTIG388	25900302_f1_4	1283	6945	585	195	844	2.2(10)-84	Escherichia coli	b1627	[pn:hypothetical protein]
CONTIG388	31770037_f1_7	1284	6946	2106	702	2255	6.5(10)-234	Escherichia coli	b1629	[pn:hypothetical protein]
CONTIG388	33594202_f1_8	1285	6947	1053	351	1560	2.8(10)-160	Escherichia coli	b1630	[pn:hypothetical protein] [gn:ydgq]
CONTIG388	4416068_f1_9	1286	6948	696	232	874	1.3(10)-87	Escherichia coli	b1632	[pn:hypothetical protein] [gn:ydgq]
CONTIG388	1269557_f1_12	1287	6949	1548	516	2011	4.7(10)-208	Escherichia coli	b1634	[pn:hypothetical protein]
CONTIG388	24849011_f1_13	1288	6950	639	213	850	5.0(10)-85	Escherichia coli	b1635	[pn:glutathione s-transferase] [gn:gst]
CONTIG388	24346900_f2_23	1289	6951	345	115	252	1.2(10)-21	Escherichia coli	b1625	[pn:hypothetical protein]
CONTIG388	32556875_f2_27	1290	6952	780	260	832	4.0(10)-83	Escherichia coli	b1631	[pn:hypothetical protein]
CONTIG388	22784386_f3_41	1291	6953	468	156	386	7.4(10)-36	Escherichia coli	b1626	[pn:hypothetical protein]

CONTIG388	25672590_f3_42	1292	6954	597	199	757	3.6(10)-75	Escherichia coli	b1628	[pn:hypothetical protein]
CONTIG388	13932707_f3_48	1293	6955	672	224	955	3.7(10)-96	Escherichia coli	b1633	[pn:endonuclease iii] [gn:nth]
CONTIG388	32522791_c1_57	1294	6956	1371	457	1780	1.3(10)-183	Escherichia coli	b1637	[pn:tyrosyl-trna synthetase] [gn:tyrs]
CONTIG388	30132800_c1_58	1295	6957	927	309	1353	2.5(10)-138	Escherichia coli	b1636	[pn:hypothetical protein]
CONTIG388	4557818_c2_70	1296	6958	1134	378	1559	3.7(10)-160	Escherichia coli	b1640	[pn:hypothetical protein]
CONTIG388	26737658_c2_71	1297	6959	360	120	399	3.1(10)-37	Escherichia coli	b1639	[pn:hypothetical protein in pdxh 5'''region] [gn:ydhx]
CONTIG388	4785791_c2_72	1298	6960	687	229	1069	3.1(10)-108	Escherichia coli	b1638	[pn:pyridoxamine 5'''-phosphate oxidase] [gn:pdxh]
CONTIG388	14511040_c3_109	1299	6961	1158	386	1601	1.3(10)-164	Escherichia coli	b1624	[pn:hypothetical protein]
CONTIG389	4557750_f1_3	1300	6962	774	258	1117	2.6(10)-113	Escherichia coli	b0652	[pn:glutamate/aspartate transport atp-binding protein gltI] [gn:gltI]
CONTIG389	2379182_f1_4	1301	6963	534	178	783	6.2(10)-78	Escherichia coli	b0651	[pn:hypothetical 33.8 kd protein in leus-gltI intergenic region] [gn:ybcK]
CONTIG389	13671885_f1_6	1302	6964	507	169	171	4.5(10)-13	Vibrio cholerae	S81006	or vibrio cholerae pn:hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nr:28 kda secreted hydrophilic protein; this sequence
CONTIG389	33634701_f1_14	1303	6965	1035	345	1390	3.0(10)-142	Escherichia coli	b0640	[pn:dna polymerase iii, delta subunit] [gn:hola]
CONTIG389	32604625_f1_16	1304	6966	1914	638	3029	0	Escherichia coli	b0635	[pn:mrda] [gn:mrda]
CONTIG389	291465_f1_17	1305	6967	528	176	572	1.5(10)-55	Escherichia coli	b0633	[pn:rare lipoprotein a precursor] [gn:rlpa]
CONTIG389	11769203_f2_18	1306	6968	828	276	1110	1.3(10)-112	Escherichia coli	b0654	[pn:glutamate/aspartate transport system permease protein gltJ] [gn:gltJ]
CONTIG389	207577_f2_19	1307	6969	675	225	971	7.5(10)-98	Escherichia coli	b0653	[pn:glutamate/aspartate transport system permease protein gltK] [gn:gltK]
CONTIG389	10751002_f2_24	1308	6970	609	203	650	7.9(10)-64	Escherichia coli	b0641	[pn:rare lipoprotein b precursor] [gn:rlpb]

CONTIG389	13714662_f2_27	1309	6971	753	251	887	6.0(10)-89	Escherichia coli	b0639	[pn:hypothetical protein] [gn:yben]
CONTIG389	26801538_f3_34	1310	6972	252	84	336	1.5(10)-30	Escherichia coli	b0655	[pn:hypothetical protein in gltj 5 ^{'''} region] [gn:ybej]
CONTIG389	9766277_f3_36	1311	6973	582	194	681	4.0(10)-67	Escherichia coli	b0651	[pn:hypothetical 33.8 kd protein in leus-glti intergenic region] [gn:ybek]
CONTIG389	24344502_f3_40	1312	6974	2712	904	4217	0	Escherichia coli	b0642	[pn:leucyl-tRNA synthetase] [gn:leus]
CONTIG389	31728136_f3_44	1313	6975	405	135	240	2.2(10)-20	Escherichia coli	b0637	[pn:hypothetical 7.7 kd protein in mrda/bopa 3 ^{'''} region] [gn:ybeb]
CONTIG389	1369165_f3_45	1314	6976	471	157	792	7.0(10)-79	Escherichia coli	b0636	[pn:hypothetical 17.3 kd protein in mrda-phpb intergenic region] [gn:ybec]
CONTIG389	33878937_f3_47	1315	6977	1149	383	1390	3.0(10)-142	Escherichia coli	b0634	[pn:rod shape-determining protein rodA] [gn:mrdb]
CONTIG389	787643_c3_97	1316	6978	525	175	688	7.4(10)-68	Escherichia coli	b0643	[pn:hypothetical 18.8 kd protein in leus-glti intergenic region] [gn:ybel]
CONTIG39	22785700_c2_2	1317	6979	444	148	575	7.0(10)-56	Escherichia coli	b1830	[pn:tail-specific protease precursor] [gn:prc]
CONTIG390	32706312_f1_12	1318	6980	354	118	95	0.0015	Kaposi's sarcoma-associated herpesvirus	U93872	[OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8] [DE:Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA replication protein, glycoprotein, DNA replication protein,
CONTIG390	24256457_f2_29	1319	6981	843	281	635	3.1(10)-62	Bacillus subtilis	yusA	[pn:hypothetical protein]
CONTIG390	6926543_f2_30	1320	6982	228	76	274	5.5(10)-24	Escherichia coli	b1675	[pn:hypothetical protein]
CONTIG390	4959691_f3_43	1321	6983	1032	344	816	2.0(10)-81	Bacillus subtilis	yusC	[pn:hypothetical protein]
CONTIG390	9782192_f3_44	1322	6984	663	221	387	5.7(10)-36	Bacillus subtilis	yusB	[pn:hypothetical protein]
CONTIG390	14642966_c1_54	1323	6985	864	288	339	7.0(10)-31	Bacillus subtilis	glnH	[pn:glutamine abc transporter]

CONTIG390	31304138_c1_56	1324	6986	909	303	273	7.0(10)-24	Escherichia coli	b0654	[pn:glutamate/aspartate transport system permease protein gltj] [gn:gltj]
CONTIG390	23722712_c2_72	1325	6987	828	276	645	2.7(10)-63	Bacillus subtilis	glmQ	[pn:glutamine abc transporter]
CONTIG390	30602341_c2_74	1326	6988	735	245	264	6.2(10)-23	Bacillus subtilis	glmP	[pn:glutamine abc transporter]
CONTIG390	35833276_c2_81	1327	6989	876	292	1193	2.2(10)-121	Escherichia coli	b1676	[pn:pyruvate kinase] [gn:pykf]
CONTIG390	4422550_c3_92	1328	6990	1602	534	554	1.7(10)-57	Saccharomyces cerevisiae	YGR155W	[pn:cystathionine beta-synthase] [gn:cys4]
CONTIG390	24401712_c3_93	1329	6991	1158	386	980	8.4(10)-99	Helicobacter pylori	HP0106	[pn:cystathionine gamma-synthase] [gn:metb]
CONTIG391	16620843_f1_1	1330	6992	855	285	211	3.2(10)-35	Escherichia coli	b1559	[pn:hypothetical protein]
CONTIG391	12928328_f1_4	1331	6993	363	121	158	1.1(10)-11	Bacteriophage phi-105	1.35561	or bacteriophage phi-105 pn:holin le:796 re 1170 di:direct sr:bacteriophage phi-105 dna nt:ori2; potential dual start motif; putative
CONTIG391	319222906_f1_6	1332	6994	1770	590	611	1.1(10)-59	Escherichia coli	b1149	[pn:hypothetical protein]
CONTIG391	3230287_f1_9	1333	6995	876	292	106	0.00067	Helicobacter pylori	HP0794	[pn:atp-dependent clp protease proteolytic component] [gn:clpp]
CONTIG391	3913318_f1_10	1334	6996	1221	407	591	1.3(10)-57	Bacteriophage HK97	P49861	major capsid protein precursor (gp5) (head protein).
CONTIG391	26817202_f2_16	1335	6997	666	222	241	1.7(10)-20	Haemophilus influenzae	HI1415	[pn:hypothetical protein]
CONTIG391	21775277_f2_18	1336	6998	948	316	372	2.2(10)-34	Bacteriophage phi-80	S43823	hypothetical protein - phage phi-80
CONTIG391	5156338_f2_21	1337	6999	486	162	101	9.4(10)-5	Mycobacterium tuberculosis	Z95586	unknown,,mcy336.26,mcy336.26. len
CONTIG391	35329530_f3_35	1338	7000	1326	442	524	1.8(10)-50	Bacteriophage HK97	P49859	portal protein (gp3).
CONTIG392	5162802_f1_5	1339	7001	471	157	214	1.3(10)-17	Escherichia coli	b1160	[pn:hypothetical protein]
CONTIG392	33447837_f1_6	1340	7002	1335	445	1719	4.0(10)-177	Escherichia coli	b1609	[pn:unknown sensor protein in terminator region] [gn:rstb]
CONTIG392	5315675_f2_15	1341	7003	1419	473	1891	2.5(10)-195	Escherichia coli	b1605	[pn:hypothetical protein]

CONTIG392	26757882_f2_16	1342	7004	735	245	994	2.7(10)-100	Escherichia coli	b1606	[pn:hypothetical protein] [gn:ydgb]
CONTIG392	7161263_f2_17	1343	7005	765	255	924	7.2(10)-93	Escherichia coli	b1608	[pn:rsta] [gn:rsta]
CONTIG392	22054561_f3_28	1344	7006	990	330	1008	9.0(10)-102	Escherichia coli	b1604	[pn:hypothetical protein]
CONTIG392	15761550_f3_30	1345	7007	942	314	1161	5.5(10)-118	Escherichia coli	b1610	[pn:dna replication terminus site-binding protein, dna sequence-specific contrahelase] [gn:tus]
CONTIG392	1385410_f3_36	1346	7008	1215	405	1645	2.8(10)-169	Escherichia coli	b1613	[pn:mannose-6-phosphate isomerase] [gn:mana]
CONTIG392	282081_f3_37	1347	7009	1608	536	1656	2.0(10)-170	Escherichia coli	b1614	[pn:hypothetical protein]
CONTIG392	4960968_c1_51	1348	7010	345	115	425	5.5(10)-40	Escherichia coli	b1607	[pn:hypothetical protein] [gn:ydgc]
CONTIG392	4806553_c2_63	1349	7011	1398	466	1910	2.3(10)-197	Escherichia coli	b1611	[pn:fumarate hydratase class ii] [gn:fumc]
CONTIG392	23438526_c3_81	1350	7012	1716	572	2604	6.7(10)-271	Escherichia coli	b1612	[pn:fumarate hydratase class i] [gn:fuma]
CONTIG393	5265713_f1_2	1351	7013	939	313	1400	2.6(10)-143	Escherichia coli	b0003	[pn:homoserine kinase] [gn:thrb]
CONTIG393	2931566_f1_3	1352	7014	1290	430	2030	4.5(10)-210	Escherichia coli	b0004	[pn:threonine synthase] [gn:thrc]
CONTIG393	14258462_f1_8	1353	7015	969	323	1541	3.0(10)-158	Escherichia coli	b0008	[pn:transaldolase b] [gn:talb]
CONTIG393	25651656_f2_19	1354	7016	537	179	188	7.0(10)-15	Escherichia coli	b0005	[pn:hypothetical protein]
CONTIG393	22382155_f2_22	1355	7017	1350	450	323	3.5(10)-29	Escherichia coli	b3523	[pn:hypothetical metabolite transport protein in tcf-kdgk intergenic region] [gn:yhje]
CONTIG393	6900287_f3_25	1356	7018	2466	822	3632	0	Escherichia coli	b0002	[pn:aspartokinase i/homoserine dehydrogenase i] [gn:thra]
CONTIG393	31411253_f3_34	1357	7019	750	250	900	2.5(10)-90	Escherichia coli	b0009	[pn:molybdopterin biosynthesis mog protein] [gn:mog]
CONTIG393	30210303_c2_62	1358	7020	1500	500	1004	2.3(10)-101	Escherichia coli	b0007	[pn:hypothetical 51.7 kd protein in thr-talb intergenic region] [gn:yaa]
CONTIG393	5162711_c2_63	1359	7021	840	280	1183	2.6(10)-120	Escherichia coli	b0006	[pn:hypothetical 29.6 kd protein in thr-talb intergenic region] [gn:yaaa]

CONTIG393	29850786_c3_74	1360	7022	564	188	759	2.2(10)-75	Escherichia coli	b0010	[pn:hypothetical 20.1 kd protein in mog-hga intergenic region] [gn:yaah]
CONTIG394	25932_f2_20	1361	7023	906	302	1412	1.3(10)-144	Escherichia coli	b0819	[pn:hypothetical protein]
CONTIG394	6447130_f2_33	1362	7024	1008	336	1393	1.5(10)-142	Escherichia coli	b0815	[pn:hypothetical protein] [gn:ybip]
CONTIG394	12145327_c1_51	1363	7025	1110	370	1327	1.3(10)-135	Escherichia coli	b0818	[pn:hypothetical protein] [gn:ybir]
CONTIG394	26852088_c1_57	1364	7026	1551	517	364	1.6(10)-33	Escherichia coli	b4080	[pn:hypothetical 53.4 kd protein in fdhf-phnp intergenic region]
CONTIG394	5199068_c1_64	1365	7027	726	242	467	1.8(10)-44	Bacillus subtilis	ydhQ	[pn:hypothetical protein]
CONTIG394	4802193_c2_68	1366	7028	483	161	707	7.2(10)-70	Escherichia coli	b0817	[pn:hypothetical protein]
CONTIG394	21773532_c2_73	1367	7029	1590	530	762	1.1(10)-75	Haemophilus influenzae	H10897	[pn:multidrug resistance protein] [gn:emrb]
CONTIG394	24253551_c2_77	1368	7030	1398	466	871	3.0(10)-87	Bacillus subtilis	yckE	[pn:hypothetical protein]
CONTIG394	10336090_c2_78	1369	7031	1338	446	528	6.7(10)-51	Bacillus subtilis	ywbA	[pn:hypothetical protein] [gn:ipa-16d]
CONTIG394	26306507_c3_85	1370	7032	1098	366	330	6.5(10)-35	Haemophilus influenzae	H10898	[pn:multidrug resistance protein] [gn:emra]
CONTIG395	29766093_f1_9	1371	7033	1062	354	1078	3.5(10)-109	Escherichia coli	b1428	[pn:hypothetical protein]
CONTIG395	13865937_f2_24	1372	7034	1254	418	703	1.8(10)-69	Bacillus subtilis	pepT	[pn:peptidase t]
CONTIG395	32509638_f3_45	1373	7035	846	282	328	1.0(10)-29	Escherichia coli	b2808	[pn:regulatory protein for glycine cleavage pathway] [gn:gcva]
CONTIG395	24804715_c1_50	1374	7036	1524	508	481	6.4(10)-46	Bacillus subtilis	pnbA	[pn:intracellular esterase b] [gn:estb]
CONTIG395	21520675_c1_53	1375	7037	1200	400	932	1.0(10)-93	Escherichia coli	b0600	[pn:hypothetical protein]
CONTIG395	1171956_c1_54	1376	7038	1746	582	2562	1.8(10)-266	Escherichia coli	b1424	[pn:hypothetical protein]
CONTIG395	7271905_c1_55	1377	7039	645	215	627	2.2(10)-61	Escherichia coli	b1427	[pn:ribosomal-protein-serine acetyltransferase] [gn:rim]
CONTIG395	4726568_c1_62	1378	7040	603	201	861	3.3(10)-86	Escherichia coli	b1430	[pn:tellurite resistance protein tehb] [gn:tehb]

CONTIG395	2034780_c2_74	1379	7041	861	287	565	8.0(10)-55	Escherichia coli	b2310	[pn:lysine-arginine-ornithine-binding periplasmic protein precursor] [gn:argt]
CONTIG395	24412506_c2_80	1380	7042	1008	336	1338	9.8(10)-137	Escherichia coli	b1429	[pn:tellurite resistance protein teha] [gn:teha]
CONTIG395	34181577_c3_94	1381	7043	1599	533	1893	1.5(10)-195	Escherichia coli	b3544	[pn:periplasmic dipeptide transport protein precursor] [gn:dppal]
CONTIG396	976575_f2_25	1382	7044	825	275	778	2.1(10)-77	Escherichia coli	b2558	[pn:hypothetical 53.2 kd protein in purl-dpj intergenic region] [gn:yfhd]
CONTIG396	35807756_f3_26	1383	7045	777	259	1109	1.8(10)-112	Escherichia coli	b2552	[pn:flavohepomeprotein] [gn:hmpal]
CONTIG396	36369777_f3_29	1384	7046	786	262	160	1.3(10)-10	Aeromonas hydrophila	U56832	[DE:Aeromonas hydrophila FK506 binding protein (fkpA) gene, completecds in 3.9 kb fragment.] [NT:ORF5; no significant similarity with known] [L.E.2969] [RE:3721] [DI:complement]
CONTIG396	10366717_c1_47	1385	7047	1485	495	1795	3.7(10)-185	Escherichia coli	b2556	[pn:hypothetical protein] [gn:yfhk]
CONTIG396	4410193_c1_51	1386	7048	348	116	553	1.5(10)-53	Escherichia coli	b2553	[pn:nitrogen regulatory protein p-ii] [gn:glnb]
CONTIG396	14660413_c2_56	1387	7049	1365	455	2071	2.1(10)-214	Escherichia coli	b2554	[pn:hypothetical protein in glnb 5''' region] [gn:yfha]
CONTIG396	32675833_c3_61	1388	7050	3918	1306	6216	0	Escherichia coli	b2557	[pn:phosphoribosylformylglycineamid de synthetase] [gn:purl]
CONTIG396	4883533_c3_63	1389	7051	771	257	574	8.9(10)-56	Escherichia coli	b2555	[pn:hypothetical 27.3 kd protein in glnb 5''' region] [gn:yfhg]
CONTIG397	33635886_f1_11	1390	7052	1293	431	2031	3.6(10)-210	Escherichia coli	b1136	[pn:isocitrate dehydrogenase] [gn:icd]
CONTIG397	13105186_f1_12	1391	7053	300	100	340	5.5(10)-31	Escherichia coli	b1295	[pn:hypothetical protein]
CONTIG397	25423317_f2_15	1392	7054	1035	345	1559	3.7(10)-160	Escherichia coli	b1127	[pn:peptidase t] [gn:pept]
CONTIG397	24032750_f3_46	1393	7055	282	94	332	3.8(10)-30	Escherichia coli	b1795	[pn:hypothetical protein]
CONTIG397	32459633_c1_49	1394	7056	669	223	942	9.0(10)-95	Escherichia coli	b1135	[pn:hypothetical protein] [gn:ym[c]
CONTIG397	14630207_c1_51	1395	7057	1287	429	1694	1.8(10)-174	Escherichia coli	b1133	[pn:hypothetical protein in purb 5''' region] [gn:ycfb]

CONTIG397	14297282_c1_52	1396	7058	657	219	865	1.3(10)-86	Escherichia coli	b1132	[pn:hypothetical 22.9 kd protein in purb 5 ^{'''} region] [gn:yfcf]
CONTIG397	26688338_c1_55	1397	7059	1143	381	1745	7.2(10)-180	Escherichia coli	b1128	[pn:hypothetical protein in pept-phoq intergenic region] [gn:yfd]
CONTIG397	22925191_c2_67	1398	7060	1425	475	2217	7.0(10)-230	Escherichia coli	b1131	[pn:adenylosuccinate lyase] [gn:purb]
CONTIG397	1058467_c3_71	1399	7061	297	99	227	1.2(10)-18	Escherichia coli	b1794	[pn:hypothetical protein]
CONTIG397	34025381_c3_74	1400	7062	1548	516	300	3.7(10)-24	Escherichia coli	b4061	[pn:hypothetical 60.8 kd protein in ssb-soxs intergenic region] [gn:yjce]
CONTIG397	5101693_c3_76	1401	7063	483	161	684	2.0(10)-67	Escherichia coli	b1134	[pn:hypothetical protein]
CONTIG397	6519052_c3_82	1402	7064	720	240	936	3.8(10)-94	Escherichia coli	b1130	[pn:transcriptional regulatory protein phop] [gn:phop]
CONTIG397	5367202_c3_83	1403	7065	1464	488	1829	9.0(10)-189	Escherichia coli	b1129	[pn:sensor protein phoq] [gn:phoq]
CONTIG398	22117656_f1_4	1404	7066	1431	477	1108	2.2(10)-112	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-selc intergenic region] [gn:yicj]
CONTIG398	1301712_f1_5	1405	7067	2052	684	2519	7.0(10)-262	Erwinia herbicola	Q01336	[hypothetical protein in orte 3' region (orf2) (fragment)]
CONTIG398	5324127_f1_9	1406	7068	411	137	429	2.1(10)-40	Escherichia coli	b1792	[pn:hypothetical protein]
CONTIG398	24821017_f2_13	1407	7069	279	93	110	1.3(10)-6	Escherichia coli	b1141	[pn:hypothetical protein]
CONTIG398	15728292_f2_19	1408	7070	513	171	400	2.3(10)-37	Escherichia coli	b1789	[pn:hypothetical protein]
CONTIG398	21581381_f2_26	1409	7071	711	237	754	7.5(10)-75	Escherichia coli	b1794	[pn:hypothetical protein]
CONTIG398	31382327_f3_31	1410	7072	1143	381	950	1.3(10)-95	Escherichia coli	b1140	[pn:hypothetical protein]
CONTIG398	20813561_f3_32	1411	7073	537	179	667	1.2(10)-65	Escherichia coli	b1787	[pn:hypothetical protein]
CONTIG398	4725963_f3_37	1412	7074	1197	399	1339	7.7(10)-137	Escherichia coli	b1791	[pn:hypothetical protein]
CONTIG398	30081918_c1_44	1413	7075	753	251	216	5.5(10)-17	Bacillus subtilis	ctrA	[pn:ctp synthase] [gn:pyrg]
CONTIG398	5112842_c2_61	1414	7076	267	89	211	2.6(10)-17	Escherichia coli	b1793	[pn:hypothetical protein]

CONTIG398	270387_c2_66	1415	7077	825	275	833	3.2(10)-83	Escherichia coli	b1790	[pn:hypothetical protein]
CONTIG399	13167057_f1_1	1416	7078	567	189	888	4.7(10)-89	Escherichia coli	b0860	[pn:arginine-binding periplasmic protein 2 precursor] [gn:artj]
CONTIG399	3963966_f1_20	1417	7079	333	111	357	8.8(10)-33	Haemophilus influenzae	HI1532	[pn:grx] [gn:grxa]
CONTIG399	11758450_f1_23	1418	7080	882	294	99	0.03699	Saccharomyces cerevisiae	S57378	hypothetical protein yol091w - yeast (saccharomycescerevisiae)
CONTIG399	20990640_f2_44	1419	7081	1803	601	2483	4.5(10)-258	Escherichia coli	b0847	[pn:hypothetical protein]
CONTIG399	36385956_c1_65	1420	7082	480	160	124	4.2(10)-8	Escherichia coli	P12009	multi-copy suppressor of livr.
CONTIG399	33260086_c1_66	1421	7083	528	176	373	1.8(10)-34	Escherichia coli	b0848	[pn:hypothetical protein]
CONTIG399	16525416_c1_68	1422	7084	1086	362	1365	1.3(10)-139	Escherichia coli	b0852	[pn:ribosomal protein s6 modification protein] [gn:rimg]
CONTIG399	32211630_c1_69	1423	7085	513	171	424	7.0(10)-40	Escherichia coli	b0853	[pn:hypothetical protein]
CONTIG399	26303807_c1_74	1424	7086	876	292	1150	8.1(10)-117	Escherichia coli	b0857	[pn:putrescine transport system permease protein poti] [gn:poti]
CONTIG399	20832265_c1_75	1425	7087	519	173	691	3.6(10)-68	Escherichia coli	b0858	[pn:hypothetical protein] [gn:ybj0]
CONTIG399	12932812_c1_80	1426	7088	1542	514	320	1.3(10)-26	Bacillus subtilis	phoR	[pn:two-component sensor histidine kinase]
CONTIG399	16589783_c2_88	1427	7089	1218	406	1754	8.0(10)-181	Escherichia coli	b0855	[pn:putrescine transport atp-binding protein potg] [gn:potg]
CONTIG399	4354193_c2_89	1428	7090	963	321	1321	6.2(10)-135	Escherichia coli	b0856	[pn:putrescine transport system permease protein poth] [gn:poth]
CONTIG399	4078143_c2_91	1429	7091	1137	379	1608	2.3(10)-165	Escherichia coli	b0859	[pn:hypothetical protein] [gn:ybjf]
CONTIG399	16970910_c3_101	1430	7092	813	271	994	2.7(10)-100	Escherichia coli	b0851	[pn:modulator of drug activity a] [gn:mdaa]
CONTIG399	33594691_c3_102	1431	7093	1137	379	1799	1.3(10)-185	Escherichia coli	b0854	[pn:putrescine-binding periplasmic protein precursor] [gn:potf]
CONTIG399	25431561_c3_110	1432	7094	729	243	517	9.8(10)-50	Bacillus subtilis	ycjJ	[pn:hypothetical protein]
CONTIG400	24025326_f1_5	1433	7095	2097	699	3000	0	Escherichia coli	b0984	[pn:hypothetical protein] [gn:ymca]

CONTIG400	5292787_f1_7	1434	7096	477	159	368	6.0(10)-34	Escherichia coli	b0982	[pn:hypothetical protein] [gn:yccy]
CONTIG400	3908300_f1_8	1435	7097	2187	729	2495	2.3(10)-259	Escherichia coli	b0981	[pn:hypothetical protein in appa 3'''region] [gn:yccc]
CONTIG400	15626550_f2_17	1436	7098	1818	606	1732	1.7(10)-178	Escherichia coli	b3647	[pn:hypothetical 63.2 kd protein in gmk 5'''region] [gn:yicf]
CONTIG400	31802025_f2_20	1437	7099	825	275	537	7.4(10)-52	Escherichia coli	b0985	[pn:hypothetical protein] [gn:yimb]
CONTIG400	6445327_f2_26	1438	7100	1134	378	1617	2.7(10)-166	Escherichia coli	b0983	[pn:hypothetical protein] [gn:yccz]
CONTIG400	4765950_f3_42	1439	7101	678	226	707	7.2(10)-70	Escherichia coli	b0986	[pn:hypothetical protein] [gn:ymcc]
CONTIG400	35413343_f3_45	1440	7102	249	83	130	1.0(10)-8	Escherichia coli	b0982	[pn:hypothetical protein] [gn:yccy]
CONTIG400	1268807_f3_50	1441	7103	840	280	954	4.7(10)-96	Escherichia coli	b3643	[pn:mase ph] [gn:rph]
CONTIG400	4153_f3_51	1442	7104	690	230	1030	4.2(10)-104	Escherichia coli	b3642	[pn orotate phosphoribosyltransferase] [gn:pyre]
CONTIG400	26660317_c1_57	1443	7105	219	73	250	5.2(10)-21	Escherichia coli	b3639	[pn:dip protein] [gn:dfp]
CONTIG400	24017165_c1_59	1444	7106	684	228	922	1.2(10)-92	Escherichia coli	b3641	[pn:tlk protein] [gn:ttk]
CONTIG400	25488563_c1_60	1445	7107	918	306	1362	2.7(10)-139	Escherichia coli	b3644	[pn:33.2 kd protein in dind-rph intergenic region] [gn:yicc]
CONTIG400	24397161_c1_80	1446	7108	579	193	853	2.3(10)-85	Escherichia coli	b3648	[pn:5'''guanylate kinase] [gn:gmk]
CONTIG400	2032005_c2_86	1447	7109	645	215	709	4.4(10)-70	Escherichia coli	b3646	[pn:hypothetical 22.0 kd protein in rph-gmk intergenic region] [gn:yieg]
CONTIG400	16977086_c3_99	1448	7110	570	190	737	4.7(10)-73	Escherichia coli	b3640	[pn:deoxyuridine 5'''-triphosphate nucleotidohydrolase] [gn:dut]
CONTIG401	36460400_f1_11	1449	7111	1578	526	2446	3.7(10)-254	Escherichia coli	b3749	[pn:high affinity ribose transport protein] [gn:rbsa]
CONTIG401	10256930_f1_13	1450	7112	270	90	163	8.4(10)-12	Escherichia coli	b3752	[pn:ribokinase] [gn:rbsk]
CONTIG401	14196916_f1_14	1451	7113	996	332	1421	1.6(10)-145	Escherichia coli	b3753	[pn:rbs repressor] [gn:rbsr]
CONTIG401	14337755_f2_24	1452	7114	1872	624	2382	2.2(10)-247	Escherichia coli	b3747	[pn:kup]

CONTIG401	23714652_f2_27	1453	7115	831	277	945	4.2(10)-95	Escherichia coli	b3750	[pn:high affinity ribose transport protein] [gn:rbse]
CONTIG401	14650302_f3_35	1454	7116	996	332	1573	1.2(10)-161	Escherichia coli	b3744	[pn:aspartate--ammonia ligase] [gn:asna]
CONTIG401	9817191_f3_41	1455	7117	450	150	640	9.0(10)-63	Escherichia coli	b3748	[pn:high affinity ribose transport protein rbsd] [gn:rbsd]
CONTIG401	13917556_f3_42	1456	7118	546	182	90	0.02999	Escherichia coli	b3750	[pn:high affinity ribose transport protein] [gn:rbse]
CONTIG401	2854076_f3_43	1457	7119	918	306	1354	2.0(10)-138	Escherichia coli	b3751	[pn:periplasmic ribose-binding protein precursor] [gn:rbsb]
CONTIG401	24319718_f3_44	1458	7120	897	299	1009	7.0(10)-102	Escherichia coli	b3752	[pn:ribokinase] [gn:rbsk]
CONTIG401	29800187_c1_49	1459	7121	441	147	451	9.5(10)-43	Escherichia coli	b3755	[pn:hypothetical 20.8 kd protein in rbsr-risc intergenic region] [gn:ytep]
CONTIG401	11067932_c2_80	1460	7122	1464	488	1648	1.3(10)-169	Escherichia coli	b3745	[pn:hypothetical 49.6 kd protein in asna 3''' region]
CONTIG401	24819702_c3_83	1461	7123	1434	478	1844	2.2(10)-190	Escherichia coli	b3754	[pn:hypothetical 51.5 kd protein in rbsr-risc intergenic region] [gn:yico]
CONTIG401	9880166_c3_97	1462	7124	1587	529	2038	6.5(10)-211	Escherichia coli	b3746	[pn:hypothetical 57.4 kd protein in asna-kup intergenic region] [gn:yien]
CONTIG401	4007813_c3_100	1463	7125	468	156	605	4.5(10)-59	Escherichia coli	b3743	[pn:regulatory protein] [gn:asnc]
CONTIG401	196080_c3_101	1464	7126	540	180	559	3.5(10)-54	Escherichia coli	b3742	[pn:involved in modulation of initiation at oric] [gn:mioc]
CONTIG402	7082715_f1_3	1465	7127	978	326	1390	3.0(10)-142	Escherichia coli	b2378	[pn:hypothetical protein]
CONTIG402	6837836_f1_8	1466	7128	735	245	1148	1.3(10)-116	Escherichia coli	b2381	[pn:hypothetical protein]
CONTIG402	20703533_f1_11	1467	7129	1260	420	1163	3.3(10)-118	Escherichia coli	b2389	[pn:hypothetical protein]
CONTIG402	19724077_f2_15	1468	7130	957	319	1145	2.7(10)-116	Escherichia coli	b2347	[pn:hypothetical 34.5 kd protein in argw 5''' region] [gn:yfdc]
CONTIG402	24782786_f3_31	1469	7131	381	127	94	0.00072	Pseudomonas sp.	L81125	or:pseudomonas sp. pn:monooxygenase subunit le:502 re:2016 di.direct sr:pseudomonas sp (strain imt37) dna
CONTIG402	6343752_f3_38	1470	7132	1725	575	2476	2.5(10)-257	Escherichia coli	b2380	[pn:hypothetical protein]

CONTIG402	24745641_c1_45	1471	7133	1311	437	1930	1.8(10)-199	Enterobacter cloacae	P23234	indole-3-pyruvate decarboxylase (cc 4.1.1.74) (indolepyruvate decarboxylase).
CONTIG402	25473516_c1_51	1472	7134	1254	418	2026	1.2(10)-209	Escherichia coli	b2379	[pn:hypothetical protein]
CONTIG402	33474091_c2_61	1473	7135	981	327	1556	7.7(10)-160	Escherichia coli	b2388	[pn:glucokinase] [gn:glk]
CONTIG402	11770652_c2_72	1474	7136	1416	472	1587	4.0(10)-163	Escherichia coli	b1490	[pn:hypothetical protein]
CONTIG402	7292291_c2_74	1475	7137	888	296	1111	1.1(10)-112	Escherichia coli	b2346	[pn:vac] lipoprotein precursor
CONTIG403	25567885_f1_10	1476	7138	525	175	898	4.0(10)-90	Escherichia coli	b0264	[pn:insertion element is1 protein insb] [gn:insb_2]
CONTIG403	2911290_f1_15	1477	7139	234	78	254	7.2(10)-22	Escherichia coli	S40546	hypothetical protein - escherichia coli
CONTIG403	24489756_f2_28	1478	7140	942	314	101	0.05299	Methanococcu s jannaschii	MJ1322	[pn:purine ntpase]
CONTIG403	6735393_f2_29	1479	7141	285	95	446	3.2(10)-42	Escherichia coli	b4294	[pn:insertion element is1f protein insa] [gn:insa_7]
CONTIG403	25567885_f2_36	1480	7142	525	175	829	8.5(10)-83	Escherichia coli	b0264	[pn:insertion element is1 protein insb] [gn:insb_2]
CONTIG403	2911290_f3_50	1481	7143	234	78	296	2.6(10)-26	Escherichia coli	S40546	hypothetical protein - escherichia coli
CONTIG403	6735393_f3_55	1482	7144	285	95	446	3.2(10)-42	Escherichia coli	b4294	[pn:insertion element is1f protein insa] [gn:insa_7]
CONTIG403	21666540_f3_56	1483	7145	729	243	1128	1.8(10)-114	Transposon Tn1525	M12900	or:transposon tn1525 gn:p12 le:996 re:>1721 di:direct sr:transposon tn1525 dna nt:putative
CONTIG403	14885165_c1_59	1484	7146	297	99	377	6.7(10)-35	Escherichia coli	D93826	hypothetical 11k protein (insertion sequence is1) -escherichia coli this protein is coded by the insertion sequence is1.
CONTIG403	11909633_c1_60	1485	7147	681	227	420	1.8(10)-39	Escherichia coli	b3025	[pn:hypothetical protein] [gn:ygix]
CONTIG403	35556507_c1_71	1486	7148	1413	471	1826	1.8(10)-188	Pseudomonas aeruginosa	Y10528	[PN:cyanide insensitive terminal oxidase] [GN:cioA] [DE:P aeruginosa cioA and cioB genes.] [LE:276] [RE:1742] [DI:direct]

CONTIG403	111891882_c2_73	1487	7149	738	246	1268	2.6(10)-129	Salmonella ordonez	S34451	hypothetical protein (insertion sequence is26l) - salmonellaordonez plasmid pip173
CONTIG403	14885165_c2_77	1488	7150	297	99	390	2.7(10)-36	Escherichia coli	D93826	hypothetical 11k protein (insertion sequence is1) -escherichia coli this protein is coded by the insertion sequence is1.
CONTIG403	36501937_c3_89	1489	7151	1386	462	347	1.0(10)-31	Escherichia coli	b3026	[pn:hypothetical protein] [gn:ygiy]
CONTIG403	35410666_c3_96	1490	7152	348	116	104	5.7(10)-6	Escherichia coli	Q32331	transcriptional repressor protein korc.
CONTIG403	24109468_c3_99	1491	7153	1041	347	1016	1.3(10)-102	Pseudomonas aeruginosa	Y10528	[PN:cyanide insensitive terminal oxidase] [GN:cioB] [DE:P.aeruginosa cioA and cioB genes.] [LE:1746] [RE:2753] [DI:direct]
CONTIG404	4453427_f1_14	1492	7154	501	167	253	9.1(10)-22	Escherichia coli	b1164	[pn:hypothetical protein]
CONTIG404	34413938_f1_15	1493	7155	381	127	212	2.0(10)-17	Escherichia coli	b1166	[pn:hypothetical protein]
CONTIG404	21509432_f2_40	1494	7156	2184	728	2478	1.5(10)-257	Escherichia coli	b4079	[pn:formate dehydrogenase, formate- hydrogen-lyase-linked, selenocysteine-containing polypeptide] [gn:fdhf]
CONTIG404	4882768_c1_67	1495	7157	687	229	413	1.0(10)-38	Escherichia coli	b4316	[pn:chaperone protein involved in biogenesis of type 1 fimbriae] [gn:fime]
CONTIG404	6506280_c1_68	1496	7158	2571	857	1485	2.6(10)-152	Escherichia coli	b3144	[pn:hypothetical outer membrane usher protein in agal-mtr intergenic region] [gn:yraj]
CONTIG404	16130091_c1_71	1497	7159	681	227	176	1.3(10)-13	Escherichia coli	b4319	[pn:fimg protein precursor] [gn:fimg]
CONTIG404	14485390_c1_77	1498	7160	1284	428	1312	5.5(10)-134	Escherichia coli	b1163	[pn:hypothetical protein]
CONTIG404	35431691_c1_78	1499	7161	852	284	812	5.4(10)-81	Escherichia coli	b1162	[pn:hypothetical protein]
CONTIG404	4008518_c1_79	1500	7162	378	126	563	1.3(10)-54	Escherichia coli	b1684	[pn:hypothetical protein] [gn:ydic]

CONTIG404	14900762_c1_82	1501	7163	1317	439	1843	3.0(10)-190	Escherichia coli	b1681	[pn:hypothetical protein]
CONTIG404	35335205_c2_87	1502	7164	1065	355	145	1.1(10)-9	Escherichia coli	b0530	[pn:hypothetical protein] [gn:sfma]
CONTIG404	22160268_c2_99	1503	7165	534	178	515	1.6(10)-49	Escherichia coli	b1679	[pn:hypothetical protein]
CONTIG404	12382906_c3_117	1504	7166	846	282	1343	2.8(10)-137	Escherichia coli	b1683	[pn:hypothetical protein]
CONTIG404	12681461_c3_118	1505	7167	702	234	1158	1.2(10)-117	Escherichia coli	b1683	[pn:hypothetical protein]
CONTIG404	4479693_c3_119	1506	7168	756	252	1168	1.0(10)-118	Escherichia coli	b1682	[pn:hypothetical protein]
CONTIG404	15913557_c3_120	1507	7169	1269	423	1797	2.2(10)-185	Escherichia coli	b1680	[pn:hypothetical protein]
CONTIG404	2152177_c3_122	1508	7170	609	203	740	2.2(10)-73	Escherichia coli	b1678	[pn:hypothetical protein]
CONTIG405	33886088_f1_1	1509	7171	495	165	90	0.034	Bacillus subtilis	ybfI	[pn:hypothetical protein]
CONTIG405	11050187_f1_2	1510	7172	990	330	146	7.4(10)-10	Escherichia coli	b2578	[pn:hypothetical 21.2 kd protein in smb-ung intergenic region]
CONTIG405	23833393_f1_12	1511	7173	810	270	341	4.4(10)-31	Escherichia coli	X02307	or:escherichia coli le:115 re:522 di:complement nt:urf 4
CONTIG405	36414562_f1_21	1512	7174	537	179	456	2.7(10)-43	Escherichia coli	b4144	[pn:hypothetical protein] [gn:yjei]
CONTIG405	6522338_f1_23	1513	7175	843	281	966	2.6(10)-97	Escherichia coli	b4147	[pn:elongation factor p] [gn:efp]
CONTIG405	4346033_f2_33	1514	7176	1221	407	247	4.0(10)-21	Escherichia coli	X02307	or:escherichia coli le:2104 re:2802 di:complement nt:urf 3
CONTIG405	23571887_f2_37	1515	7177	555	185	376	8.5(10)-35	Escherichia coli	b4140	[pn:hypothetical protein]
CONTIG405	12141687_f2_41	1516	7178	390	130	449	1.6(10)-42	Escherichia coli	b4142	[pn:groes protein] [gn:mopb]
CONTIG405	21523957_f3_51	1517	7179	219	73	104	2.2(10)-5	Bacillus subtilis	ybfI	[pn:hypothetical protein]
CONTIG405	24798443_f3_64	1518	7180	1659	553	2236	6.7(10)-232	Escherichia coli	b4143	[pn:60 kd chaperonin] [gn:mopa]
CONTIG405	13104628_f3_71	1519	7181	333	111	338	9.0(10)-31	Escherichia coli	b4148	[pn:suges] [gn:suge]

CONTIG405	3017827_c1_81	1520	7182	1248	416	1588	3.1(10)-163	Escherichia coli	b4141	[pn:hypothetical 44.8 kd protein in aspa-mopb intergenic region] [gn:yjeh]
CONTIG405	4353830_c1_83	1521	7183	1518	506	2253	1.1(10)-233	Escherichia coli	b4139	[pn:aspartate ammonia-lyase] [gn:aspa]
CONTIG405	2037566_c1_87	1522	7184	1722	574	2053	1.7(10)-212	Escherichia coli	b4136	[pn:thiol] [gn:dsbd]
CONTIG405	24005301_c2_98	1523	7185	1041	347	1532	2.7(10)-157	Escherichia coli	b4146	[pn:hypothetical 38.7 kd protein in mopa-efp intergenic region]
CONTIG405	19688916_c2_101	1524	7186	627	209	601	1.2(10)-58	Escherichia coli	b4329	[pn:hypothetical 16.2 kd protein in iada-mcd intergenic region]
CONTIG405	6511528_c2_102	1525	7187	1674	558	101	0.00259	Mycobacterium tuberculosis	M15467	or:mycobacterium tuberculosis pn:unknown protein le:1194 re:1670 di:complement sr:mycobacterium tuberculosis (strain erdman) dna nt.orf d158; putative
CONTIG405	2986693_c2_109	1526	7188	336	112	426	4.2(10)-40	Escherichia coli	b4137	[pn:c-type cy] [gn:cuta]
CONTIG405	30080456_c2_110	1527	7189	681	227	916	5.0(10)-92	Escherichia coli	b4135	[pn:yjdc]
CONTIG405	26777213_c3_113	1528	7190	966	322	703	1.8(10)-69	Escherichia coli	b4149	[pn:hypothetical 19.9 kd protein in suga-ampc intergenic region]
CONTIG405	16620215_c3_115	1529	7191	639	213	118	1.3(10)-5	Escherichia coli	b1951	[pn:colanic acid capsular biosynthesis activation protein a] [gn:rcsa]
CONTIG405	6291406_c3_118	1530	7192	711	237	762	1.1(10)-75	Escherichia coli	b4330	[pn:hypothetical 24.2 kd protein in iada-mcd intergenic region]
CONTIG405	10317165_c3_119	1531	7193	1191	397	1216	8.3(10)-124	Escherichia coli	b4328	[pn:isoaspartyl dipeptidase] [gn:iada]
CONTIG405	134683_c3_123	1532	7194	474	158	233	1.2(10)-19	Mycobacterium tuberculosis	M15467	or:mycobacterium tuberculosis pn:unknown protein le:242 re:769 di:complement sr:mycobacterium tuberculosis (strain erdman) dna nt.orf f175; putative
CONTIG405	7214683_c3_129	1533	7195	1317	439	1127	2.2(10)-114	Escherichia coli	b4138	[pn:anaerobic c4-dicarboxylate transporter deua] [gn:deua]
CONTIG406	15673342_f1_9	1534	7196	1734	578	2055	1.0(10)-212	Escherichia coli	b1336	[pn:hypothetical protein in ogf 5'''region] [gn:ydah]

CONTIG406	5100443_f1_10	1535	7197	525	175	717	6.2(10)-71	Escherichia coli	b1335	[pn:o6-methylguanine-dna-alkyltransferase] [gn:ogt]
CONTIG406	24103168_f1_11	1536	7198	768	256	1255	6.0(10)-128	Escherichia coli	b1334	[pn:fumarate and nitrate reduction regulatory protein] [gn:fnr]
CONTIG406	26613250_f2_21	1537	7199	1470	490	1998	1.1(10)-206	Escherichia coli	b1337	[pn:hypothetical protein]
CONTIG406	25942627_f3_28	1538	7200	1719	573	1220	3.1(10)-124	Escherichia coli	b4355	[pn:methyl-accepting chemotaxis protein ii] [gn:tsr]
CONTIG406	22345917_f3_29	1539	7201	1347	449	1668	1.0(10)-171	Escherichia coli	b1338	[pn:hypothetical protein] [gn:yda]
CONTIG406	16503_f3_36	1540	7202	999	333	1547	7.0(10)-159	Escherichia coli	b1333	[pn:35.6 kd protein in tpx-fnr intergenic region] [gn:ydaa]
CONTIG406	22073937_c2_63	1541	7203	1296	432	1811	7.4(10)-187	Escherichia coli	b1602	[pn:pyridine nucleotide transhydrogenase subunit- beta] [gn:pnth]
CONTIG406	4339527_c2_82	1542	7204	897	299	1093	9.0(10)-111	Escherichia coli	b1406	[pn:hypothetical 30.7 kd protein near the replication terminus] [gn:ydbc]
CONTIG406	23677087_c3_83	1543	7205	1230	410	1253	9.9(10)-128	Salmonella typhimurium	U94729	[dc:salmonella typhimurium oxd-6 operon, putative substrate-binding protein (oxd-6a), putative transmembrane protein (oxd-6), putative transmembrane protein (oxd-6c), putative atpase (oxd-6d), and putative atpase (oxd-6e)]
CONTIG406	3963432_c3_92	1544	7206	927	309	1201	3.2(10)-122	Escherichia coli	b1339	[pn:hypothetical protein]
CONTIG406	29328408_c3_93	1545	7207	651	217	658	1.1(10)-64	Escherichia coli	b1340	[pn:hypothetical protein]
CONTIG407	119052_f1_4	1546	7208	1410	470	971	7.5(10)-98	Bacillus subtilis	sacA	[pn:sucrase-6-phosphate hydrolase] [gn:ipa-50d]
CONTIG407	9978192_f1_6	1547	7209	1602	534	552	1.8(10)-53	Escherichia coli	b1421	[pn:methyl-accepting chemotaxis protein iii] [gn:trg]
CONTIG407	9817713_f2_19	1548	7210	873	291	1222	1.8(10)-124	Klebsiella pneumoniae	P27218	sucrose porin precursor.
CONTIG407	3237531_f2_20	1549	7211	1437	479	918	3.1(10)-92	Bacillus subtilis	sacP	[pn:phosphotransferase system] [gn:ipa-49d]
CONTIG407	34422278_f2_23	1550	7212	1023	341	1420	2.0(10)-145	Klebsiella pneumoniae	P37076	sucrose (scr) operon repressor

CONTIG407	33797292_f2_25	1551	7213	837	279	688	7.4(10)-68	Escherichia coli	b0604	[pn:hypothetical protein]
CONTIG407	34192591_f3_42	1552	7214	591	197	114	1.3(10)-5	Bacillus subtilis	sigZ	[pn:ria polymerase ccf-type sigma factor]
CONTIG407	4188967_f3_47	1553	7215	894	298	418	3.0(10)-39	Bacillus subtilis	alsR	[pn:transcriptional regulator]
CONTIG407	962827_c1_56	1554	7216	1548	516	294	2.2(10)-24	Methanobacterium thermoautotrophicum	MTH1394	[pn:conserved protein]
CONTIG407	31808341_c2_72	1555	7217	1107	369	136	8.5(10)-7	Bacillus subtilis	ymP	[pn:hypothetical protein]
CONTIG407	22657666_c3_90	1556	7218	369	123	332	3.8(10)-30	Bacillus subtilis	yhxD	[pn:hypothetical protein]
CONTIG407	14553381_c3_92	1557	7219	936	312	276	3.3(10)-24	Escherichia coli	b0076	[pn:leuo]
CONTIG407	16253767_c3_95	1558	7220	1434	478	1768	2.7(10)-182	Escherichia coli	b1491	[pn:hypothetical protein]
CONTIG407	1457626_c3_100	1559	7221	318	106	96	0.00067	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn:trae gn:trae le-44196 re.46259 di:complement
CONTIG408	34398586_f1_14	1560	7222	609	203	655	2.2(10)-64	Escherichia coli	b1806	[pn:hypothetical protein]
CONTIG408	6120461_f2_20	1561	7223	1572	524	2053	1.7(10)-212	Escherichia coli	b1816	[pn:hypothetical protein] [gn:yoe]
CONTIG408	665793_f2_34	1562	7224	1206	402	1650	8.5(10)-170	Escherichia coli	b1804	[pn:ribonuclease d] [gn:rnd]
CONTIG408	14464211_f3_46	1563	7225	195	65	261	1.3(10)-22	Escherichia coli	b1811	[pn:hypothetical protein]
CONTIG408	6364088_f3_48	1564	7226	1920	640	2813	4.9(10)-293	Escherichia coli	b1808	[pn:hypothetical protein]
CONTIG408	15660326_f3_49	1565	7227	723	241	931	1.3(10)-93	Escherichia coli	b1807	[pn:hypothetical protein]
CONTIG408	23485885_f3_51	1566	7228	1755	585	2749	2.8(10)-286	Escherichia coli	b1805	[pn:long-chain-fatty-acid--coa ligase] [gn:fadD]
CONTIG408	915878_c1_53	1567	7229	270	90	422	1.1(10)-39	Escherichia coli	b1174	[pn:cell division topological specificity factor] [gn:mne]
CONTIG408	4416061_c1_74	1568	7230	966	322	1392	1.8(10)-142	Escherichia coli	b1817	[pn:pts system, mannose-specific iiab component] [gn:manx]

CONTIG408	20789142_c2_89	1569	7231	615	205	836	1.5(10)-83	Escherichia coli	b1813	[pn:hypothetical 21.4 kd protein in pabb-sdaa intergenic region] [gn:yeab]
CONTIG408	26844406_c3_105	1570	7232	504	168	548	5.0(10)-53	Escherichia coli	b1809	[pn:hypothetical protein]
CONTIG408	16265877_c3_106	1571	7233	1380	460	1671	5.0(10)-172	Escherichia coli	b1812	[pn:para-aminobenzoate synthase component i] [gn:pabb]
CONTIG408	29845761_c3_108	1572	7234	1407	469	2040	4.0(10)-211	Escherichia coli	b1814	[pn:l-serine dehydratase 1] [gn:sdaa]
CONTIG408	9784408_c3_109	1573	7235	1728	576	1732	1.7(10)-178	Escherichia coli	b1815	[pn:hypothetical protein]
CONTIG409	23714651_f1_16	1574	7236	573	191	95	0.03799	Thermus thermophilus	Y15464	[de:thermus thermophilus phes, phet genes and 5 orf ^{ms} .] [pn:ferredoxin oxidoreductase-like (gamma and alpha) [gn:orf2]
CONTIG409	26352002_f1_17	1575	7237	792	264	245	1.2(10)-20	Escherichia coli	b3442	[pn:hypothetical 44.2 kd protein in gntr-ggt intergenic region] [gn:yhbz]
CONTIG409	406255_f2_27	1576	7238	495	165	293	5.2(10)-26	Escherichia coli	b1183	[pn umud protein] [gn:umud]
CONTIG409	14885165_f3_46	1577	7239	297	99	390	2.7(10)-36	Escherichia coli	D93826	hypothetical 11k protein (insertion sequence is1) -escherichia coli this protein is coded by the insertion sequence is1.
CONTIG409	16486527_f3_48	1578	7240	1272	424	959	1.3(10)-96	Escherichia coli	b1184	[pn:umuc protein] [gn:umuc]
CONTIG409	33460927_f3_53	1579	7241	570	190	194	1.6(10)-15	Escherichia coli	Z68186	or-escherichia coli pn:bfpb gn:bfpb le:9044 re:9490 di:direct
CONTIG409	14578162_f3_54	1580	7242	228	76	181	1.7(10)-13	Escherichia coli	b3442	[pn:hypothetical 44.2 kd protein in gntr-ggt intergenic region] [gn:yhbz]
CONTIG409	4322963_f3_55	1581	7243	516	172	135	2.8(10)-9	Escherichia coli	b3443	[pn:hypothetical protein] [gn:ytha]
CONTIG409	24410340_c1_63	1582	7244	1500	500	214	5.0(10)-15	Plasmid F	M24492	or:plasmid f pn:periplasmic protein gn:trah le:550 re:1629 di:direct sr:plasmid f dna
CONTIG409	6735393_c1_72	1583	7245	285	95	446	3.2(10)-42	Escherichia coli	b4294	[pn:insertion element is1f protein insa] [gn:insa_7]
CONTIG409	15897332_c1_75	1584	7246	1959	653	115	0.00309	Lycopersicon esculentum	Y07861	or:lycopersicon esculentum pn:mfp1 protein gn:mfp1 le:6 re:2099 di:direct sr:tomato

CONTIG409	2047880_c1_76	1585	7247	315	105	369	4.7(10)-34	Yersinia pestis	AF053945	[de:yersinia pestis plasmid ppepl, complete plasmid sequence.] [pn:transposase]
CONTIG409	4901068_c2_80	1586	7248	759	253	347	1.0(10)-31	Escherichia coli	b2893	[pn:disulfide interchange protein, precursor] [gn:dsbc]
CONTIG409	34178880_c2_83	1587	7249	909	303	238	3.6(10)-20	Coxiella burnetii	A49232	outer membrane protein - coxiella burnetii
CONTIG409	2911290_c2_86	1588	7250	234	78	296	2.6(10)-26	Escherichia coli	S40546	hypothetical protein - escherichia coli
CONTIG409	25480326_c3_91	1589	7251	3963	1321	111	0.032	Bombyx mori	S52714	sericin1b - silkworm
CONTIG409	25567885_c3_96	1590	7252	525	175	898	4.0(10)-90	Escherichia coli	b0264	[pn:insertion element isl protein insb] [gn:insb_2]
CONTIG41	14492812_f1_1	1591	7253	453	151	410	2.1(10)-38	Escherichia coli	b0097	[pn:hypothetical 16.0 kd protein in lpxc-seca intergenic region] [gn:yaca]
CONTIG41	26688902_f3_3	1592	7254	213	71	278	2.1(10)-24	Escherichia coli	b0096	[pn:udp-3-o-3-hydroxymyristoyl n-acetylglucosamine deacetylase] [gn:lpxc]
CONTIG410	26593890_f1_19	1593	7255	1506	502	523	8.0(10)-58	Bacillus subtilis	yusP	[pn:hypothetical protein]
CONTIG410	20587883_f2_38	1594	7256	462	154	293	5.2(10)-26	Erwinia amylovora	L25828	or. erwinia amylovora le:10466 re:10885 di:direct nt:orf 12
CONTIG410	26449211_f3_46	1595	7257	963	321	218	5.7(10)-18	Escherichia coli	b2714	[pn:asc operon repressor protein] [gn:aseg]
CONTIG410	34070927_c1_67	1596	7258	672	224	155	2.2(10)-11	Escherichia coli	b1013	[pn:hypothetical protein] [gn:ycdc]
CONTIG410	24423367_c1_72	1597	7259	3141	1047	2558	5.0(10)-266	Escherichia coli	b0462	[pn:acriflavin resistance protein b] [gn:acrb]
CONTIG410	16828927_c1_73	1598	7260	1164	388	433	7.7(10)-41	Bacillus subtilis	ydgK	[pn:hypothetical protein]
CONTIG410	10948818_c1_76	1599	7261	327	109	182	3.1(10)-14	Bacillus subtilis	ydhM	[pn:hypothetical protein]
CONTIG410	34416581_c2_80	1600	7262	576	192	146	2.0(10)-10	Escherichia coli	b1618	[pn:glucuronide repressor] [gn:uidr]
CONTIG410	3396086_c2_81	1601	7263	1155	385	831	5.2(10)-83	Escherichia coli	b0463	[pn:acriflavin resistance protein a precursor] [gn:acra]
CONTIG410	12692683_c3_105	1602	7264	1386	462	744	8.5(10)-74	Escherichia coli	b0572	[pn:hypothetical protein] [gn:yicb]

CONTIG410	3016317_c3_113	1603	7265	1284	428	539	4.5(10)-52	Bacillus subtilis	ywbA	[pn:hypothetical protein] [gn:ipa-16d]
CONTIG411	24650302_f1_1	1604	7266	1062	354	1374	1.5(10)-140	Escherichia coli	b0929	[pn:outer membrane protein f precursor] [gn:ompf]
CONTIG411	22520135_f1_15	1605	7267	666	222	648	1.3(10)-63	Escherichia coli	b0920	[pn:hypothetical protein in kdsb-kicb intergenic region] [gn:ycbc]
CONTIG411	24851430_f2_17	1606	7268	1209	403	1930	1.8(10)-199	Escherichia coli	b0928	[pn:aspartate aminotransferase] [gn:aspc]
CONTIG411	35814061_c1_59	1607	7269	816	272	1089	2.3(10)-110	Escherichia coli	b0921	[pn:hypothetical 29.8 kd protein in kdsb-kicb intergenic region] [gn:smta]
CONTIG411	25663880_c1_60	1608	7270	1326	442	2147	1.8(10)-222	Escherichia coli	b0922	[pn:mukf protein] [gn:mukf]
CONTIG411	34274216_c1_61	1609	7271	4464	1488	6395	0	Escherichia coli	b0924	[pn:mukb]
CONTIG411	15686_c1_65	1610	7272	582	194	820	7.5(10)-82	Escherichia coli	b0926	[pn:hypothetical protein] [gn:ycbk]
CONTIG411	30730282_c2_75	1611	7273	801	267	1108	2.2(10)-112	Escherichia coli	b0923	[pn:muke protein] [gn:muke]
CONTIG411	13088555_c2_76	1612	7274	225	75	93	8.3(10)-5	Homo sapiens	S40543	or:homo sapiens pn:low density lipoprotein receptor le:1 re:177 dr:direct sr:human nt:description: low density lipoprotein receptor, ldl cell division protein mukb.
CONTIG411	33839465_c2_79	1613	7275	330	110	136	9.3(10)-8	Escherichia coli	P22523	
CONTIG411	16542168_c3_89	1614	7276	1908	636	2340	6.5(10)-243	Escherichia coli	b0925	[pn:hypothetical protein in mukb 3''' region] [gn:ycbb]
CONTIG411	35683285_c3_90	1615	7277	693	231	981	6.5(10)-99	Escherichia coli	b0927	[pn:hypothetical protein] [gn:ycbl]
CONTIG411	1442568_c3_91	1616	7278	1218	406	393	1.3(10)-36	Pseudomonas aeruginosa	U50396	or:pseudomonas aeruginosa pn:wbpn gn:wbpn le:22302 re:23693 di:direct
CONTIG412	13087788_f1_13	1617	7279	1392	464	543	1.7(10)-52	Bacillus subtilis	ycnF	[pn:hypothetical protein]
CONTIG412	31344415_f1_14	1618	7280	1586	529	1902	1.7(10)-196	Escherichia coli	b4340	[pn:hypothetical 53.0 kd protein in iada-merd intergenic region]
CONTIG412	24431531_f2_15	1619	7281	1275	425	1574	9.5(10)-162	Escherichia coli	b4336	[pn:hypothetical 48.2 kd protein in iada-merd intergenic region]
CONTIG412	4957168_f3_36	1620	7282	528	176	183	2.3(10)-14	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:catr le:59 re:580 di:direct nt:orf2

CONTIG412	31431505_f3_38	1621	7283	906	302	510	5.4(10)-49	Escherichia coli	b0900	[pn:hypothetical protein] [gn:yea]
CONTIG412	26432281_c1_50	1622	7284	1050	350	276	3.3(10)-24	Bacillus subtilis	ydfG	[pn:hypothetical protein]
CONTIG412	13783340_c1_57	1623	7285	495	165	208	5.4(10)-17	Escherichia coli	b1642	[pn:hypothetical protein] [gn:slya]
CONTIG412	5119091_c2_74	1624	7286	744	248	373	1.8(10)-34	Bacillus subtilis	ydfF	[pn:hypothetical protein]
CONTIG412	22895156_c3_78	1625	7287	189	63	161	5.2(10)-12	Escherichia coli	b4341	[pn:hypothetical protein] [gn:yjis]
CONTIG412	3407211_c3_84	1626	7288	1449	483	687	9.4(10)-68	Escherichia coli	b0312	[pn:betaine aldehyde dehydrogenase] [gn:betb]
CONTIG412	2081292_c3_85	1627	7289	399	133	96	4.0(10)-5	Bacillus subtilis	yqjZ	[pn:hypothetical protein]
CONTIG412	4883288_c3_87	1628	7290	1077	359	267	3.0(10)-23	Escherichia coli	b4082	[pn:hypothetical 36.9 kd protein in fdhF-phn intergenic region]
CONTIG413	22370937_f1_4	1629	7291	948	316	1266	4.2(10)-129	Escherichia coli	b2131	[pn:hypothetical 32.6 kd protein in molr-bglx intergenic region] [gn:yeHz]
CONTIG413	16986091_f1_5	1630	7292	1170	390	662	4.2(10)-65	Escherichia coli	b2130	[pn:hypothetical abc transporter permease protein yehY] [gn:yeHy]
CONTIG413	17058580_f2_17	1631	7293	1104	368	1257	3.7(10)-128	Escherichia coli	b2129	[pn:hypothetical abc transporter in molr-bglx intergenic region] [gn:yeHx]
CONTIG413	3227158_f2_24	1632	7294	771	257	1035	1.3(10)-104	Escherichia coli	b2125	[pn:hypothetical 27.9 kd protein in molr-bglx intergenic region]
CONTIG413	14255177_f3_28	1633	7295	285	95	441	1.1(10)-41	Escherichia coli	b2134	[pn:penicillin-binding protein 7 precursor] [gn:pbpg]
CONTIG413	7223781_f3_34	1634	7296	2391	797	3750	0	Escherichia coli	b2132	[pn:periplasmic beta-glucosidase precursor] [gn:bglx]
CONTIG413	30666041_f3_39	1635	7297	741	247	821	6.0(10)-82	Escherichia coli	b2128	[pn:hypothetical 25.5 kd protein in molr-bglx intergenic region] [gn:yeHw]
CONTIG413	1431637_f3_40	1636	7298	1704	568	2269	2.2(10)-235	Escherichia coli	b2126	[pn:hypothetical 62.1 kd protein in molr-bglx intergenic region] [gn:yeHu]
CONTIG413	14642543_f3_42	1637	7299	525	175	642	5.5(10)-63	Escherichia coli	b2124	[pn:hypothetical 18.0 kd protein in molr-bglx intergenic region] [gn:yeHs]

CONTIG413	21565658_c1_45	1638	7300	1182	394	1740	2.5(10)-179	Escherichia coli	b2114	[pn:methionyl-trna synthetase] [gn:metg]
CONTIG413	24397250_c1_48	1639	7301	825	275	890	2.8(10)-89	Escherichia coli	b2127	[pn:hypothetical transcriptional regulator in molr-bglx intergenic region] [gn:yehv]
CONTIG413	16620831_c2_85	1640	7302	1923	641	2678	9.8(10)-279	Escherichia coli	b2133	[pn:d-lactate dehydrogenase] [gn:dlld]
CONTIG413	23847008_c2_86	1641	7303	636	212	488	1.2(10)-46	Alcaligenes faecalis	P31668	phosphinothricin-resistance protein (ptc-resistance protein).
CONTIG414	25829787_f1_1	1642	7304	900	300	1364	1.7(10)-139	Escherichia coli	b4161	[pn:hypothetical 37 7 kd protein in psd-amib intergenic region]
CONTIG414	23567037_f1_9	1643	7305	417	139	472	5.7(10)-45	Escherichia coli	b4152	[pn:fumarate reductase, membrane anchor polypeptide] [gn:frdc]
CONTIG414	3162711_f1_12	1644	7306	1254	418	1245	7.0(10)-127	Escherichia coli	b4150	[pn:beta-lactamase precursor] [gn:ampc]
CONTIG414	2439512_f2_13	1645	7307	1044	348	1600	1.7(10)-164	Escherichia coli	b4160	[pn:phosphatidylserine decarboxylase proenzyme] [gn:psd]
CONTIG414	33206957_f2_21	1646	7308	1842	614	2810	1.0(10)-292	Escherichia coli	b4154	[pn:fumarate reductase flavoprotein subunit] [gn:frda]
CONTIG414	10948336_f2_22	1647	7309	417	139	535	1.2(10)-51	Escherichia coli	b4151	[pn:fumarate reductase, membrane anchor polypeptide] [gn:frdd]
CONTIG414	16879681_f3_26	1648	7310	3483	1161	4253	0	Escherichia coli	b4159	[pn:hypothetical 123.8 kd protein in genx-psd intergenic region]
CONTIG414	32131937_f3_35	1649	7311	810	270	1239	3.0(10)-126	Escherichia coli	b4153	[pn:fumarate reductase iron-sulfur protein] [gn:frdb]
CONTIG414	37576_c1_41	1650	7312	903	301	1516	1.3(10)-155	Enterobacter cloacae	A25686	ampr protein - enterobacter cloacae
CONTIG414	26056526_c1_48	1651	7313	981	327	1573	1.2(10)-161	Escherichia coli	b4155	[pn:lysyl-trna synthetase analog] [gn:yjea]
CONTIG414	163931_c2_66	1652	7314	1563	521	1981	7.0(10)-205	Escherichia coli	b4156	[pn:hypothetical 56.3 kd protein in genx-psd intergenic region]
CONTIG415	23572162_f1_1	1653	7315	642	214	883	1.6(10)-88	Serratia marcescens	U59131	or:serratia marcescens le:1362 re:1982 di:direct nt:orfb
CONTIG415	4876425_f1_10	1654	7316	306	102	418	3.0(10)-39	Escherichia coli	b2105	[pn:hypothetical protein] [gn:yohl]
CONTIG415	32230063_f1_19	1655	7317	1311	437	172	3.1(10)-9	Saccharomyces cerevisiae	YDL058 W	[pn:intracellular protein transport protein] [gn:usol]
CONTIG415	23928775_f2_26	1656	7318	765	255	1195	1.3(10)-121	Serratia marcescens	U59131	or:serratia marcescens pn:sbba gn:sbba le:313 re:1350 di:direct

CONTIG415	19572828_f2_27	1657	7319	1416	472	2236	6.7(10)-232	Escherichia coli	S70165	,
CONTIG415	6297128_f2_34	1658	7320	825	275	102	0.016	Serratia marcescens	U60283	or:serratia marcescens pn:restriction methylase gn:trg1 le:84 re:1775 di:direct nt:putative restriction methylase
CONTIG415	24744778_f2_39	1659	7321	447	149	237	4.5(10)-20	Escherichia coli	P09183	very hypothetical 20.3 kd protein in dem 3'region (orf 3).
CONTIG415	6439528_f3_43	1660	7322	255	85	358	6.9(10)-33	Escherichia coli	I77547	hypothetical protein 2 (insertion sequence is903) -escherichia coli
CONTIG415	20984450_f3_49	1661	7323	468	156	618	1.8(10)-60	Escherichia coli	S70162	,
CONTIG415	4875376_f3_58	1662	7324	585	195	265	4.9(10)-23	Haemophilus influenzae	I111296	[pn:partitioning system protein] [gn:parb]
CONTIG415	21726630_c1_67	1663	7325	1536	512	802	6.2(10)-80	Rhizobium sp.	P55501	hypothetical 57.2 kd protein y4ja/y4ne/y4se,
CONTIG415	31532840_c2_86	1664	7326	1101	367	787	2.3(10)-78	Yersinia pestis	AF053947	[de:yersinia pestis plasmid pm1, complete plasmid sequence.] [pn:transposase]
CONTIG415	14704677_c2_87	1665	7327	990	330	1597	3.5(10)-164	Escherichia coli	X02527	or:escherichia coli le:199 re:1122 di:direct nt:orf1 (aa 1-307)
CONTIG415	33992155_c3_92	1666	7328	1482	494	1385	1.0(10)-141	Escherichia coli	b1961	[pn:dna-cytosine methyltransferase] [gn:dem]
CONTIG415	15750433_c3_99	1667	7329	786	262	474	3.5(10)-45	Rhizobium sp.	P55500	putative insertion sequence atp-binding protein y4iq/y4nd/y4sd,
CONTIG415	5117806_c3_101	1668	7330	1131	377	498	3.8(10)-93	Escherichia coli	b2106	[pn:hypothetical protein]
CONTIG416	16260012_f1_8	1669	7331	1026	342	1058	4.5(10)-107	Escherichia coli	b3196	[pn:hypothetical 34.7 kd protein in murz-rpon intergenic region] [gn:yrbg]
CONTIG416	32547880_f1_9	1670	7332	606	202	869	4.9(10)-87	Escherichia coli	b3198	[pn:hypothetical 20.0 kd protein in murz-rpon intergenic region] [gn:yrbg]
CONTIG416	1445325_f1_10	1671	7333	576	192	655	2.2(10)-64	Escherichia coli	b3200	[pn:17.3 kd protein in rpon 5'''region precursor] [gn:yhbh]
CONTIG416	16828525_f1_11	1672	7334	732	244	1175	1.8(10)-119	Escherichia coli	b3201	[pn:probable abc transporter in ntra/rpon 5'''region] [gn:yhbh]
CONTIG416	29928931_f1_12	1673	7335	417	139	339	7.0(10)-31	Escherichia coli	b3203	[pn:probable signal] [gn:yhbh]

CONTIG416	35556932_f1_13	1674	7336	372	124	438	2.2(10)-41	Escherichia coli	b3206	[pn:phosphocarrier protein npr] [gn:ptso]
CONTIG416	13127067_f2_22	1675	7337	891	297	1242	1.5(10)-126	Escherichia coli	b3187	[pn:octaprenyl pyro] [gn:ispb]
CONTIG416	17540_f2_23	1676	7338	342	114	389	3.6(10)-36	Escherichia coli	b3188	[pn:ner-like protein] [gn:nlp]
CONTIG416	212966_f2_31	1677	7339	1062	354	1444	5.7(10)-148	Escherichia coli	b3197	[pn:hypothetical 35.2 kd protein in murz-rpon intergenic region] [gn:yrbh]
CONTIG416	25678166_f2_36	1678	7340	507	169	753	9.5(10)-75	Escherichia coli	b3204	[pn:enzyme liant] [gn:ptsn]
CONTIG416	36524205_f2_37	1679	7341	900	300	1357	9.5(10)-139	Escherichia coli	b3205	[pn:hypothetical protein] [gn:yhbj]
CONTIG416	17070418_f3_58	1680	7342	594	198	770	1.5(10)-76	Escherichia coli	b3199	[pn:hypothetical 21.7 kd protein in murz-rpon intergenic region] [gn:yrbk]
CONTIG416	21756342_f3_60	1681	7343	1473	491	1867	8.5(10)-193	Escherichia coli	b3202	[pn:sigma-n] [gn:rpon]
CONTIG416	34395429_c1_70	1682	7344	833	277	1192	2.8(10)-121	Escherichia coli	b4262	[pn:hypothetical 39.8 kd protein in pepa-gntv intergenic region] [gn:yjgc]
CONTIG416	24412837_c1_73	1683	7345	501	167	617	2.5(10)-60	Escherichia coli	b3210	[pn:aerobic respiration control sensor protein arch] [gn:arcb]
CONTIG416	35438562_c1_74	1684	7346	759	253	917	4.0(10)-92	Escherichia coli	b3208	[pn:hypothetical 27.3 kd protein in pto-arcb intergenic region] [gn:yrbm]
CONTIG416	13078568_c1_89	1685	7347	798	266	1236	6.2(10)-126	Escherichia coli	b3194	[pn:hypothetical 27.9 kd protein in murz-rpon intergenic region] [gn:yrbf]
CONTIG416	35750840_c1_90	1686	7348	357	119	371	2.8(10)-34	Escherichia coli	b3191	[pn:hypothetical 14.4 kd protein in murz-rpon intergenic region] [gn:yrbf]
CONTIG416	20875000_c1_91	1687	7349	381	127	412	1.3(10)-38	Escherichia coli	b3190	[pn:hypothetical 9.5 kd protein in murz-rpon intergenic region] [gn:yrbf]
CONTIG416	7930_c2_96	1688	7350	702	234	792	7.0(10)-79	Escherichia coli	b3209	[pn:sigma cross-reacting protein 27a] [gn:yhbl]
CONTIG416	4978140_c2_108	1689	7351	567	189	610	1.3(10)-59	Escherichia coli	b3193	[pn:hypothetical protein] [gn:yrbd]

CONTIG416	24823250_c2_109	1690	7352	654	218	1004	2.3(10)-101	Escherichia coli	b3192	[pn:hypothetical 24.0 kd protein in murz-rpon intergenic region] [gn:yrbcb]
CONTIG416	34381303_c3_112	1691	7353	1977	659	2853	2.7(10)-297	Escherichia coli	b3210	[pn:aerobic respiration control sensor protein arcB] [gn:arcB]
CONTIG416	14630327_c3_127	1692	7354	813	271	1182	3.2(10)-120	Escherichia coli	b3195	[pn:hypothetical protein] [gn:yrbf]
CONTIG416	16211468_c3_132	1693	7355	1305	435	1930	1.8(10)-199	Escherichia coli	b3189	[pn:udp-n-acetylglucosamine 1-carboxyvinyltransferase] [gn:mura]
CONTIG417	33376713_f1_3	1694	7356	1020	340	108	1.2(10)-5	coliphage T4	P39506	hypothetical 9.5 kd protein in frd-gp32 intergenic region.
CONTIG417	10976425_f2_30	1695	7357	201	67	94	6.5(10)-5	Escherichia coli	b1565	[pn:hypothetical protein]
CONTIG417	21775383_f2_45	1696	7358	300	100	505	1.8(10)-48	Bacteriophage lambda	J01735	ori:bacteriophage lambda le 525 re:851 di:direct sr:bacteriophage lambda kh100 is5 element nt:small gene
CONTIG417	21877261_f2_46	1697	7359	252	84	327	1.3(10)-29	Escherichia coli	b1371	[pn:hypothetical protein]
CONTIG417	33691012_c1_72	1698	7360	855	285	508	8.8(10)-49	Rhizobium sp.	P55373	putative transposase y4bf,
CONTIG417	4299217_c2_88	1699	7361	642	214	903	1.2(10)-90	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG417	2118828_c2_89	1700	7362	1053	351	301	4.2(10)-26	Mycobacterium leprae	Z97369	[PN:hypothetical protein MLCB250.18c] [GN.MLCB250.18c] [DE:Mycobacterium leprae cosmid B250] [NT:MLCB250.18c, unknown, len: 596 aa; highly similar] [LE:5885] [RE:7675] [DI: complement]
CONTIG417	30204130_c2_90	1701	7363	279	93	109	9.8(10)-6	Escherichia coli	U95365	transposase, is5b,
CONTIG417	34629052_c2_96	1702	7364	690	230	236	5.7(10)-20	Escherichia coli	b1567	[pn:hypothetical protein]
CONTIG417	160080_c2_97	1703	7365	948	316	747	4.0(10)-74	Synechocystis sp	P74068	[GN.SL11263] [SR:PCC 6803,] [DE:HYPOTHETICAL 33.3 KD PROTEIN SLL11263] [SP:P74068]

CONTIG417	16837632_c2_98	1704	7366	294	98	473	4.5(10)-45	Escherichia coli	b1563	[pn:hypothetical rele protein] [gn:rele]
CONTIG417	4339135_c3_104	1705	7367	1026	342	1767	3.3(10)-182	Escherichia coli	b1994	[pn:insertion element is5 hypothetical 39.3 kd protein]
CONTIG417	25830_c3_115	1706	7368	1374	458	278	1.0(10)-22	Streptomyces coelicolor	P14707	mini-circle hypothetical 45.7 kd protein.
CONTIG417	33494038_c3_116	1707	7369	243	81	387	5.7(10)-36	Escherichia coli	b1564	[pn:relb protein] [gn:relb]
CONTIG417	628161_c3_117	1708	7370	189	63	127	2.1(10)-8	Escherichia coli	P23587	f1mc protein homolog.
CONTIG418	35314451_f1_2	1709	7371	1212	404	1621	1.0(10)-166	Escherichia coli	b2028	[pn:hypothetical protein] [gn:ugd]
CONTIG418	14635416_f1_7	1710	7372	468	156	194	1.6(10)-15	Escherichia coli	D90840	or:escherichia coli gn:ylh028w le:12646 re:12942 dt:complement sr:escherichia coli (strain:k12) dna, clone_lib.kohara lambda minise nt:orf_id:o350#11; similar to [swissprot accession]
CONTIG418	2776938_f1_15	1711	7373	351	117	102	0.00046	Homo sapiens	AC004493	[de:homo sapiens chromosome 16, cosmid clone 373c8 (lam)], complete sequence.] [pn:kiaa0324] [gn:kiaa0324]
CONTIG418	17051316_f2_18	1712	7374	1143	381	1544	1.3(10)-158	Escherichia coli	b2041	[pn:tdp-glucose 4,6-dehydratase] [gn:rbb]
CONTIG418	32229077_f2_19	1713	7375	882	294	1314	3.3(10)-134	Escherichia coli	b2039	[pn:tdp-glucose pyrophosphorylase] [gn:rba]
CONTIG418	6057958_f2_31	1714	7376	876	292	1133	5.2(10)-115	Escherichia coli	b2016	[pn:hypothetical protein]
CONTIG418	32553165_f3_32	1715	7377	1449	483	2300	1.1(10)-238	Escherichia coli	b2029	[pn:6-phosphogluconate dehydrogenase, decarboxylating] [gn:gnd]
CONTIG418	15113290_f3_39	1716	7378	1143	381	901	2.0(10)-90	Escherichia coli	b2027	[pn:hypothetical protein]
CONTIG418	31739687_c1_53	1717	7379	984	328	1450	1.3(10)-148	Escherichia coli	b2019	[pn:atp phosphoribosyltransferase] [gn:hig]
CONTIG418	34188291_c1_58	1718	7380	1089	363	1666	1.7(10)-171	Escherichia coli	b2022	[pn:histidinol phosphatase] [gn:hishb]
CONTIG418	32424192_c1_59	1719	7381	933	311	1268	2.6(10)-129	Escherichia coli	b2025	[pn:hishf protein] [gn:hishf]

CONTIG418	31922662_c2_70	1720	7382	1140	380	1608	2.3(10)-165	Escherichia coli	b2021	[pn:imidazole] [gn:hisc]
CONTIG418	32678126_c2_75	1721	7383	816	272	915	6.5(10)-92	Escherichia coli	b2024	[pn:phosphoribosylformimino-5-aminoimidazole carboxamide ribotide] [gn:hisa]
CONTIG418	15734716_c2_77	1722	7384	330	110	97	3.1(10)-5	Salmonella typhimurium	X03976	or:salmonella typhimurium le:1 re:>173 di:direct nt:chimeric protein of hisf and hisie genes (57 aa)
CONTIG418	16620952_c2_80	1723	7385	1017	339	1466	2.7(10)-150	Escherichia coli	Q04871	hypothetical 37.6 kD protein in cld 5'region (orf2).
CONTIG418	35361063_c3_88	1724	7386	1326	442	1927	3.7(10)-199	Escherichia coli	b2020	[pn:histidinol dehydrogenase] [gn:hisd]
CONTIG418	2469541_c3_90	1725	7387	621	207	961	8.6(10)-97	Escherichia coli	b2023	[pn:amidotransferase] [gn:hish]
CONTIG418	6445253_c3_91	1726	7388	654	218	897	5.2(10)-90	Escherichia coli	b2026	[pn:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase] [gn:hisi]
CONTIG419	4350678_f1_1	1727	7389	531	177	93	0.26	Caenorhabditis elegans	L46861	or:caenorhabditis elegans pn.talin le:2 re:7663 di:direct sr:caenorhabditis elegans (strain bristol) (tissue library: whol
CONTIG419	22558287_f1_9	1728	7390	2559	853	2822	5.4(10)-294	Escherichia coli	b0496	[pn:hypothetical protein] [gn:ybbp]
CONTIG419	16458166_f2_24	1729	7391	735	245	814	3.2(10)-81	Escherichia coli	b0490	[pn:hypothetical protein] [gn:ybbj]
CONTIG419	33847266_f2_32	1730	7392	741	247	959	1.3(10)-96	Escherichia coli	b0495	[pn:hypothetical abc transporter] [gn:ybba]
CONTIG419	24791562_f2_42	1731	7393	642	214	581	1.6(10)-56	Escherichia coli	U82664	or:escherichia coli le:133380 re:134066 di:direct nt:hypothetical protein
CONTIG419	21525291_f3_54	1732	7394	864	288	909	2.7(10)-91	Escherichia coli	b0491	[pn:hypothetical protein] [gn:ybbm]
CONTIG419	21644141_f3_63	1733	7395	1167	389	99	0.033	Escherichia coli	b1377	[pn:hypothetical protein]
CONTIG419	24853550_f3_70	1734	7396	1581	527	2192	3.1(10)-227	Escherichia coli	b0526	[pn:cysteineyl-trna synthetase] [gn:cyss]
CONTIG419	2750412_c1_77	1735	7397	1554	518	1039	4.7(10)-105	Bacillus subtilis	pisG	[pn:phosphotransferase system]

CONTIG419	162701_c1_79	1736	7398	564	188	774	5.7(10)-77	Escherichia coli	b0527	[pn:hypothetical protein in cyss-fold intergenic region] [gn:ybcj]
CONTIG419	31719580_c1_84	1737	7399	645	215	735	7.7(10)-73	Escherichia coli	b0523	[pn:phosphoribosylaminoimidazole carboxylase catalytic subunit] [gn:pure]
CONTIG419	1272192_c1_95	1738	7400	297	99	92	0.00011	Entamoeba histolytica	Y14328	[PN:3E1 protein] [DE:Entamoeba histolytica mRNA for 3E1 protein.] [LE:32] [RE:418] [DI:direct]
CONTIG419	31369027_c1_98	1739	7401	813	271	1203	2.0(10)-122	Escherichia coli	b0493	[pn:hypothetical protein] [gn:ybbv]
CONTIG419	13015666_c1_103	1740	7402	531	177	553	1.5(10)-53	Escherichia coli	b0489	[pn:hypothetical protein] [gn:ybbk]
CONTIG419	33848817_c2_104	1741	7403	342	114	324	2.7(10)-29	Escherichia coli	b0528	[pn:hypothetical 7.4 kd protein in cyss-fold intergenic region] [gn:ybcj]
CONTIG419	34173532_c2_126	1742	7404	876	292	1141	7.2(10)-116	Escherichia coli	b0492	[pn:hypothetical protein] [gn:ybbn]
CONTIG419	11228205_c3_134	1743	7405	249	83	330	6.4(10)-30	Escherichia coli	b0529	[pn:methyltetrahydrofolate dehydrogenase] [gn:fold]
CONTIG419	36048591_c3_138	1744	7406	1173	391	498	1.0(10)-47	Escherichia coli	b1620	[pn:repressor protein] [gn:mali]
CONTIG419	4004186_c3_142	1745	7407	558	186	829	8.5(10)-83	Escherichia coli	b0525	[pn:peptidyl-prolyl cis-trans isomerase b] [gn:ppib]
CONTIG419	14978525_c3_143	1746	7408	726	242	1045	1.1(10)-105	Escherichia coli	b0524	[pn:hypothetical 26.9 kd protein in pure-ppib intergenic region]
CONTIG419	16102281_c3_144	1747	7409	1089	363	1634	4.2(10)-168	Escherichia coli	b0522	[pn:phosphoribosylaminoimidazole carboxylase apase subunit] [gn:purk]
CONTIG419	16113178_c3_145	1748	7410	1155	385	1365	1.3(10)-139	Escherichia coli	b0503	[pn:hypothetical 41.1 kd protein in rhd-gcl intergenic region] [gn:ybbb]
CONTIG419	24039076_c3_150	1749	7411	888	296	990	7.4(10)-100	Escherichia coli	b0494	[pn:acyl-coa thioesterase i] [gn:tesa]
CONTIG420	14629541_c1_70	1750	7412	630	210	722	1.8(10)-71	Escherichia coli	b2051	[pn:hypothetical 18.4 kd protein in cpsb 5'''region] [gn:yefc]
CONTIG420	886252_c1_73	1751	7413	1422	474	2149	1.1(10)-222	Escherichia coli	b2048	[pn:phosphomannomutase] [gn:manb]
CONTIG420	32682807_c1_74	1752	7414	1497	499	2158	1.2(10)-223	Escherichia coli	b2046	[pn:hypothetical protein]
CONTIG420	17004375_c1_75	1753	7415	1296	432	1937	3.2(10)-200	Escherichia coli	b2045	[pn:hypothetical protein] [gn:wack]

CONTIG420	24427167_c2_79	1754	7416	1035	345	1509	7.4(10)-155	Escherichia coli	b2052	[pn:hypothetical 36.1 kd protein in cpsb 5''' region] [gn:yefb]
CONTIG420	20330425_c2_94	1755	7417	936	312	1389	3.8(10)-142	Escherichia coli	b2042	[pn:utp-glucose-1-phosphate uridylyltransferase] [gn:galf]
CONTIG420	24251592_c3_95	1756	7418	1134	378	1888	5.0(10)-195	Escherichia coli	b2053	[pn:gdp-mannose 4,6-dehydratase] [gn:yefa]
CONTIG420	36417061_c3_98	1757	7419	1275	425	1634	4.2(10)-168	Escherichia coli	b2050	[pn:hypothetical 44.9 kd protein in cpsb 5''' region] [gn:yefd]
CONTIG420	21759652_c3_99	1758	7420	1440	480	2174	2.5(10)-225	Escherichia coli	b2049	[pn:mannose-1-phosphate guanylyltransferase] [gn:mane]
CONTIG420	11800807_c3_103	1759	7421	1467	489	2060	3.0(10)-213	Escherichia coli	b2047	[pn:hypothetical protein] [gn:wca]
CONTIG420	31505387_c3_109	1760	7422	1392	464	1689	6.2(10)-174	Escherichia coli	b2044	[pn:hypothetical protein] [gn:wcal]
CONTIG420	3158143_c3_110	1761	7423	1398	466	1857	9.8(10)-192	Escherichia coli	b2043	[pn:hypothetical protein] [gn:wcam]
CONTIG420	30672166_c3_111	1762	7424	1011	337	234	1.7(10)-18	Saccharomyces cerevisiae	YGL001C	[pn:putative 3-beta-hydroxysteroid dehydrogenase]
CONTIG421	16991042_f1_3	1763	7425	438	146	91	0.00839	Saccharomyces cerevisiae	YJR151C	[pn:similarity to mucin proteins, yk1224c, sta1p] [gn:j2223]
CONTIG421	33331650_f1_5	1764	7426	696	232	907	4.5(10)-91	Escherichia coli	b0046	[pn:hypothetical nadph oxidoreductase in fixc-kefc intergenic region] [gn:yabf]
CONTIG421	6679631_f2_15	1765	7427	288	96	182	3.1(10)-14	Escherichia coli	b2809	[pn:hypothetical protein]
CONTIG421	31646007_f2_22	1766	7428	1977	659	2127	2.3(10)-220	Escherichia coli	b0047	[pn:glutathione-regulated potassium-efflux system protein kefc] [gn:kefc]
CONTIG421	964590_f2_23	1767	7429	513	171	804	3.7(10)-80	Escherichia coli	b0048	[pn:dihydrofolate reductase type i] [gn:fola]
CONTIG421	20996093_f3_33	1768	7430	834	278	1308	1.5(10)-133	Escherichia coli	b0032	[pn:carbamoyl-phosphate synthase small chain] [gn:carA]
CONTIG421	25524180_f3_34	1769	7431	3243	1081	5312	0	Escherichia coli	b0033	[pn:carbamoyl-phosphate synthase large chain] [gn:carb]
CONTIG421	34180387_c1_57	1770	7432	1299	433	1816	2.2(10)-187	Escherichia coli	b0053	[pn:survival protein sura precursor] [gn:sura]
CONTIG421	33866441_c1_66	1771	7433	501	167	98	0.0011	Helicobacter pylori	AC000108	or:helicobacter pylori pn:orf33
CONTIG421	2371025_c2_75	1772	7434	1437	479	2091	1.6(10)-216	Escherichia coli	b0054	[pn:organic solvent tolerance protein precursor] [gn:imp]

CONTIG421	14881910_c2_76	1773	7435	828	276	1320	7.9(10)-135	Escherichia coli	b0051	[pn:dimethyladenosine transferase] [gn:ksga]
CONTIG421	25431533_c2_77	1774	7436	381	127	506	1.3(10)-48	Escherichia coli	b0050	[pn:apag protein] [gn:apag]
CONTIG421	24083442_c3_91	1775	7437	1050	350	1384	1.3(10)-141	Escherichia coli	b0052	[pn:pyridoxal phosphate biosynthetic protein pda] [gn:pda]
CONTIG421	31664075_c3_92	1776	7438	969	323	1366	1.1(10)-139	Escherichia coli	b0049	[pn:bis] [gn:apah]
CONTIG421	35285415_c3_97	1777	7439	471	157	100	0.0076	Caenorhabditis elegans	AF022974	[de:caenorhabditis elegans cosmid f26g5.1] [gn:f26g5.9] [nt:contains similarity to c3hc4-type zinc
CONTIG421	23626562_c3_100	1778	7440	3102	1034	441	4.5(10)-65	Escherichia coli	b1509	[pn:hypothetical protein]
CONTIG422	10971967_f1_3	1779	7441	1221	407	2054	1.3(10)-212	Escherichia coli	b2290	[pn:hypothetical protein]
CONTIG422	21759631_f1_4	1780	7442	603	201	950	1.3(10)-95	Escherichia coli	b2291	[pn:hypothetical protein]
CONTIG422	2931592_f1_21	1781	7443	435	145	183	4.5(10)-14	Escherichia coli	b3438	[pn:gtnkr operon regulator] [gn:gtnr]
CONTIG422	25833401_f1_22	1782	7444	624	208	262	1.0(10)-22	Escherichia coli	b3438	[pn:gtnkr operon regulator] [gn:gtnr]
CONTIG422	33203141_f2_34	1783	7445	1239	413	1902	1.7(10)-196	Escherichia coli	b2296	[pn:acetate kinase] [gn:acka]
CONTIG422	31728532_f2_35	1784	7446	2145	715	3368	0	Escherichia coli	b2297	[pn:phosphate acetyltransferase] [gn:pta]
CONTIG422	31678191_c1_71	1785	7447	636	212	795	3.3(10)-79	Escherichia coli	b2299	[pn:hypothetical protein]
CONTIG422	2786715_c1_75	1786	7448	306	102	94	6.5(10)-5	Escherichia coli	b4194	[pn:hypothetical 10.9 kd protein in aidb-rpsf intergenic region] [gn:yjft]
CONTIG422	26620418_c1_76	1787	7449	1404	468	435	4.7(10)-41	Escherichia coli	b4193	[pn:hypothetical 52.9 kd protein in aidb-rpsf intergenic region] [gn:yjfs]
CONTIG422	16683451_c1_77	1788	7450	1008	336	462	6.5(10)-44	Methanococcus jannaschii	MJ0679	[pn:transketolase""""]
CONTIG422	4429018_c1_84	1789	7451	465	155	738	3.7(10)-73	Escherichia coli	b2295	[pn:hypothetical protein]
CONTIG422	26681415_c2_108	1790	7452	678	226	703	1.8(10)-69	Escherichia coli	b2293	[pn:hypothetical protein]
CONTIG422	6039811_c2_109	1791	7453	1845	615	2338	1.1(10)-242	Escherichia coli	b2292	[pn:hypothetical protein] [gn:yfbs]

CONTIG422	5111062_c2_111	1792	7454	894	298	1222	1.8(10)-124	Escherichia coli	b2289	[pn:nadh dehydrogenase operon transcriptional regulator] [gn:lrha]
CONTIG422	2931576_c3_112	1793	7455	555	185	835	2.0(10)-83	Escherichia coli	b2300	[pn:hypothetical protein] [gn:yfcc]
CONTIG422	23853437_c3_114	1794	7456	447	149	238	3.6(10)-20	Escherichia coli	b4195	[pn:hypothetical phosphotransferase enzyme ii] [gn:ptxa]
CONTIG422	24507291_c3_117	1795	7457	858	286	462	6.5(10)-44	Methanococcus jannaschii	MJ0681	[pn:transketolase ^{III}]
CONTIG422	13725686_c3_122	1796	7458	549	183	797	2.1(10)-79	Escherichia coli	b2294	[pn:hypothetical protein]
CONTIG423	36125431_f1_7	1797	7459	216	72	105	4.5(10)-6	Bacteriophage phi-80	P17651	adsorption-inhibiting cor protein.
CONTIG423	24222277_f2_27	1798	7460	1383	461	1955	4.0(10)-202	Escherichia coli	b1784	[pn:hypothetical protein]
CONTIG423	7151578_f3_45	1799	7461	264	88	429	3.7(10)-40	Escherichia coli	b1783	[pn:hypothetical protein]
CONTIG423	30522566_c1_70	1800	7462	3363	1121	248	6.0(10)-20	Salmonella typhimurium	AF007380	[PN:lambdaphage II tail component homolog] [DE:Salmonella typhimurium lambdaphage K tail component homolog gene, partial cds, lambdaphage L tail component homolog, copper-zinc superoxide dismutase (sodC), attachment and invasion prote
CONTIG423	6286331_c1_74	1801	7463	4020	1340	1029	2.7(10)-115	Bacteriophage lambda	P03749	host specificity protein j.
CONTIG423	665907_c2_89	1802	7464	762	254	329	8.1(10)-30	Yersinia pestis	AF053947	[de:yersinia pestis plasmid pmtI, complete plasmid sequence.]
CONTIG423	36534812_c2_91	1803	7465	609	203	128	2.3(10)-8	Bacteriophage lambda	P03730	[pn:phage lambda minor tail protein I homolog]
CONTIG423	20916702_c2_100	1804	7466	672	224	93	0.066	Bacillus subtilis	yhaU	tail assembly protein i.
CONTIG423	26584831_c2_102	1805	7467	360	120	91	0.00013	Salmonella typhimurium	P23831	[pn:hypothetical protein]
CONTIG423	22948562_c3_106	1806	7468	1122	374	581	1.6(10)-56	Bacteriophage HK97	P49861	sama protein (ec 3.4.21.-).
CONTIG423										major capsid protein precursor (gp5) (head protein).

CONTIG423	31728755_c3_112	1807	7469	387	129	136	2.2(10)-9	Bacteriophage lambda	P03737	minor tail protein m.
CONTIG423	25524180_c3_114	1808	7470	723	241	387	5.7(10)-36	Coxiella burnetii	Y15898	[de:coxiella burnetii plasmid qprs dna.] [pn:hypothetical protein] [gn:orf 248]
CONTIG424	33641631_fl_6	1809	7471	1398	466	1791	9.6(10)-185	Escherichia coli	b1002	[pn:glucose-1-phosphatase precursor] [gn:agp]
CONTIG424	2846890_fl_8	1810	7472	195	65	210	3.2(10)-17	Escherichia coli	b1259	[pn:hypothetical protein in tonb-trpa intergenic region] [gn:ycig]
CONTIG424	33807708_fl_15	1811	7473	666	222	908	3.6(10)-91	Escherichia coli	b1013	[pn:hypothetical protein] [gn:yedc]
CONTIG424	9776952_fl_19	1812	7474	651	217	136	2.2(10)-9	Azospirillum brasiliense	X70360	or:azospirillum brasiliense gn:car le:59 re:580 di:direct nt:orf2
CONTIG424	9964202_f2_33	1813	7475	534	178	151	5.9(10)-11	Helicobacter pylori	HP0571	[pn:conserved hypothetical integral membrane protein]
CONTIG424	33235452_f2_54	1814	7476	1509	503	2172	4.0(10)-225	Escherichia coli	b1015	[pn:sodium/proline symporter] [gn:putp]
CONTIG424	23862882_f3_62	1815	7477	975	325	151	1.3(10)-8	Bacillus subtilis	yovV	[pn:hypothetical protein]
CONTIG424	22266038_c1_80	1816	7478	1092	364	1129	1.3(10)-114	Escherichia coli	b2393	[pn:nucleoside permease nupc] [gn:nupc]
CONTIG424	13067881_c1_86	1817	7479	324	108	91	0.00479	Escherichia coli	I53597	proline dehydrogenase (ec 1.5.99.8) - escherichia coli
CONTIG424	32290750_c1_93	1818	7480	441	147	596	4.2(10)-58	Escherichia coli	b1010	[pn:hypothetical protein]
CONTIG424	32425751_c1_100	1819	7481	1116	372	870	3.7(10)-87	Providencia stuartii	U23806	or:providencia stuartii le:343 re:1413 di:direct nt:extended orf of mgte gene; transcription from this
CONTIG424	14455001_c1_101	1820	7482	537	179	97	0.0038	Bacillus subtilis	yxlJ	[pn:hypothetical protein]
CONTIG424	4803205_c2_105	1821	7483	4092	1364	5754	0	Escherichia coli	b1014	[pn:proline oxidase] [gn:puta]
CONTIG424	23564416_c2_106	1822	7484	447	149	207	6.9(10)-17	Sinorhizobium meliloti	P42879	hypothetical 15.0 kd protein in ureb- urec intergenic region (orf5).
CONTIG424	31813125_c2_110	1823	7485	783	261	1104	6.0(10)-112	Escherichia coli	b1011	[pn:hypothetical protein]
CONTIG424	32619542_c2_111	1824	7486	858	286	1022	3.0(10)-103	Escherichia coli	b1009	[pn:hypothetical protein]

CONTIG424	16614702_c2_112	1825	7487	591	197	874	1.3(10)-87	Escherichia coli	b1008	[pn:hypothetical protein]
CONTIG424	16835915_c2_120	1826	7488	603	201	807	1.8(10)-80	Escherichia coli	b1004	[pn:trp repressor binding protein] [gn:wrba]
CONTIG424	34645256_c2_121	1827	7489	246	82	366	9.8(10)-34	Escherichia coli	b1003	[pn:hypothetical 8.5 kd protein in agp 3'''region] [gn:yccj]
CONTIG424	32661281_c3_132	1828	7490	183	61	117	8.1(10)-6	Escherichia coli	I53597	proline dehydrogenase (ec 1.5.99.8) - escherichia coli
CONTIG424	23625786_c3_138	1829	7491	1179	393	1701	3.2(10)-175	Escherichia coli	b1012	[pn:hypothetical protein]
CONTIG424	4332318_c3_141	1830	7492	504	168	707	7.2(10)-70	Escherichia coli	b1007	[pn:hypothetical protein]
CONTIG424	33601030_c3_142	1831	7493	1344	448	1835	2.1(10)-189	Escherichia coli	b1006	[pn:hypothetical protein] [gn:yedg]
CONTIG425	22659426_f1_1	1832	7494	2682	894	3783	0	Escherichia coli	b1834	[pn:hypothetical protein]
CONTIG425	11176451_f1_4	1833	7495	285	95	350	4.9(10)-32	Escherichia coli	b1836	[pn:hypothetical protein]
CONTIG425	35599132_f1_5	1834	7496	1104	368	524	1.8(10)-50	Escherichia coli	b0877	[pn:hypothetical protein]
CONTIG425	7159682_f1_10	1835	7497	273	91	333	3.1(10)-30	Escherichia coli	b1842	[pn:dna polymerase iii, theta subunit] [gn:hole]
CONTIG425	26050762_f1_11	1836	7498	684	228	332	2.0(10)-41	Escherichia coli	b1843	[pn:hypothetical protein]
CONTIG425	32635763_f1_12	1837	7499	678	226	1052	2.0(10)-106	Escherichia coli	b1844	[pn:hypothetical protein]
CONTIG425	4803751_f3_44	1838	7500	1314	438	1773	7.7(10)-183	Escherichia coli	b1833	[pn:hypothetical protein]
CONTIG425	29781327_f3_46	1839	7501	1464	488	2052	2.1(10)-212	Escherichia coli	b1835	[pn:hypothetical protein]
CONTIG425	24349067_f3_54	1840	7502	1275	425	1599	2.2(10)-164	Escherichia coli	b1849	[pn:phosphoribosylglycinamide formyltransferase 2] [gn:put]

CONTIG425	33494665_c1_58	1841	7503	285	95	91	0.0027	Triticum aestivum	JN0690	glutenin, high-molecular-weight bx7 chain precursor - wheat the main wheat storage proteins are divided into two groups. the glutenins, composed of high- and low-molecular weight families, and the gliadins, composed of alpha or beta, gamma and omega fam
CONTIG425	3158387_c1_62	1842	7504	876	292	545	1.1(10)-52	Escherichia coli	b1840	[pn:hypothetical protein]
CONTIG425	7228508_c2_77	1843	7505	687	229	529	5.2(10)-51	Escherichia coli	b1846	[pn:hypothetical 23.7 kd protein in put 5'''region] [gn:yebe]
CONTIG425	32225388_c2_78	1844	7506	2103	701	2793	6.4(10)-291	Escherichia coli	b1845	[pn:protease ii] [gn:ptrb]
CONTIG425	24415886_c2_82	1845	7507	342	114	444	5.2(10)-42	Escherichia coli	b1839	[pn:hypothetical protein]
CONTIG425	24025302_c2_93	1846	7508	501	167	754	7.5(10)-75	Escherichia coli	b1832	[pn:hypothetical protein]
CONTIG425	196055_c2_94	1847	7509	516	172	325	2.2(10)-29	Haemophilus influenzae	HI1670	[pn:conjugative transfer co-repressor] [gn:fino]
CONTIG425	4976566_c3_104	1848	7510	390	130	272	9.0(10)-24	Escherichia coli	b1841	[pn:hypothetical protein]
CONTIG425	24897717_c3_110	1849	7511	777	259	704	1.5(10)-69	Escherichia coli	b1838	[pn:hypothetical protein] [gn:prpa]
CONTIG426	26460813_f1_27	1850	7512	216	72	178	8.1(10)-14	Escherichia coli	b3537	[pn:hypothetical protein] [gn:yhit]
CONTIG426	25987562_f2_49	1851	7513	1587	529	2040	4.0(10)-211	Escherichia coli	b3536	[pn:hypothetical 59.4 kd protein in dcta-dppf intergenic region]
CONTIG426	31666653_f2_50	1852	7514	1713	571	2368	7.0(10)-246	Escherichia coli	b3538	[pn:hypothetical 62.0 kd protein in dcta-dppf intergenic region]
CONTIG426	19556892_c1_85	1853	7515	1014	338	1364	1.7(10)-139	Escherichia coli	b3973	[pn:bifunctional protein] [gn:bira]
CONTIG426	16691707_c1_92	1854	7516	2643	881	3852	0	Escherichia coli	b3533	[pn:hypothetical 101.6 kd protein in dcta-dppf intergenic region]
CONTIG426	35657127_c1_98	1855	7517	3507	1169	4218	0	Escherichia coli	b3530	[pn:hypothetical 125.7 kd protein in dcta-dppf intergenic region]
CONTIG426	23455028_c1_99	1856	7518	2100	700	2387	6.7(10)-248	Escherichia coli	b3529	[pn:hypothetical 73.1 kd protein in dcta-dppf intergenic region]

CONTIG426	16598131_c1_100	1857	7519	567	189	570	2.3(10)-55	Escherichia coli	b3528	[pn:c4-dicarboxylate transport protein] [gn:dcta]
CONTIG426	33719693_c2_102	1858	7520	1176	392	1474	3.7(10)-151	Escherichia coli	b3972	[pn:udp-n-acetylenolpyruvoylglucosamine reductase] [gn:murb]
CONTIG426	14551878_c2_107	1859	7521	783	261	897	5.2(10)-90	Escherichia coli	b3534	[pn:hypothetical protein] [gn:yhiq]
CONTIG426	21769375_c2_111	1860	7522	2541	847	2874	0	Escherichia coli	b3532	[pn:hypothetical 86.0 kd protein in dcta-dppf intergenic region]
CONTIG426	24650458_c2_112	1861	7523	1113	371	1417	4.2(10)-145	Escherichia coli	b3531	[pn:hypothetical 41.7 kd protein in dcta-dppf intergenic region] [gn:yhim]
CONTIG426	32319840_c3_124	1862	7524	249	83	245	6.5(10)-21	Escherichia coli	b3535	[pn:hypothetical protein] [gn:yhir]
CONTIG426	32035966_c3_137	1863	7525	348	116	94	0.00095	Pseudomonas sp	D10769	or:pseudomonas sp. pn:maltopentaose forming any/lase le:717 re:2561 di:direct sr:pseudomonas sp. (strain ko-8940) (library: lambda 147) dna
CONTIG427	4152178_f1_8	1864	7526	1020	340	1216	8.3(10)-124	Escherichia coli	b1320	[pn:hypothetical protein]
CONTIG427	4823265_f2_20	1865	7527	807	269	1160	7.0(10)-118	Escherichia coli	b1326	[pn:hypothetical protein] [gn:yji]
CONTIG427	24265676_f2_22	1866	7528	531	177	727	5.5(10)-72	Escherichia coli	b1324	[pn:thiol peroxidase] [gn:tpx]
CONTIG427	31681349_c1_59	1867	7529	838	279	1209	4.5(10)-123	Escherichia coli	b1313	[pn:hypothetical protein]
CONTIG427	5350202_c1_60	1868	7530	1077	359	1412	1.3(10)-144	Escherichia coli	b1315	[pn:hypothetical protein]
CONTIG427	7314416_c1_66	1869	7531	765	255	596	4.2(10)-58	Escherichia coli	b1317	[pn:hypothetical protein]
CONTIG427	32842_c1_68	1870	7532	927	309	990	7.4(10)-100	Escherichia coli	b1319	[pn:hypothetical protein] [gn:ompg]
CONTIG427	10634640_c1_76	1871	7533	1032	344	1162	4.4(10)-118	Escherichia coli	b1325	[pn:hypothetical protein]
CONTIG427	5165892_c2_81	1872	7534	858	286	1201	3.2(10)-122	Escherichia coli	b1314	[pn:hypothetical protein]
CONTIG427	35236466_c2_84	1873	7535	1125	375	1378	5.5(10)-141	Escherichia coli	b1318	[pn:hypothetical protein]

CONTIG427	14885377_c2_89	1874	7536	1059	353	1256	4.7(10)-128	Escherichia coli	b1322	[pn:hypothetical protein in pspe-tyrr intergenic region] [gn:ycjfl]
CONTIG427	3411330_c2_90	1875	7537	1638	546	2210	3.8(10)-229	Escherichia coli	b1323	[pn:transcriptional regulatory protein tyrr] [gn:tyrr]
CONTIG427	24505167_c3_96	1876	7538	2310	770	2548	5.9(10)-265	Escherichia coli	b1316	[pn:hypothetical protein]
CONTIG427	5213467_c3_100	1877	7539	1407	469	2285	4.4(10)-237	Escherichia coli	b1321	[pn:hypothetical protein]
CONTIG427	4157968_c3_108	1878	7540	1626	542	2510	6.2(10)-261	Escherichia coli	b1329	[pn:hypothetical protein]
CONTIG428	16932050_f1_22	1879	7541	1098	366	538	5.7(10)-52	Bacillus subtilis	yesQ	[pn:hypothetical protein]
CONTIG428	13867963_f1_23	1880	7542	1140	380	818	1.2(10)-81	Bacillus subtilis	msmX	[pn:multiple sugar-binding transport atp-binding protein] [gn:yxkg]
CONTIG428	4807327_f2_30	1881	7543	1023	341	1503	3.2(10)-154	Escherichia coli	b2837	[pn:galactose operon repressor] [gn:galr]
CONTIG428	32149135_f2_38	1882	7544	957	319	1322	4.7(10)-135	Escherichia coli	b2839	[pn:transcriptional activator protein lysr] [gn:lysr]
CONTIG428	24427336_f2_41	1883	7545	336	112	218	4.7(10)-18	Erwinia chrysanthemi	Q05527	pectin degradation protein kdgf.
CONTIG428	4345932_f2_47	1884	7546	1350	450	327	1.3(10)-29	Bacillus subtilis	yesO	[pn:hypothetical protein]
CONTIG428	2468768_f3_59	1885	7547	1119	373	692	2.7(10)-68	Escherichia coli	b2714	[pn:asc operon repressor protein] [gn:aseg]
CONTIG428	24642553_f3_65	1886	7548	897	299	775	4.5(10)-77	Bacillus subtilis	yesP	[pn:hypothetical protein]
CONTIG428	24026430_c1_81	1887	7549	1425	475	609	1.7(10)-59	Bacillus subtilis	licC	[pn:phosphotransferase system] [gn:celb]
CONTIG428	21587562_c2_104	1888	7550	1494	498	958	1.8(10)-96	Bacillus subtilis	ydhP	[pn:hypothetical protein]
CONTIG428	14257826_c2_105	1889	7551	795	265	560	2.7(10)-54	Haemophilus influenzae	H10054	[pn:uxu operon regulator] [gn:uxur]
CONTIG428	4962950_c2_110	1890	7552	2322	774	3240	0	Escherichia coli	b2836	[pn:2-acylglycerophosphoethanolamine acyltransferase / acyl-acyl carrier protein synthetase] [gn:aas]
CONTIG428	9943775_c3_117	1891	7553	1215	405	1077	4.4(10)-109	Escherichia coli	b0587	[pn:ferric enterobactin transport protein fepe] [gn:fepe]

CONTIG428	34179511_c3_118	1892	7554	1185	395	895	8.5(10)-90	Escherichia coli	b2840	[pn:hypothetical 25.2 kd protein in lysr-arae intergenic region] [gn:ygea]
CONTIG428	4376958_c3_120	1893	7555	1365	455	1906	6.2(10)-197	Escherichia coli	b2838	[pn:diaminopimelate decarboxylase] [gn:lysa]
CONTIG428	1413592_c3_136	1894	7556	930	310	1155	2.3(10)-117	Escherichia coli	b2835	[pn:hypothetical protein in mth-aas intergenic region] [gn:yged]
CONTIG429	34664655_f1_2	1895	7557	540	180	420	1.8(10)-39	Escherichia coli	b0419	[pn:hypothetical protein] [gn:yajo]
CONTIG429	3414166_f1_3	1896	7558	363	121	225	1.1(10)-18	Escherichia coli	b0419	[pn:hypothetical protein] [gn:yajo]
CONTIG429	19964657_f1_22	1897	7559	609	203	217	6.0(10)-18	Bacillus subtilis	yjaR	[pn:hypothetical protein]
CONTIG429	428316_f1_23	1898	7560	591	197	461	8.4(10)-44	Bacillus subtilis	yxD	[pn:hypothetical protein]
CONTIG429	21955468_f2_24	1899	7561	1209	403	325	2.2(10)-29	Bacillus subtilis	iolS	[pn:hypothetical protein] [gn:yxbf]
CONTIG429	2819755_f2_25	1900	7562	1074	358	480	8.0(10)-46	Synechocystis sp.	S76674	[PN:hypothetical protein] [OR Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR PCC 6803, I]
CONTIG429	4890901_f2_26	1901	7563	582	194	291	8.6(10)-26	Escherichia coli	b0046	[pn:hypothetical nadph oxidoreductase in fixc-kefc intergenic region] [gn:yabf]
CONTIG429	6750016_f2_31	1902	7564	642	214	215	9.8(10)-18	Bacillus subtilis	ywrO	[pn:hypothetical protein]
CONTIG429	24222287_f3_54	1903	7565	762	254	91	0.00052	Escherichia coli	b1518	[pn:hypothetical protein]
CONTIG429	5353556_f3_55	1904	7566	819	273	137	4.0(10)-9	Methanobacterium thermoautotrophicum	MTH234	[pn:gamma-carboxymuconolactone decarboxylase]
CONTIG429	30156668_f3_58	1905	7567	1491	497	597	3.2(10)-58	Escherichia coli	b1828	[pn:hypothetical protein]
CONTIG429	30329136_c1_90	1906	7568	549	183	398	4.0(10)-37	Mycobacterium tuberculosis	Z95210	unknown., mtey21c12.13. mtey21c12.13. len
CONTIG429	33867840_c2_103	1907	7569	2484	828	965	1.3(10)-117	Arthrobacter sp.	S65769	maltooligosyl trehalose synthase - arthrobacter sp. (strain q36)
CONTIG429	14730330_c2_104	1908	7570	2091	697	1423	9.5(10)-146	Escherichia coli	b3431	[pn:glycogen operon protein glgx] [gn:glgx]

CONTIG429	10551037_c2_112	1909	7571	963	321	168	2.7(10)-10	Escherichia coli	b0076	[pn:leuo]
CONTIG429	20157792_c2_113	1910	7572	294	98	129	1.3(10)-8	Mycobacterium tuberculosis	Z95210	unknown_mtey21c12.12.mtey21c12.12.len
CONTIG429	33601702_c3_120	1911	7573	1788	596	826	1.8(10)-82	Sulfolobus solfataricus	S73087	[pn:alpha-amylase, precursor]
CONTIG43	34018765_f2_1	1912	7574	663	221	1034	1.6(10)-104	Escherichia coli	b3320	[pn:50s ribosomal subunit protein 13]
CONTIG43	36517717_f3_3	1913	7575	368	123	510	5.4(10)-49	Escherichia coli	b3319	[pn:50s ribosomal subunit protein 14]
CONTIG430	25570176_f1_3	1914	7576	921	307	1276	3.6(10)-130	Escherichia coli	b0428	[pn:cytochrome o ubiquinol oxidase c subunit] [gn:cyoc]
CONTIG430	7089132_f1_4	1915	7577	1374	458	1801	8.5(10)-186	Escherichia coli	b0427	[pn:hypothetical protein] [gn:yajr]
CONTIG430	10835913_f1_18	1916	7578	615	205	677	1.1(10)-66	Escherichia coli	b0412	[pn:hypothetical 21.8 kd protein in tsx-ribd intergenic region] [gn:yaji]
CONTIG430	24869658_f2_19	1917	7579	2031	677	3197	0	Escherichia coli	b0431	[pn:cytochrome o ubiquinol oxidase subunit ii] [gn:cyob]
CONTIG430	20801331_f2_20	1918	7580	423	141	297	2.0(10)-26	Escherichia coli	b0429	[pn:cytochrome o ubiquinol oxidase c subunit] [gn:cyod]
CONTIG430	5196068_f2_23	1919	7581	921	307	1376	9.1(10)-141	Escherichia coli	b0425	[pn:apba protein] [gn:apba]
CONTIG430	235707_f2_26	1920	7582	1005	335	1531	3.5(10)-157	Escherichia coli	b0419	[pn:hypothetical protein] [gn:yajo]
CONTIG430	14587812_f3_37	1921	7583	618	206	937	3.0(10)-94	Escherichia coli	b0430	[pn:cytochrome o ubiquinol oxidase subunit iii] [gn:cyoc]
CONTIG430	34648537_f3_44	1922	7584	609	203	905	7.5(10)-91	Escherichia coli	b0424	[pn:thij protein] [gn:thij]
CONTIG430	12922775_f3_47	1923	7585	249	83	357	8.8(10)-33	Escherichia coli	b0422	[pn:exodeoxyribonuclease small subunit] [gn:xseb]
CONTIG430	10157952_f3_48	1924	7586	900	300	1234	1.0(10)-125	Escherichia coli	b0421	[pn:geranyltransferase] [gn:ispa]
CONTIG430	2147132_f3_49	1925	7587	1887	629	2952	0	Escherichia coli	b0420	[pn:hypothetical protein] [gn:yajp]
CONTIG430	5161562_c1_60	1926	7588	1209	403	1658	1.2(10)-170	Escherichia coli	b0414	[pn:riboflavin biosynthesis protein ribd] [gn:ribd]
CONTIG430	4182842_c1_61	1927	7589	480	160	580	2.1(10)-56	Escherichia coli	b0415	[pn:probable riboflavin synthase beta chain] [gn:ribh]

CONTIG430	23671875_c1_62	1928	7590	441	147	661	5.4(10)-65	Escherichia coli	b0416	[pn:n utilization substance protein b] [gn:nusb]
CONTIG430	19781883_c2_99	1929	7591	555	185	775	4.5(10)-77	Escherichia coli	b0426	[pn:hypothetical protein] [gn:yaiaq]
CONTIG430	31430461_c3_108	1930	7592	462	154	723	1.3(10)-71	Escherichia coli	b0413	[pn:hypothetical 17.2 kd protein in tsx-ribd intergenic region] [gn:ybad]
CONTIG430	30212766_c3_109	1931	7593	975	325	1449	1.7(10)-148	Escherichia coli	b0417	[pn:hypothetical protein] [gn:thil]
CONTIG430	34005008_c3_116	1932	7594	1473	491	2182	3.6(10)-226	Escherichia coli	b0423	[pn:hypothetical protein] [gn:yaik]
CONTIG431	32236592_f1_4	1933	7595	2160	720	3307	0	Escherichia coli	b2675	[pn:ribonucleoside-diphosphate reductase 2 alpha chain] [gn:nrde]
CONTIG431	5320443_f1_5	1934	7596	969	323	1465	3.3(10)-150	Escherichia coli	b2676	[pn:ribonucleoside-diphosphate reductase 2 beta chain] [gn:nrdl]
CONTIG431	2067336_f1_7	1935	7597	1221	407	1908	3.8(10)-197	Escherichia coli	b2677	[pn:glycine betaine/l-proline transport atp-binding protein prov]
CONTIG431	10343930_f1_11	1936	7598	1212	404	954	4.7(10)-96	Escherichia coli	b2681	[pn:hypothetical protein]
CONTIG431	35604561_f1_14	1937	7599	1224	408	1632	6.7(10)-168	Escherichia coli	b2685	[pn:multidrug resistance protein a] [gn:emra]
CONTIG431	113537_f2_25	1938	7600	486	162	676	1.3(10)-66	Escherichia coli	b2670	[pn:hypothetical protein]
CONTIG431	31767930_f2_27	1939	7601	546	182	633	5.0(10)-62	Escherichia coli	b2674	[pn:hypothetical protein] [gn:nrdi]
CONTIG431	36604152_f2_31	1940	7602	1083	361	1416	5.2(10)-145	Escherichia coli	b2678	[pn:glycine betaine/l-proline transport system permease protein p] [gn:prox]
CONTIG431	5194693_f2_32	1941	7603	1005	335	1470	1.0(10)-150	Escherichia coli	b2679	[pn:glycine betaine-binding periplasmic protein precursor] [gn:prox]
CONTIG431	13007717_f2_34	1942	7604	1581	527	2347	1.2(10)-243	Escherichia coli	b2686	[pn:multidrug resistance protein b] [gn:emrb]
CONTIG431	22383582_f3_45	1943	7605	354	118	278	2.1(10)-24	Escherichia coli	b2672	[pn:hypothetical protein] [gn:ygam]
CONTIG431	32461077_f3_46	1944	7606	255	85	325	2.2(10)-29	Escherichia coli	b2673	[pn:hypothetical protein] [gn:nrdh]
CONTIG431	35166511_f3_57	1945	7607	627	209	872	2.3(10)-87	Escherichia coli	b2684	[pn:transcriptional repressor mpra] [gn:mpra]

CONTIG431	14070762_f3_59	1946	7608	1695	565	1454	5.0(10)-149	Saccharomyces cerevisiae	YNL104C	[pn:2-isopropylmalate synthase] [gn:leu4]
CONTIG431	26046955_c1_66	1947	7609	435	145	559	3.5(10)-54	Escherichia coli	b2690	[pn:hypothetical protein]
CONTIG431	35355165_c1_67	1948	7610	462	154	576	5.5(10)-56	Escherichia coli	b2689	[pn:hypothetical protein]
CONTIG431	23681890_c1_69	1949	7611	885	295	301	7.5(10)-27	Escherichia coli	b1790	[pn:hypothetical protein]
CONTIG431	4117193_c1_89	1950	7612	354	118	527	8.5(10)-51	Escherichia coli	b2671	[pn:hypothetical 13.1 kd protein in sta-nrde intergenic region] [gn:ygacl]
CONTIG431	33838307_c2_94	1951	7613	315	105	297	2.0(10)-26	Escherichia coli	b2690	[pn:hypothetical protein]
CONTIG431	1275266_c2_97	1952	7614	519	173	845	1.7(10)-84	Escherichia coli	b2687	[pn:hypothetical protein in emb3 3' region] [gn:ygacl]
CONTIG431	25390686_c3_117	1953	7615	1572	524	2378	6.0(10)-247	Escherichia coli	b2688	[pn:glutamate--cysteine ligase] [gn:gshal]
CONTIG432	24425931_f1_4	1954	7616	357	119	296	2.6(10)-26	Escherichia coli	b4023	[pn:hypothetical 10.5 kd protein in pepe-lysc intergenic region]
CONTIG432	5917286_f2_24	1955	7617	1362	454	1766	4.2(10)-182	Escherichia coli	b4024	[pn:lysine-sensitive aspartokinase iii] [gn:lysc]
CONTIG432	5162807_f2_25	1956	7618	1020	340	559	3.5(10)-54	Bacillus subtilis	yocS	[pn:hypothetical protein]
CONTIG432	30198511_f2_37	1957	7619	933	311	1323	3.7(10)-135	Escherichia coli	b4018	[pn:acetate operon repressor] [gn:iclr]
CONTIG432	34663402_f3_48	1958	7620	318	106	220	2.8(10)-18	Haemophilus influenzae	1111419	[pn:hypothetical protein]
CONTIG432	22692827_f3_49	1959	7621	294	98	179	6.4(10)-14	Haemophilus influenzae	H11420	[pn:hypothetical protein]
CONTIG432	7218818_c1_67	1960	7622	942	314	1568	4.0(10)-161	Escherichia coli	b4013	[pn:homoserine o-succinyltransferase] [gn:meta]
CONTIG432	17051906_c1_71	1961	7623	1365	455	2134	4.4(10)-221	Escherichia coli	b4015	[pn:isocitrate lyase] [gn:acea]
CONTIG432	12203130_c1_72	1962	7624	1803	601	2698	7.5(10)-281	Escherichia coli	b4016	[pn:isocitrate dehydrogenase kinase/phosphatase] [gn:acekl]
CONTIG432	36415708_c1_75	1963	7625	3702	1234	5941	0	Escherichia coli	b4019	[pn:b12-dependent homocysteine-n5-methyltetrahydrofolate transmethyase] [gn:meth]

CONTIG432	2207187_c1_78	1964	7626	954	318	1276	3.6(10)-130	Escherichia coli	b4022	[pn:hypothetical 32.5 kd protein in pepe-lysc intergenic region]
CONTIG432	13708462_c2_87	1965	7627	225	75	124	5.2(10)-7	Escherichia coli	M18974	or:escherichia coli gn:acek ie:472 re:2205 di:direct sr:c.coli (strain k12) dna nt:isocitrate dehydrogenase kinase/phosphatase
CONTIG432	86625_c3_104	1966	7628	1629	543	2464	4.7(10)-256	Escherichia coli	b4014	[pn:malate synthase a] [gn:aceb]
CONTIG432	12930443_c3_113	1967	7629	1647	549	2060	3.0(10)-213	Escherichia coli	b4020	[pn:hypothetical 59.5 kd protein in meth-pepe intergenic region] [gn:yjbb]
CONTIG433	783_f1_7	1968	7630	432	144	631	8.0(10)-62	Escherichia coli	b3167	[pn:ribosome-binding factor a] [gn:rbfa]
CONTIG433	14901591_f1_9	1969	7631	525	175	413	1.0(10)-38	Escherichia coli	b3165	[pn:30s ribosomal subunit protein s15] [gn:rpso]
CONTIG433	33364211_f1_20	1970	7632	555	185	762	1.1(10)-75	Escherichia coli	b3157	[pn:hypothetical 19.7 kd protein in soha-mtr intergenic region] [gn:yhbt]
CONTIG433	13677326_f2_28	1971	7633	492	164	740	2.2(10)-73	Escherichia coli	b3170	[pn:hypothetical 16.8 kd protein in nusa-mety intergenic region] [gn:yhbc]
CONTIG433	32694807_f2_34	1972	7634	1011	337	1485	2.6(10)-152	Escherichia coli	b3163	[pn:hypothetical 33.6 kd protein in dead-pnp intergenic region] [gn:yhbm]
CONTIG433	13129803_f2_35	1973	7635	1935	645	2085	3.2(10)-256	Escherichia coli	b3162	[pn:dead] [gn:dead]
CONTIG433	35656427_f2_42	1974	7636	723	241	867	8.0(10)-87	Escherichia coli	b3152	[pn:hypothetical 24.8 kd protein in agai-mtr intergenic region] [gn:yrar]
CONTIG433	13086018_f3_47	1975	7637	1518	506	2280	1.5(10)-236	Escherichia coli	b3169	[pn:n utilization substance protein a] [gn:nusa]
CONTIG433	36069132_f3_48	1976	7638	2709	903	2853	0	Escherichia coli	b3168	[pn:protein chain initiation factor 2] [gn:infb]
CONTIG433	32317906_f3_49	1977	7639	978	326	1389	3.8(10)-142	Escherichia coli	b3166	[pn:uma pseudouridine 55 synthase] [gn:trub]
CONTIG433	30367705_f3_50	1978	7640	2220	740	3047	0	Escherichia coli	b3164	[pn:polynucleotide phosphorylase] [gn:pnp]
CONTIG433	16833293_f3_55	1979	7641	1251	417	1821	6.4(10)-188	Escherichia coli	b3161	[pn:tryptophan-specific permease] [gn:mtr]
CONTIG433	5103407_f3_60	1980	7642	507	169	753	9.5(10)-75	Escherichia coli	b3156	[pn:hypothetical protein] [gn:yhbs]

CONTIG433	24742838_f3_61	1981	7643	447	149	607	2.7(10)-59	Escherichia coli	b3154	[pn.hypothetical 16.8 kd protein in soha-mtr intergenic region]
CONTIG433	36422036_f3_64	1982	7644	738	246	757	3.6(10)-75	Escherichia coli	b3151	[pn.hypothetical 37.3 kd protein in agai-mtr intergenic region] [gn.yraq]
CONTIG433	6745840_c1_68	1983	7645	363	121	349	6.2(10)-32	Escherichia coli	b3155	[pn.hypothetical 11.3 kd protein in soha-mtr intergenic region]
CONTIG433	22902158_c1_72	1984	7646	1038	346	1437	3.2(10)-147	Escherichia coli	b3159	[pn.hypothetical 33.2 kd protein in soha-mtr intergenic region]
CONTIG433	14873383_c1_73	1985	7647	1014	338	1451	1.0(10)-148	Escherichia coli	b3160	[pn.hypothetical 37.1 kd protein in soha-mtr intergenic region] [gn.yhbw]
CONTIG433	7071032_c2_91	1986	7648	456	152	98	0.00479	Caenorhabditis elegans	Z93395	[de:caenorhabditis elegans cosmid zc101, complete sequence] [pn:zc101 1] [nt:similar to low-density lipoprotein receptor]
CONTIG433	24023542_c2_92	1987	7649	540	180	794	4.2(10)-79	Escherichia coli	b3153	[pn.hypothetical 20.3 kd protein in soha-mtr intergenic region]
CONTIG433	12001058_c2_128	1988	7650	1125	375	1780	1.3(10)-183	Escherichia coli	b3172	[pn:argininosuccinate synthetase] [gn:argg]
CONTIG433	3337752_c3_133	1989	7651	999	333	1494	2.8(10)-153	Escherichia coli	b3158	[pn:putative protease in soha-mtr intergenic region] [gn.yhbu]
CONTIG433	21675430_c3_166	1990	7652	321	107	406	5.7(10)-38	Escherichia coli	b3172	[pn:argininosuccinate synthetase] [gn:argg]
CONTIG434	16053507_f1_2	1991	7653	474	158	481	6.4(10)-46	Escherichia coli	b1104	[pn.hypothetical protein]
CONTIG434	4876342_f1_9	1992	7654	270	90	314	3.2(10)-28	Escherichia coli	b1112	[pn.hypothetical protein]
CONTIG434	25520382_f1_20	1993	7655	1269	423	1490	7.5(10)-153	Escherichia coli	b1118	[pn.hypothetical protein]
CONTIG434	33330125_f1_21	1994	7656	966	322	1287	2.5(10)-131	Escherichia coli	b1119	[pn.hypothetical protein] [gn.yefx]
CONTIG434	23478157_f2_28	1995	7657	651	217	757	3.6(10)-75	Escherichia coli	b1105	[pn.hypothetical protein]
CONTIG434	11072040_f2_29	1996	7658	1068	356	1580	2.2(10)-162	Escherichia coli	b1107	[pn.hypothetical protein]
CONTIG434	7323500_f2_30	1997	7659	1320	440	1937	3.2(10)-200	Escherichia coli	b1109	[pn.nadh dehydrogenase] [gn.ndh]
CONTIG434	640966_f2_40	1998	7660	1944	648	1372	2.3(10)-140	Escherichia coli	b1116	[pn.hypothetical protein]

CONTIG434	7226712_f3_49	1999	7661	372	124	584	7.7(10)-57	Escherichia coli	b1103	[pn:hypothetical protein in flue-ndh intergenic region] [gn:ycff]
CONTIG434	33605040_f3_52	2000	7662	864	288	879	4.2(10)-88	Escherichia coli	b1106	[pn:hypothetical protein]
CONTIG434	15049141_f3_53	2001	7663	555	185	938	2.3(10)-94	Escherichia coli	b1108	[pn:hypothetical protein]
CONTIG434	421905_f3_55	2002	7664	612	204	697	8.1(10)-69	Escherichia coli	b1110	[pn:hypothetical 18.9 kd protein in ndh-mfd intergenic region] [gn:ycff]
CONTIG434	14973833_f3_63	2003	7665	900	300	1044	1.3(10)-105	Escherichia coli	b1120	[pn:hypothetical protein]
CONTIG434	29329666_f3_70	2004	7666	279	93	251	3.0(10)-21	Escherichia coli	b1127	[pn:peptidase t] [gn:pept]
CONTIG434	10195287_c1_74	2005	7667	1059	353	1637	2.0(10)-168	Escherichia coli	b1123	[pn:spermidine/putrescine-binding periplasmic protein precursor] [gn:potd]
CONTIG434	1195910_c1_84	2006	7668	1155	385	1221	2.3(10)-124	Escherichia coli	b1115	[pn:hypothetical protein]
CONTIG434	12362887_c2_99	2007	7669	1212	404	1650	8.5(10)-170	Escherichia coli	b1126	[pn:spermidine/putrescine transport atp-binding protein pota] [gn:pota]
CONTIG434	16689813_c2_101	2008	7670	807	269	943	7.0(10)-95	Escherichia coli	b1124	[pn:spermidine/putrescine transport system permease protein potc] [gn:potc]
CONTIG434	6485817_c2_108	2009	7671	3513	1171	5326	0	Escherichia coli	b1114	[pn:transcription-repair coupling factor] [gn:mfd]
CONTIG434	14460050_c2_109	2010	7672	1020	340	1377	7.2(10)-141	Escherichia coli	b1113	[pn:hypothetical protein]
CONTIG434	34657312_c3_120	2011	7673	882	294	1258	2.8(10)-128	Escherichia coli	b1125	[pn:spermidine/putrescine transport system permease protein potb] [gn:potb]
CONTIG434	24018801_c3_140	2012	7674	669	223	875	1.1(10)-87	Escherichia coli	b1111	[pn:hypothetical protein]
CONTIG435	21774136_f1_3	2013	7675	846	282	205	1.1(10)-16	Bacillus subtilis	ylbO	[pn:hypothetical protein]
CONTIG435	5214541_f1_9	2014	7676	2742	914	1145	2.7(10)-116	Escherichia coli	b2592	[pn:clpb protein] [gn:clpb]
CONTIG435	26681587_f1_10	2015	7677	1437	479	159	4.0(10)-8	Saccharomyces cerevisiae	YOL045W	[pn:similarity to ser/thr protein kinase]
CONTIG435	25782568_f1_12	2016	7678	789	263	139	9.4(10)-8	Serratia liquefaciens	P18954	phlb protein precursor.

CONTIG435	32303567_f1_14	2017	7679	1194	398	223	1.6(10)-15	Escherichia coli	AF044503	[de:escherichia coli strain ec11 unknown (498), hcp gene, complete cds;and rhsg accessory genetic element vrg protein, core component anddsorf-g1 genes, complete cds.] [pn:vrg protein]
CONTIG435	22832555_f2_15	2018	7680	1797	599	96	0.04399	Bos taurus	U92535	neuronal axonal membrane protein,,nap-22 homolog
CONTIG435	16588251_f3_48	2019	7681	453	151	326	1.7(10)-29	Escherichia coli	b2055	[pn:hypothetical protein] [gn:wcae]
CONTIG436	292882_f2_49	2020	7682	1164	388	353	2.2(10)-32	Azorhizobium caulinodans	S52856	arae-like protein - azorhizobium caulinodans
CONTIG436	95380_f2_50	2021	7683	1089	363	955	3 7(10)-96	Bacillus subtilis	gap	[pn:glyceraldehyde-3-phosphate dehydrogenase]
CONTIG436	11198311_f2_51	2022	7684	1725	575	2264	7 2(10)-235	Escherichia coli	b1197	[pn:periplasmic trehalase precursor] [gn:trear]
CONTIG436	29383457_c1_83	2023	7685	1725	575	391	2 8(10)-63	Escherichia coli	b0150	[pn:ferrichrome-iron receptor precursor] [gn:fhua]
CONTIG436	36035686_c1_93	2024	7686	3666	1222	170	3.3(10)-21	Legionella pneumophila	Y15044	[de:legionella pneumophila 22kb dna fragment from icm gene cluster.] [pn:icmf protein] [gn:icmf]
CONTIG436	14511687_c2_100	2025	7687	270	90	103	0.00012	Escherichia coli	b0150	[pn:ferrichrome-iron receptor precursor] [gn:fhua]
CONTIG436	4957906_c2_110	2026	7688	1269	423	165	4.2(10)-10	Bacillus subtilis	motB	[pn:motility protein b] [gn:mot]
CONTIG437	24870905_f1_1	2027	7689	1032	344	766	4.0(10)-76	Escherichia coli	b3826	[pn:yigl]
CONTIG437	10995841_f1_11	2028	7690	660	220	828	1.1(10)-82	Escherichia coli	b3834	[pn:hypothetical 22.3 kd protein in udp-rfah intergenic region] [gn:yigp]
CONTIG437	19956350_f1_15	2029	7691	282	94	288	1.8(10)-25	Escherichia coli	b3836	[pn:hypothetical 11 3 kd protein in udp-rfah intergenic region]
CONTIG437	25791025_f1_16	2030	7692	546	182	472	5 7(10)-45	Escherichia coli	b3838	[pn:hypothetical 15.6 kd protein in udp-rfah intergenic region]
CONTIG437	2112687_f1_22	2031	7693	520	174	686	1.2(10)-67	Escherichia coli	b3554	[pn:hypothetical 30.2 kd protein in bisccspa intergenic region] [gn:yiaf]
CONTIG437	4569713_f2_23	2032	7694	912	304	1307	1.8(10)-133	Escherichia coli	b3827	[pn:hypothetical 33.7 kd protein in pldb-metr intergenic region] [gn:yigm]

CONTIG437	197802_f2_25	2033	7695	2289	763	3781	0	Escherichia coli	b3829	[pn:5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase] [gn:metc]
CONTIG437	50892_f2_28	2034	7696	810	270	1241	1.8(10)-126	Escherichia coli	b3831	[pn:uridine phosphorylase] [gn:udp]
CONTIG437	12694067_f2_32	2035	7697	831	277	758	2.7(10)-75	Escherichia coli	b3840	[pn:yigw]
CONTIG437	33751042_f2_33	2036	7698	1515	505	2515	1.8(10)-261	Escherichia coli	b3843	[pn:hypothetical 55.3 kd protein in rfah-rfe intergenic region] [gn:yigc]
CONTIG437	22519382_f2_34	2037	7699	723	241	1083	1.0(10)-109	Escherichia coli	b3844	[pn:flavin reductase] [gn:ubib]
CONTIG437	36017000_f2_35	2038	7700	1638	546	654	3.0(10)-64	Streptomyces lincolnensis	S69834	,
CONTIG437	25595458_f3_37	2039	7701	228	76	334	2.3(10)-30	Escherichia coli	b3825	[pn:lysophospholipase l2] [gn:pldb]
CONTIG437	2032755_f3_47	2040	7702	1602	534	2022	3.2(10)-209	Escherichia coli	b3832	[pn:hypothetical 54.7 kd protein in udp 3''' region precursor] [gn:yign]
CONTIG437	10444800_f3_48	2041	7703	771	257	1228	4.4(10)-125	Escherichia coli	b3833	[pn:hypothetical 28.1 kd protein in udp-rfah intergenic region] [gn:yigo]
CONTIG437	22062915_f3_49	2042	7704	1677	559	2532	2.8(10)-263	Escherichia coli	b3835	[pn:hypothetical 63.2 kd protein in udp-rfah intergenic region]
CONTIG437	4491042_f3_50	2043	7705	780	260	1000	6.4(10)-101	Escherichia coli	b3839	[pn:hypothetical 29.0 kd protein in udp-rfah intergenic region] [gn:yigu]
CONTIG437	6102030_c1_58	2044	7706	318	106	310	8.4(10)-28	Escherichia coli	b3555	[pn:hypothetical 11.0 kd protein in bise-cspa intergenic region]
CONTIG437	22128816_c1_65	2045	7707	546	182	678	8.5(10)-67	Escherichia coli	b3842	[pn:transcriptional activator] [gn:rfah]
CONTIG437	19971006_c1_79	2046	7708	861	287	850	5.0(10)-85	Escherichia coli	b3830	[pn:hypothetical protein]
CONTIG437	16830043_c2_110	2047	7709	444	148	157	4.9(10)-11	Escherichia coli	b3830	[pn:hypothetical protein]
CONTIG437	4297842_c2_114	2048	7710	963	321	1466	2.7(10)-150	Escherichia coli	b3828	[pn:trans-activator of mete and meth] [gn:metr]
CONTIG438	12601687_f1_3	2049	7711	1506	502	566	6.2(10)-55	Bacillus subtilis	yhdl	[pn:hypothetical protein]
CONTIG438	32204502_f1_13	2050	7712	666	222	750	2.0(10)-74	Escherichia coli	b0464	[pn:potential acraB operon repressor] [gn:acrr]

CONTIG438	13719682_fl_18	2051	7713	618	206	889	3.7(10)-89	Escherichia coli	b0469	[pn:adenine phosphoribosyltransferase] [gn:apt]
CONTIG438	34257891_fl_20	2052	7714	354	118	324	2.7(10)-29	Escherichia coli	b0471	[pn:hypothetical 12.0 kd protein in dnax-recr intergenic region] [gn:ybab]
CONTIG438	11816261_f2_52	2053	7715	1974	658	2630	1.2(10)-273	Escherichia coli	b0470	[pn:dna polymerase iii subunits gamma and tau] [gn:dnax]
CONTIG438	22554702_f2_54	2054	7716	1875	625	2946	0	Escherichia coli	b0473	[pn:heat shock protein htpg] [gn:htpg]
CONTIG438	10750312_f2_55	2055	7717	678	226	1060	2.7(10)-107	Escherichia coli	b0474	[pn:adenylate kinase] [gn:adk]
CONTIG438	22517057_f2_57	2056	7718	1410	470	2087	4.2(10)-216	Escherichia coli	b0477	[pn:inosine-guanosine kinase] [gn:gsk]
CONTIG438	12210058_f3_78	2057	7719	3483	1161	3978	0	Escherichia coli	b0465	[pn:hypothetical protein] [gn:aefa]
CONTIG438	268831_f3_79	2058	7720	405	135	359	5.4(10)-33	Escherichia coli	b0468	[pn:hypothetical 14.8 kd protein in pric-apt intergenic region] [gn:yban]
CONTIG438	1988513_f3_82	2059	7721	618	206	906	5.9(10)-91	Escherichia coli	b0472	[pn:recombination protein recr] [gn:recr]
CONTIG438	16970952_f3_86	2060	7722	963	321	1377	7.2(10)-141	Escherichia coli	b0475	[pn:ferrochelatase] [gn:hcmh]
CONTIG438	16604206_f3_87	2061	7723	270	90	109	8.3(10)-6	Escherichia coli	JU0314	hypothetical 34.6k protein (visa 3 region) - escherichiacoli
CONTIG438	33636577_f3_89	2062	7724	792	264	115	0.0014	Saccharomyces cerevisiae	YIR019C	[pn:extracellular alpha-1,4-glucan glucosidase] [gn:sta1]
CONTIG438	20369535_c1_96	2063	7725	312	104	90	0.0011	Homo sapiens	P29966	myristoylated alanine-rich c-kinase substrate (marks) (protein kinase c substrate, 80 kd protein, light chain) (pkcs1) (80k-1 protein).
CONTIG438	29901058_c1_103	2064	7726	519	173	277	2.6(10)-24	Escherichia coli	U82664	or:escherichia coli lc:73500 re:73877 di:complement nt:hypothetical
CONTIG438	110457_c1_109	2065	7727	555	185	486	1.8(10)-46	Escherichia coli	b0467	[pn:primosomal replication protein n] [gn:pric]
CONTIG438	3229836_c1_110	2066	7728	189	63	168	9.4(10)-13	Escherichia coli	b0466	[pn:hypothetical 6.0 kd protein in acrr-pric intergenic region]
CONTIG438	33851510_c1_116	2067	7729	1266	422	1539	4.9(10)-158	Escherichia coli	b0463	[pn:acrilavin resistance protein a precursor] [gn:acra]

CONTIG438	5085917_c1_120	2068	7730	201	67	103	7.2(10)-6	Escherichia coli	U82664	or:escherichia coli pn:hha protein gn:hha le:59538 re:5957 di:complement
CONTIG438	33673537_c1_121	2069	7731	573	191	761	1.3(10)-75	Escherichia coli	b0459	[pn:hypothetical protein] [gn:ylad]
CONTIG438	20100019_c2_126	2070	7732	278	92	277	2.6(10)-24	Escherichia coli	b0479	[pn:fosmidomycin resistance protein] [gn:fsr]
CONTIG438	23540913_c2_159	2071	7733	3114	1038	4072	0	Escherichia coli	b0462	[pn:acriflavin resistance protein b] [gn:acrb]
CONTIG438	31437757_c3_164	2072	7734	1740	580	2165	2.2(10)-224	Escherichia coli	b0478	[pn:hypothetical protein in gsk 3'''region] [gn:ybal]
CONTIG438	34431890_c3_188	2073	7735	414	138	633	5.0(10)-62	Escherichia coli	b0461	[pn:hypothetical 14.6 kd protein in hha-acrb intergenic region] [gn:ybaj]
CONTIG438	3914143_c3_189	2074	7736	228	76	357	8.8(10)-33	Escherichia coli	b0460	[pn:haemolysin expression modulating protein] [gn:hha]
CONTIG438	4882717_c3_190	2075	7737	477	159	510	5.4(10)-49	Escherichia coli	b0458	[pn:hypothetical protein] [gn:ylac]
CONTIG438	2164755_c3_194	2076	7738	744	248	635	3.1(10)-62	Saccharomyces cerevisiae	P40586	hypothetical 27.4 kd protein in hyr1 3' region.
CONTIG439	22395066_f1_2	2077	7739	798	266	1095	5.5(10)-111	Escherichia coli	b0763	[pn:24 aa signal peptide] [gn:moda]
CONTIG439	836680_f1_7	2078	7740	1008	336	1444	5.7(10)-148	Escherichia coli	b0767	[pn:hypothetical 36.3 kd protein in mode-bioa intergenic region] [gn:ybhe]
CONTIG439	22297577_f1_11	2079	7741	1257	419	730	2.6(10)-72	Bacillus subtilis	hutI	[pn:imidazolonepropionase] [gn:ee57b]
CONTIG439	10599075_f1_13	2080	7742	888	296	988	1.2(10)-99	Klebsiella aerogenes	P12380	histidine utilization repressor.
CONTIG439	34161325_f1_15	2081	7743	1581	527	1849	6.9(10)-191	Pseudomonas putida	A35251	histidine ammonia-lyase (ec 4.3.1.3)
CONTIG439	31820791_f1_19	2082	7744	1194	398	1163	3.3(10)-118	Escherichia coli	b0776	pseudomonas putida [pn:8-amino-7-oxononanoate synthase] [gn:biof]
CONTIG439	26845457_f2_29	2083	7745	1077	359	1508	9.5(10)-155	Escherichia coli	b0765	[pn:molybdenum transport atp-binding protein mode] [gn:mode]
CONTIG439	32441655_f2_30	2084	7746	354	118	202	2.2(10)-16	Escherichia coli	U27192	or:escherichia coli pn:modd gn:modd le:5360 re:6055 di:direct
CONTIG439	29398902_f2_36	2085	7747	1761	587	1861	3.7(10)-192	Bacillus subtilis	hutU	[pn:urocanate hydratase] [gn:ee57a]

CONTIG439	14945407_f2_46	2086	7748	1080	360	1602	1.0(10)-164	Escherichia coli	b0775	[pn:biotin synthetase] [gn:biob]
CONTIG439	22913166_f2_49	2087	7749	810	270	741	1.8(10)-73	Escherichia coli	b0777	[pn:biotin synthesis protein bioc] [gn:bioc]
CONTIG439	5334457_f3_56	2088	7750	717	239	713	1.7(10)-70	Escherichia coli	b0764	[pn:molybdenum transport system permease protein modb] [gn:modb]
CONTIG439	5164052_f3_59	2089	7751	270	90	159	8.4(10)-12	Escherichia coli	D90715	or:escherichia coli pn:putative molybdenum transport protein modd gn.modd le:4270 re:4410 di:direct sr:escherichia coli(strain:k12) dna, clone:kohara clone #180
CONTIG439	32033513_f3_63	2090	7752	999	333	643	4.2(10)-63	Klebsiella aerogenes	P19452	formiminoglutamase (cc 3.5.3.8) (formiminoglutamate hydrolase) (histidine utilization protein g) (fragment).
CONTIG439	14320833_f3_76	2091	7753	837	279	858	7.2(10)-86	Escherichia coli	b0778	[pn:dethiobiotin synthetase] [gn:biob]
CONTIG439	12582512_f3_77	2092	7754	351	117	364	8.5(10)-33	Escherichia coli	b0779	[pn:excision nuclease abc subunit b] [gn:uvrb]
CONTIG439	23531503_c1_78	2093	7755	828	276	275	4.2(10)-24	Escherichia coli	b3454	[pn:high-affinity branched-chain amino acid transport atp-binding] [gn:livf]
CONTIG439	25970953_c1_87	2094	7756	498	166	705	1.2(10)-69	Escherichia coli	b0773	[pn:hypothetical 17.1 kd protein in bioa 5'''region] [gn:ybbb]
CONTIG439	2945417_c1_101	2095	7757	1137	379	1440	1.5(10)-147	Escherichia coli	b0772	[pn:hypothetical protein in bioa 5'''region] [gn:ybbc]
CONTIG439	31306950_c2_119	2096	7758	1350	450	1866	1.1(10)-192	Escherichia coli	b0774	[pn:adenosylmethionine-8-amino-7-oxononanoate aminotransferase] [gn:bioa]
CONTIG439	16601510_c2_135	2097	7759	501	167	258	6.2(10)-22	Escherichia coli	b0772	[pn:hypothetical protein in bioa 5'''region] [gn:ybbc]
CONTIG439	31694127_c3_162	2098	7760	903	301	1093	9.0(10)-111	Escherichia coli	b0766	[pn:hypothetical 30.2 kd protein in mode-bioa intergenic region] [gn:ybha]
CONTIG44	29432965_f3_3	2099	7761	555	185	220	2.7(10)-17	Escherichia coli	b3966	[pn:vitamin b12 receptor precursor] [gn:btub]
CONTIG440	29298500_f1_1	2100	7762	258	86	400	2.3(10)-37	Escherichia coli	b3637	[pn:50s ribosomal subunit protein l28] [gn:rpmb]

CONTIG440	24814713_fl_28	2101	7763	775	259	257	3.5(10)-22	Haemophilus influenzae	HI0653	[pn:pir]
CONTIG440	23633567_f3_46	2102	7764	183	61	246	5.0(10)-21	Escherichia coli	b3636	[pn:50s ribosomal subunit protein 133] [gn:rpmg]
CONTIG440	4141380_f3_47	2103	7765	876	292	1324	3.0(10)-135	Escherichia coli	b3635	[pn:formamidopyrimidine-dna glycosylase] [gn:mutm]
CONTIG440	31525267_f3_67	2104	7766	1395	465	1853	2.6(10)-191	Escherichia coli	b3617	[pn:2-amino-3-ketobutyrate coenzyme a ligase] [gn:kbl]
CONTIG440	5127068_f3_68	2105	7767	1038	346	1563	1.3(10)-160	Escherichia coli	b3616	[pn:threonine 3-dehydrogenase] [gn:tdh]
CONTIG440	31901006_c1_81	2106	7768	1137	379	1636	2.6(10)-168	Escherichia coli	b3620	[pn:adp-heptose-lps heptosyltransferase ii] [gn:rfaf]
CONTIG440	7290966_c1_82	2107	7769	987	329	1267	3.2(10)-129	Escherichia coli	b3621	[pn:lipopolysaccharide heptosyltransferase-1] [gn:rfac]
CONTIG440	19806531_c1_83	2108	7770	1113	371	164	1.3(10)-9	Helicobacter pylori	HP1191	[pn:adp-heptose-lps heptosyltransferase ii] [gn:rfaf]
CONTIG440	25910910_c1_92	2109	7771	1086	362	716	8.0(10)-71	Escherichia coli	b3632	[pn:lipopolysaccharide core biosynthesis protein rfaq] [gn:rfag]
CONTIG440	12892041_c1_95	2110	7772	1047	349	606	3.6(10)-59	Escherichia coli	b3615	[pn:hypothetical 40.5 kd protein in scb-tdh 5''' region] [gn:yibd]
CONTIG440	16893762_c1_96	2111	7773	1311	437	1727	5.9(10)-178	Escherichia coli	b3633	[pn:3-deoxy-d-manno-octulosonic-acid transferase] [gn:kdta]
CONTIG440	9979011_c2_99	2112	7774	1221	407	198	3.2(10)-13	Methanococcus jannaschii	MJ1059	[pn:capsular polysaccharide biosynthesis protein m]
CONTIG440	20603766_c2_103	2113	7775	975	325	1601	1.3(10)-164	Escherichia coli	b3619	[pn:adp-l-glycero-d-mannoheptose-6-epimerase] [gn:rfad]
CONTIG440	26594043_c2_110	2114	7776	1218	406	219	2.2(10)-16	Escherichia coli	b3622	[pn:rfal]
CONTIG440	23860312_c2_114	2115	7777	1152	384	192	1.3(10)-12	Methanococcus jannaschii	MJ1059	[pn:capsular polysaccharide biosynthesis protein m]
CONTIG440	4691452_c3_124	2116	7778	576	192	103	0.0038	Homo sapiens	Z34277	or:homo sapiens pn:mucin gn:muc5ac le:<1 re:>1431 di:direct
CONTIG440	32285666_c3_130	2117	7779	930	310	126	1.5(10)-5	Haemophilus influenzae	HI1578	[pn:glycosyl transferase] [gn:lgtd]
CONTIG440	2205040_c3_132	2118	7780	1161	387	224	1.8(10)-16	Escherichia coli	b3631	[pn:lipopolysaccharide core biosynthesis protein rfaq] [gn:rfag]
CONTIG440	10672642_c3_136	2119	7781	849	283	637	1.8(10)-62	Haemophilus influenzae	HI0653	[pn:pir]

CONTIG440	14337783_c3_137	2120	7782	483	161	685	1.5(10)-67	Escherichia coli	b3634	[pn:lipopolysaccharide core biosynthesis protein kdtb] [gn:kdtb]
CONTIG441	31447255_f1_8	2121	7783	402	134	280	1.3(10)-24	Escherichia coli	b2824	[pn:hypothetical 13.5 kd protein in ppdc-ppdb intergenic region] [gn:ygdb]
CONTIG441	25645890_f1_15	2122	7784	2907	969	4170	0	Escherichia coli	b2821	[pn:protease iii precursor] [gn:ptr]
CONTIG441	19585327_f1_22	2123	7785	1338	446	1912	1.5(10)-197	Escherichia coli	b2817	[pn:hypothetical protein]
CONTIG441	33790961_f2_25	2124	7786	879	293	1386	8 0(10)-142	Escherichia coli	b2828	[pn:prolipoprotein diacylglycerol transferase] [gn:lgf]
CONTIG441	24644068_f2_26	2125	7787	801	267	1401	2.1(10)-143	Escherichia coli	b2827	[pn:thymidylate synthetase] [gn:thya]
CONTIG441	34645790_f2_28	2126	7788	579	193	495	2 1(10)-47	Escherichia coli	b2825	[pn:prepilin peptidase dependent protein b precursor] [gn:ppdb]
CONTIG441	33828506_f2_36	2127	7789	1851	617	2175	2.0(10)-225	Escherichia coli	b2819	[pn:exonuclease v alpha-subunit] [gn:reec]
CONTIG441	477291_f3_40	2128	7790	360	120	541	2.7(10)-52	Escherichia coli	b2830	[pn:hypothetical protein] [gn:ygdp]
CONTIG441	4869633_f3_41	2129	7791	2259	753	3278	0	Escherichia coli	b2829	[pn:phosphoenolpyruvate-protein phosphotransferase] [gn:ptsp]
CONTIG441	281892_f3_46	2130	7792	516	172	410	2.1(10)-38	Escherichia coli	b2826	[pn:prepilin peptidase dependent protein a precursor] [gn:ppda]
CONTIG441	16182818_f3_48	2131	7793	336	112	239	2.7(10)-20	Escherichia coli	b2823	[pn:prepilin peptidase dependent protein c precursor] [gn:ppdc]
CONTIG441	1305455_f3_49	2132	7794	3387	1129	4626	0	Escherichia coli	b2822	[pn:exonuclease v subunit] [gn:reec]
CONTIG441	14883438_f3_51	2133	7795	3549	1183	4526	0	Escherichia coli	b2820	[pn:exonuclease v subunit] [gn:reec]
CONTIG441	23550057_c3_124	2134	7796	1353	451	2120	1.3(10)-219	Escherichia coli	b2818	[pn:amino-acid acetyltransferase] [gn:arga]
CONTIG442	35750680_f1_1	2135	7797	726	242	1115	4.2(10)-113	Escherichia coli	b2777	[pn:hypothetical protein] [gn:ygcf]
CONTIG442	33463508_f1_10	2136	7798	1752	584	2661	6.2(10)-277	Escherichia coli	b2763	[pn:nadph hemoprotein alpha subunit] [gn:cysi]
CONTIG442	7242681_f1_11	2137	7799	750	250	1236	6.2(10)-126	Escherichia coli	b2762	[pn:3'-phosphoadenosine 5'-phosphosulfate sulfotransferase] [gn:cysb]

CONTIG442	6769537_f1_18	2138	7800	375	125	403	1.2(10)-37	Escherichia coli	b2748	[pn:hypothetical protein]
CONTIG442	25664010_f1_19	2139	7801	558	186	578	3.3(10)-56	Escherichia coli	b2746	[pn:hypothetical 16.9 kd protein in sure-cysc intergenic region]
CONTIG442	19806956_f1_20	2140	7802	843	281	1240	2.3(10)-126	Escherichia coli	b2744	[pn:stationary-phase survival protein sure] [gn:sure]
CONTIG442	11760791_f1_21	2141	7803	199	67	109	3.0(10)-6	Escherichia coli	b2743	[pn:l-isoaspartyl protein carboxyl methyltransferase type ii]
CONTIG442	36017966_f2_22	2142	7804	642	214	274	5.5(10)-24	Escherichia coli	b3223	[pn:hypothetical protein] [gn:yhcj]
CONTIG442	14880191_f2_29	2143	7805	1812	604	2693	2.5(10)-280	Escherichia coli	b2764	[pn:nadph flavoprotein beta subunit] [gn:cysj]
CONTIG442	16109558_f2_41	2144	7806	651	217	876	8.9(10)-88	Escherichia coli	b2750	[pn:adenosine 5-phosphosulfate kinase] [gn:cysc]
CONTIG442	17052176_f2_42	2145	7807	810	270	1063	1.3(10)-107	Escherichia coli	b2747	[pn:hypothetical protein]
CONTIG442	17010938_f3_44	2146	7808	273	91	197	5.0(10)-15	Escherichia coli	b1101	[pn:pts system, glucose-specific ilbc component] [gn:ptsg]
CONTIG442	16679686_f3_50	2147	7809	2397	799	150	7.2(10)-7	Bacillus subtilis	yesS	[pn:hypothetical protein]
CONTIG442	11753301_f3_57	2148	7810	1443	481	975	5.9(10)-107	Escherichia coli	b3368	[pn:siroheme synthase] [gn:cysg]
CONTIG442	3963443_f3_58	2149	7811	918	306	1473	4.7(10)-151	Escherichia coli	b2752	[pn:atp sulfurylase] [gn:cysd]
CONTIG442	4426068_f3_59	2150	7812	1434	478	2131	9.0(10)-221	Escherichia coli	b2751	[pn:atp sulfurylase] [gn:cysn]
CONTIG442	14119653_f3_61	2151	7813	348	116	407	4.4(10)-38	Escherichia coli	b2749	[pn:hypothetical protein in sure-cysc intergenic region] [gn:ygbe]
CONTIG442	16298917_f3_64	2152	7814	1080	360	1563	1.3(10)-160	Escherichia coli	b2745	[pn:hypothetical protein] [gn:ybgo]
CONTIG442	35596015_f3_65	2153	7815	363	121	453	5.9(10)-43	Escherichia coli	b2743	[pn:l-isoaspartyl protein carboxyl methyltransferase type ii]
CONTIG442	4018943_c2_107	2154	7816	1053	351	1448	2.2(10)-148	Escherichia coli	b2753	[pn:iap] [gn:iap]
CONTIG442	4142201_c2_120	2155	7817	1293	431	573	1.1(10)-55	Bacillus subtilis	yhaA	[pn:hypothetical protein]
CONTIG442	9866650_c2_121	2156	7818	1425	475	271	2.2(10)-21	Bacillus subtilis	mmr	[pn:methylenomycin a resistance protein]

CONTIG442	400675_c3_148	2157	7819	534	178	634	3.8(10)-62	Escherichia coli	b2765	[pn:hypothetical protein]
CONTIG443	17050011_f1_1	2158	7820	324	108	555	9.1(10)-54	Plasmid R478	L38824	or:plasmid r478 gn:tera lc:751 re:1776 di:direct sr:plasmid r478 dna nt:putative
CONTIG443	3932668_f1_13	2159	7821	306	102	97	3.1(10)-5	Escherichia coli	b1508	[pn:hipb protein] [gn:hipb]
CONTIG443	23870438_f1_15	2160	7822	828	276	93	0.065	Rattus norvegicus	S15674	cell surface glycoprotein ox47 precursor - rat
CONTIG443	25567885_f1_18	2161	7823	525	175	898	4.0(10)-90	Escherichia coli	b0264	[pn:insertion element isl protein insb] [gn:insb_2]
CONTIG443	16914082_f2_23	2162	7824	588	196	749	2.5(10)-74	Plasmid R478	L38824	or:plasmid r478 gn:terb lc:1799 re:2254 di:direct sr:plasmid r478 dna nt:putative
CONTIG443	12268751_f2_25	2163	7825	633	211	429	2.1(10)-40	Bacillus subtilis	yceD	[pn:hypothetical protein]
CONTIG443	33632805_f2_26	2164	7826	1263	421	2036	1.1(10)-210	Plasmid R478	L38824	or:plasmid r478 gn:terf lc:5017 re:6258 di:direct sr:plasmid r478 dna nt:putative
CONTIG443	22676377_f2_38	2165	7827	1359	453	832	4.0(10)-83	Escherichia coli	b1507	[pn:hipa protein] [gn:hipa]
CONTIG443	6735393_f2_43	2166	7828	285	95	446	3.2(10)-42	Escherichia coli	b4294	[pn:insertion element isl f protein insa] [gn:insa_7]
CONTIG443	9822137_f3_46	2167	7829	1044	348	1530	4.4(10)-157	Plasmid R478	L38824	or:plasmid r478 gn:terc lc:2277 re:3317 di:direct sr:plasmid r478 dna nt:putative
CONTIG443	23547182_f3_47	2168	7830	606	202	549	4.0(10)-53	Bacillus subtilis	yceD	[pn:hypothetical protein]
CONTIG443	2911290_f3_65	2169	7831	234	78	370	3.7(10)-34	Escherichia coli	S40546	hypothetical protein - escherichia coli
CONTIG443	23947168_c1_88	2170	7832	2043	681	328	2.0(10)-26	Bacillus subtilis	yjeD	[pn:hypothetical protein]
CONTIG443	16125182_c2_94	2171	7833	2448	816	3998	0	Escherichia coli	P08504	transposase for transposon tn2501.
CONTIG443	31284383_c2_95	2172	7834	1026	342	1577	4.5(10)-162	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn:tnpa gn:tnpa lc:10303 re:11307 di:complement

CONTIG443	14885165_c2_97	2173	7835	297	99	390	2.7(10)-36	Escherichia coli	D93826	hypothetical 11k protein (insertion sequence is1) -escherichia coli this protein is coded by the insertion sequence is1.
CONTIG443	22313533_c2_113	2174	7836	1083	361	100	0.027	Saccharomyces cerevisiae	P25040	hypothetical protein in ifm1 3'region (fragment).
CONTIG444	6341_f1_13	2175	7837	2628	876	4054	0	Escherichia coli	b3806	[pn:adenylate cyclase] [gn:cyaA]
CONTIG444	25886466_f1_14	2176	7838	888	296	1326	1.8(10)-135	Escherichia coli	b3809	[pn:diaminopimelate epimerase] [gn:dapF]
CONTIG444	10677291_f1_17	2177	7839	750	250	1051	2.5(10)-106	Escherichia coli	b3812	[pn:hypothetical 27.1 kd protein in xerc-uvrd intergenic region]
CONTIG444	14656965_f1_23	2178	7840	1023	341	1516	1.3(10)-155	Escherichia coli	b3816	[pn:magnesium and cobalt transport protein cora] [gn:corA]
CONTIG444	15097887_f1_26	2179	7841	924	308	1440	1.5(10)-147	Escherichia coli	b3821	[pn:phospholipase a1 precursor] [gn:plda]
CONTIG444	1368832_f1_27	2180	7842	1896	632	2840	6.7(10)-296	Escherichia coli	b3822	[pn:dna-dependent atpase, dna helicase] [gn:recq]
CONTIG444	36619627_f1_30	2181	7843	471	157	703	1.8(10)-69	Escherichia coli	b3825	[pn:lysophospholipase l2] [gn:pldb]
CONTIG444	11932643_f2_46	2182	7844	459	153	206	8.8(10)-17	Escherichia coli	P39166	hypothetical 7.2 kd protein in cyay-dapf intergenic region.
CONTIG444	14877083_f2_48	2183	7845	909	303	1308	1.5(10)-133	Escherichia coli	b3811	[pn:integrase/recombinase xerc] [gn:xerc]
CONTIG444	35158586_f2_50	2184	7846	2217	739	3493	0	Escherichia coli	b3813	[pn:dna helicase ii] [gn:uvrd]
CONTIG444	829026_f2_57	2185	7847	651	217	446	3.2(10)-42	Escherichia coli	b3823	[pn:hypothetical 13.3 kd protein in recq 3''' region] [gn:yigj]
CONTIG444	11875466_f3_72	2186	7848	723	241	992	4.5(10)-100	Escherichia coli	b3810	[pn:hypothetical 26.7 kd protein in dapf-xerc intergenic region]
CONTIG444	5198312_c1_89	2187	7849	645	215	547	6.5(10)-53	Escherichia coli	b3824	[pn:hypothetical 15.4 kd protein in recq-pldb intergenic region]
CONTIG444	22520812_c1_120	2188	7850	1254	418	1123	5.9(10)-114	Escherichia coli	b3803	[pn:uroporphyrinogen iii methylase] [gn:hcmx]
CONTIG444	11744501_c2_126	2189	7851	555	185	727	5.5(10)-72	Escherichia coli	b3820	[pn:hypothetical 17.1 kd protein in rad-plda intergenic region] [gn:yigj]
CONTIG444	12109716_c2_127	2190	7852	909	303	1197	8.5(10)-122	Escherichia coli	b3819	[pn:rard protein] [gn:rard]

CONTIG444	12242841_c2_141_2191	7853	756	252	924	7.2(10)-93	Escherichia coli	b3804	[pn:uroporphyrinogen iii synthase] [gn:hemd]
CONTIG444	15735641_c3_169_2192	7854	360	120	431	1.3(10)-40	Escherichia coli	b3807	[pn:cyay protein] [gn:cyay]
CONTIG444	4728191_c3_173_2193	7855	966	322	1447	2.7(10)-148	Escherichia coli	b3805	[pn:porphobilinogen deaminase] [gn:heme]
CONTIG444	16145837_c3_177_2194	7856	1224	408	1682	3.3(10)-173	Escherichia coli	b3802	[pn:hemy protein] [gn:hemy]
CONTIG444	6282962_c3_178_2195	7857	1224	408	189	2.1(10)-13	Erwinia herbicola	Q01334	hypothetical 29.9 kd protein in crte 3'region (orf3).
CONTIG445	23634781_f1_4_2196	7858	3081	1027	485	1.6(10)-52	Serratia marcescens	JC5568	[pn:serine proteinase h1, precursor] [gn:ssp-h1]
CONTIG445	10052331_f1_15_2197	7859	819	273	737	4.7(10)-73	Escherichia coli	b2805	[pn:l-fucose operon activator] [gn:fuc]
CONTIG445	24868825_f1_24_2198	7860	348	116	128	1.6(10)-8	Escherichia coli	b3004	[pn:hypothetical protein]
CONTIG445	32035208_f2_31_2199	7861	2013	671	1321	2.0(10)-186	Escherichia coli	b1023	[pn:hypothetical protein] [gn:ycdr]
CONTIG445	9948592_f2_34_2200	7862	447	149	208	5.4(10)-17	Yersinia pestis	U22837	or:yersinia pestis pn-hmss gn:hmss le:7025 re:7492 di:direct nt:hypothetical and essential protein, pi 6.68; 17.5
CONTIG445	16613762_f2_39_2201	7863	1212	404	1574	9.5(10)-162	Escherichia coli	b3001	[pn:hypothetical protein]
CONTIG445	6410751_f3_44_2202	7864	2424	808	1529	5.5(10)-157	Escherichia coli	b1024	[pn:hypothetical protein] [gn:ycds]
CONTIG445	24304207_f3_48_2203	7865	1434	478	1459	1.5(10)-149	Escherichia coli	b1022	[pn:hypothetical protein] [gn:ycdq]
CONTIG445	441008_f3_51_2204	7866	537	179	91	0.049	Klebsiella pneumoniae	P06218	nitrogen regulation protein ntrb (ec 2.7.3.-)
CONTIG445	7241576_f3_53_2205	7867	981	327	1332	4.2(10)-136	Escherichia coli	b2989	[pn:hypothetical protein]
CONTIG445	25990684_c1_61_2206	7868	281	93	274	5.5(10)-24	Escherichia coli	b3005	[pn:biopolymer transport exbd protein] [gn:exbd]
CONTIG445	32604711_c1_81_2207	7869	531	177	91	0.03599	Neisseria gonorrhoeae	S16613	[PN:opacity protein opaB]
CONTIG445	11854837_c1_85_2208	7870	645	215	198	6.2(10)-16	Haemophilus influenzae	H10726	[pn:nitrate/nitrite response regulator protein] [gn:narp]

CONTIG445	33615888_c2_87	2209	7871	528	176	749	2.5(10)-74	Escherichia coli	b3002	[pn:hypothetical protein] [gn:yqha]
CONTIG445	14659377_c2_90	2210	7872	1677	559	746	5.2(10)-74	Escherichia coli	b1421	[pn:methyl-accepting chemotaxis protein iii] [gn:trg]
CONTIG445	4477253_c2_94	2211	7873	1872	624	2696	1.2(10)-280	Escherichia coli	b2988	[pn:glutathionylspermidine synthetase/amidase] [gn:gsp]
CONTIG445	24862907_c3_110	2212	7874	390	130	157	5.7(10)-11	Pseudomonas sp.	P18896	increased glyphosate resistance protein.
CONTIG446	14222077_f1_7	2213	7875	1062	354	1563	1.3(10)-160	Escherichia coli	b4269	[pn:hypothetical zinc-type alcohol dehydrogenase- like protein] [gn:yjgb]
CONTIG446	35711006_f2_24	2214	7876	2880	960	4657	0	Escherichia coli	b4258	[pn:valyl-trna synthetase] [gn:vals]
CONTIG446	475468_f2_25	2215	7877	597	199	422	1.1(10)-39	Escherichia coli	b4256	[pn:hypothetical protein]
CONTIG446	21992143_f3_40	2216	7878	603	201	708	5.5(10)-70	Escherichia coli	b4259	[pn:dna polymerase iii chi subunit] [gn:holc]
CONTIG446	16172193_f3_50	2217	7879	1572	524	2108	2.5(10)-218	Escherichia coli	b4263	[pn:hypothetical 54.3 kd protein in pepa-gntv intergenic region]
CONTIG446	36381892_f3_52	2218	7880	4503	1501	7200	0	Escherichia coli	b3212	[pn:glutamate synthase] [gn:gltb]
CONTIG446	5250318_f3_53	2219	7881	1428	476	2377	7.7(10)-247	Escherichia coli	b3213	[pn:glutamate synthase] [gn:gltd]
CONTIG446	29304682_c1_71	2220	7882	1665	555	1540	3.7(10)-158	Citrobacter freundii	P45510	dihydroxyacetone kinase (ec 2.7.1.29) (glycerone kinase).
CONTIG446	33682087_c2_90	2221	7883	1032	344	1515	1.7(10)-155	Escherichia coli	b3211	[pn:hypothetical 34.6 kd protein in arcb-gltb intergenic region]
CONTIG446	21954086_c2_91	2222	7884	948	316	181	5.0(10)-12	Pseudomonas aeruginosa	D86947	[dc:pseudomonas aeruginosa gene for chemotactic transducer, completecds.] [pn:hydrophilic protein] [nt:orf1]
CONTIG446	24415936_c3_102	2223	7885	675	225	244	8.3(10)-21	Escherichia coli	b3219	[pn:hypothetical protein] [gn:yhcf]
CONTIG447	15125800_f1_1	2224	7886	540	180	801	7.7(10)-80	Escherichia coli	b0812	[pn:dna protection during starvation protein] [gn:dps]
CONTIG447	25604712_f1_3	2225	7887	741	247	1104	6.0(10)-112	Escherichia coli	b0809	[pn:glutamine transport apb-binding protein glnq] [gn:glnq]
CONTIG447	26285806_f1_4	2226	7888	2328	776	2857	1.1(10)-297	Escherichia coli	b0808	[pn:hypothetical protein]

CONTIG447	12586088_f1_6	2227	7889	300	100	285	3.7(10)-25	Escherichia coli	b0806	[pn:hypothetical protein]
CONTIG447	861407_f1_9	2228	7890	2583	861	1504	2.5(10)-154	Escherichia coli	b3144	[pn:hypothetical outer membrane usher protein in agal-mtr intergenic region] [gn:yraj]
CONTIG447	4488453_f1_11	2229	7891	513	171	197	7.9(10)-16	Escherichia coli	b4319	[pn:fimg protein precursor] [gn:fimg]
CONTIG447	13161462_f1_24	2230	7892	1224	408	1395	8.9(10)-143	Escherichia coli	b0793	[pn:hypothetical protein]
CONTIG447	25964387_f2_25	2231	7893	816	272	1210	3.6(10)-123	Escherichia coli	b0811	[pn:glutamine-binding periplasmic protein precursor] [gn:glnh]
CONTIG447	16853916_f2_26	2232	7894	729	243	744	8.5(10)-74	Escherichia coli	b0810	[pn:glutamine transport system permease protein glnp] [gn:glnp]
CONTIG447	36033312_f2_38	2233	7895	582	194	209	4.2(10)-17	Escherichia coli	b4314	[pn:type 1 fimbrial subunit] [gn:fma]
CONTIG447	3909688_f2_39	2234	7896	684	228	408	3.5(10)-38	Escherichia coli	b3143	[pn:hypothetical 25.7 kd fimbrial chaperone in agal- mtr intergeni] [gn:yrai]
CONTIG447	24494091_f2_46	2235	7897	1065	355	114	7.4(10)-5	Escherichia coli	b0942	[pn:hypothetical protein]
CONTIG447	15720380_f2_56	2236	7898	1035	345	1194	1.8(10)-121	Escherichia coli	b0795	[pn:hypothetical protein]
CONTIG447	26736057_f3_73	2237	7899	285	95	401	1.8(10)-37	Escherichia coli	b0803	[pn:hypothetical 9.8 kd protein in ding/rarb 3'''region] [gn:ybi]
CONTIG447	14650256_f3_74	2238	7900	264	88	193	2.1(10)-15	Escherichia coli	b0802	[pn:hypothetical 8.6 kd protein in ding/rarb 3'''region] [gn:ybi]
CONTIG447	23437800_f3_89	2239	7901	696	232	874	1.3(10)-87	Escherichia coli	b0796	[pn:hypothetical transcriptional regulator in moae-rhle intergenic region] [gn:ybi]
CONTIG447	24900957_f3_92	2240	7902	1755	585	2686	1.3(10)-279	Escherichia coli	b0794	[pn:hypothetical protein]
CONTIG447	32713215_c2_138	2241	7903	1407	469	1801	8.5(10)-186	Escherichia coli	b0797	[pn:putative atp-dependent rna helicase] [gn:rhle]
CONTIG447	5177157_c3_156	2242	7904	309	103	378	5.2(10)-35	Entamoeba histolytica	Y14328	[PN:3E1 protein] [DE:Entamoeba histolytica mRNA for 3E1 protein.] [LE:32] [RE:418] [DI:direct]

CONTIG447	29933406_c3_157	2243	7905	435	145	95	0.05299	Caenorhabditis elegans	U39852	or:caenorhabditis elegans gn:k10c2.1 le:join(2542 re:2988,309 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna cm20c9; coded for by
CONTIG447	136417_c3_164	2244	7906	2256	752	3206	0	Escherichia coli	b0799	[pn:probable atp-dependent helicase ding] [gn:ding]
CONTIG447	15829811_c3_172	2245	7907	996	332	1122	7.5(10)-114	Escherichia coli	b0800	[pn:hypothetical 35.0 kd protein in ding/rarb 3'''region] [gn:ybib]
CONTIG447	26206586_c3_174	2246	7908	1026	342	1341	4.7(10)-137	Escherichia coli	b0807	[pn:hypothetical protein]
CONTIG448	2510268_f1_7	2247	7909	444	148	137	1.8(10)-9	Escherichia coli	b4347	[pn:hypothetical 14.6 kd protein in mcrb-hsds intergenic region]
CONTIG448	26251502_f1_14	2248	7910	735	245	96	0.01499	Escherichia coli	b4365	[pn:hypothetical 27.0 kd protein in dnat-hold intergenic region]
CONTIG448	35807665_f1_15	2249	7911	771	257	385	9.5(10)-36	Escherichia coli	b0939	[pn:hypothetical protein]
CONTIG448	24408336_f1_21	2250	7912	1110	370	155	9.6(10)-11	Escherichia coli	b4314	[pn:type 1 fimbrial subunit] [gn:fima]
CONTIG448	17007156_f1_25	2251	7913	1209	403	97	0.05899	Helicobacter pylori	HP1079	[pn:h]
CONTIG448	25432962_f2_37	2252	7914	498	166	164	2.5(10)-12	Vibrio cholerae	S81006	or:vibrio cholerae pn:hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nt:28 kda secreted hydrophilic protein; this sequence
CONTIG448	12766056_f2_42	2253	7915	645	215	193	2.1(10)-15	Escherichia coli	b4314	[pn:type 1 fimbrial subunit] [gn:fima]
CONTIG448	32599061_f2_45	2254	7916	693	231	240	2.2(10)-20	Escherichia coli	b0943	[pn:hypothetical protein]
CONTIG448	473413_f2_50	2255	7917	753	251	481	6.4(10)-46	Escherichia coli	b2127	[pn:hypothetical transcriptional regulator in molt-bglx intergenic region] [gn:yehv]
CONTIG448	31250052_f2_51	2256	7918	474	158	354	1.8(10)-32	Escherichia coli	b1970	[pn:hypothetical protein]
CONTIG448	7245763_f2_52	2257	7919	978	326	405	7.2(10)-38	Escherichia coli	b0707	[pn:hypothetical 20.2 kd protein in phrb 5'''region] [gn:ybga]
CONTIG448	5963256_f3_72	2258	7920	252	84	96	0.0004	Volvox carteri	S22697	extensin - volvox carteri (fragment)

CONTIG448	36568816_f3_74	2259	7921	2598	866	1593	9.3(10)-164	Escherichia coli	b0940	[pn:hypothetical protein]
CONTIG448	4494031_c1_99	2260	7922	783	261	644	3.3(10)-63	Bacillus subtilis	yddR	[pn:hypothetical protein]
CONTIG448	1055337_c1_127	2261	7923	504	168	349	6.2(10)-32	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-selc intergenic region] [gn:yicj]
CONTIG448	24659636_c2_131	2262	7924	1257	419	180	3.7(10)-11	Escherichia coli	P22519	colicin v secretion protein cvaa.
CONTIG448	26758592_c2_133	2263	7925	1005	335	146	8.3(10)-8	Haemophilus influenzae	HI1052	[pn:arac-like transcription regulator]
CONTIG448	21960077_c2_149	2264	7926	855	285	274	5.5(10)-24	Escherichia coli	b2847	[pn:hypothetical protein]
CONTIG448	6132827_c2_150	2265	7927	990	330	152	1.8(10)-8	Bacillus subtilis	yfil	[pn:hypothetical protein]
CONTIG448	22272552_c2_151	2266	7928	492	164	231	2.0(10)-19	Escherichia coli	b4012	[pn:hypothetical 16.4 kd protein in rrfc-meta intergenic region]
CONTIG448	16135200_c2_155	2267	7929	1161	387	1062	1.7(10)-107	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-selc intergenic region] [gn:yicj]
CONTIG448	2506660_c3_162	2268	7930	1200	400	374	4.0(10)-34	Bacillus subtilis	yknV	[pn:hypothetical protein]
CONTIG448	6929702_c3_177	2269	7931	540	180	614	5.0(10)-60	Escherichia coli	b4149	[pn:hypothetical 19.9 kd protein in sugc-ampc intergenic region]
CONTIG448	33334717_c3_184	2270	7932	492	164	123	5.5(10)-8	Escherichia coli	b2848	[pn:hypothetical protein]
CONTIG448	9900640_c3_190	2271	7933	435	145	541	2.7(10)-52	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-selc intergenic region] [gn:yicj]
CONTIG448	34582963_c3_191	2272	7934	2379	793	3661	0	Escherichia coli	b3656	[pn:hypothetical 88.1 kd protein in glts-selc intergenic region] [gn:yicj]
CONTIG449	14843818_f2_51	2273	7935	1017	339	921	1.5(10)-92	Escherichia coli	b2321	[pn:div protein] [gn:div]
CONTIG449	7235901_f2_77	2274	7936	1017	339	818	9.4(10)-126	Escherichia coli	b2344	[pn:long-chain fatty acid transport protein precursor] [gn:fadI]
CONTIG449	16065700_f3_78	2275	7937	183	61	110	1.3(10)-6	Escherichia coli	D90862	or escherichia coli pn:glycine-rich cell wall structural protein gn:dedd le:14996 re:15160 di:direct sr:escherichia coli (strain:k12) dna, clone_lib.kohara lambda minise nt:similar to [swissprot accession number p27483]

CONTIG449	16285206_f3_89	2276	7938	303	101	95	0.00025	Rattus norvegicus	S24169	mucin - rat
CONTIG449	6431430_f3_95	2277	7939	2172	724	2644	3.8(10)-275	Escherichia coli	b2324	[pn:hypothetical protein]
CONTIG449	24415941_f3_102	2278	7940	555	185	900	2.5(10)-90	Escherichia coli	b2331	[pn:hypothetical protein]
CONTIG449	30729686_c1_117	2279	7941	501	167	745	6.7(10)-74	Escherichia coli	b2340	[pn:hypothetical protein]
CONTIG449	111308_c1_121	2280	7942	822	274	1148	1.3(10)-116	Escherichia coli	b2327	[pn:hypothetical 28.6 kd protein in mepa 5'''region] [gn:yfca]
CONTIG449	19558455_c1_123	2281	7943	366	122	369	4.7(10)-34	Escherichia coli	b2325	[pn:hypothetical protein]
CONTIG449	15882827_c1_127	2282	7944	1218	406	1807	2.0(10)-186	Escherichia coli	b2323	[pn:3-oxoacyl-acyl-carrier-protein synthase i] [gn:fabb]
CONTIG449	897890_c1_138	2283	7945	1002	334	1330	6.9(10)-136	Escherichia coli	b2316	[pn:acetyl-coa carboxylase beta subunit] [gn:accd]
CONTIG449	21913887_c2_142	2284	7946	372	124	96	0.00025	Escherichia coli	D90864	or:escherichia coli pn:mitochondrial trifunctional enzyme beta subunit gn:hadhb lc:13075 re:14127 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to swissprot accession number
CONTIG449	14665927_c2_145	2285	7947	2151	717	2730	3.0(10)-284	Escherichia coli	b2341	[pn:hypothetical protein]
CONTIG449	16850312_c2_148	2286	7948	216	72	174	1.2(10)-12	Escherichia coli	b2330	[pn:hypothetical adenine-specific methylase in aroc 3'''region] [gn:yfcb]
CONTIG449	22048513_c2_149	2287	7949	975	325	1123	5.9(10)-114	Escherichia coli	b2328	[pn:penicillin-insensitive murein endopeptidase precursor] [gn:mepa]
CONTIG449	6767933_c2_162	2288	7950	912	304	1251	1.6(10)-127	Escherichia coli	b2318	[pn:pseudouridylylase synthase i] [gn:trua]
CONTIG449	4588311_c2_166	2289	7951	1281	427	1748	3.5(10)-180	Escherichia coli	b2315	[pn:folypolyglutamate synthase] [gn:folc]
CONTIG449	23712758_c3_168	2290	7952	288	96	411	1.7(10)-38	Escherichia coli	b2343	[pn:hypothetical protein]
CONTIG449	24088515_c3_169	2291	7953	1344	448	1984	3.3(10)-205	Escherichia coli	b2342	[pn:hypothetical protein]

CONTIG449	14976381_c3_172	2292	7954	1023	341	1544	1.3(10)-158	Escherichia coli	b2330	[pn: hypothetical adenine-specific methylase in aroC 3'"' region] [gn:yfcb]
CONTIG449	3411530_c3_173	2293	7955	1146	382	1557	6.0(10)-160	Escherichia coli	b2329	[pn: chorismate synthase] [gn: aroc]
CONTIG449	10751892_c3_176	2294	7956	540	180	134	7.0(10)-9	Escherichia coli	D90863	or: escherichia coli le: 14845 re: 15579 di: complement sr: escherichia coli (strain: k12) dna, clone_lib: kohara lambda minise nt: similar to [swissprot accession number]
CONTIG449	15085211_c3_177	2295	7957	588	196	914	8.3(10)-92	Escherichia coli	b2326	[pn: hypothetical protein]
CONTIG449	33470092_c3_183	2296	7958	1239	413	1402	1.6(10)-143	Escherichia coli	b2322	[pn: hypothetical protein]
CONTIG449	2348128_c3_185	2297	7959	1167	389	1630	1.1(10)-167	Escherichia coli	b2320	[pn: erythronate-4-phosphate dehydrogenase] [gn: pdxb]
CONTIG449	10972782_c3_186	2298	7960	1020	340	1386	8.0(10)-142	Escherichia coli	b2319	[pn: -l protein] [gn: usg]
CONTIG449	24037543_c3_187	2299	7961	672	224	756	4.5(10)-75	Escherichia coli	b2317	[pn: dcdA protein] [gn: deda]
CONTIG449	36588465_c3_190	2300	7962	339	113	251	1.5(10)-21	Escherichia coli	b2314	[pn: dcdD protein] [gn: dedd]
CONTIG45	20132828_f3_3	2301	7963	771	257	301	8.0(10)-31	Escherichia coli	b2412	[pn: hypothetical protein] [gn: zipa]
CONTIG450	16897627_f1_1	2302	7964	813	271	1166	1.6(10)-118	Escherichia coli	b4364	[pn: hypothetical 30.5 kd protein in dnat-hold intergenic region]
CONTIG450	24067318_f1_12	2303	7965	1479	493	2489	1.0(10)-258	Escherichia coli	Z37980	or: escherichia coli pn: 5-carboxy-2-hydroxymuconate semialdehyde gn: hpae le: 2137 re: 3603 di: direct
CONTIG450	32052067_f1_16	2304	7966	330	110	90	0.0015	Zea mays	U28017	or: zea mays pn: globulin1 gn: glb1 le: join(421 re: 922, 1010 di: direct sr: maize nt: allele glb1-hb; a null allele caused by the
CONTIG450	35713343_f1_30	2305	7967	342	114	344	2.1(10)-31	Escherichia coli	b4353	[pn: hypothetical 7.7 kd protein in mrr-ts intergenic region] [gn: yjix]
CONTIG450	5897876_f2_34	2306	7968	489	163	320	7.2(10)-29	Bacillus subtilis	ykmA	[pn: hypothetical protein]

CONTIG450	12714138_f2_35	2307	7969	444	148	593	8.5(10)-58	Acinetobacter calcoaceticus	Y09102	or:acinetobacter calcoaceticus pn:unknown protein le:621 re:1052 di:direct nt:orf2
CONTIG450	34469090_f2_36	2308	7970	756	252	1072	1.5(10)-108	Escherichia coli	b4361	[pn:dna replication protein dnac] [gn:dnac]
CONTIG450	24640902_f2_37	2309	7971	489	163	348	7.9(10)-32	Escherichia coli	b4360	[pn:hypothetical 17.5 kd protein in mdob-dnac intergenic region] [gn:yjia]
CONTIG450	22861262_f2_39	2310	7972	531	177	113	6.2(10)-7	Bacillus subtilis	yvbK	[pn:hypothetical protein]
CONTIG450	31835762_f2_43	2311	7973	1314	438	1646	2.2(10)-169	Escherichia coli	Z37980	or:escherichia coli pn:5-oxo-1,2,5- tricarboxylic-3-penten acid gn:hpag le:851 re:2140 di:direct
CONTIG450	4120187_f2_48	2312	7974	819	273	1318	1.3(10)-134	Escherichia coli	AF036583	[de:escherichia coli 2-oxo-hept-4-ene- 1,7-dioate hydratase (hpcg) gene, complete cds] [pn:2-oxo-hept- 4-ene-1,7-dioate hydratase] [gn:hpcg] [nt:ohed hydratase]
CONTIG450	4891633_f2_59	2313	7975	540	180	764	6.5(10)-76	Escherichia coli	C55349	4-hydroxyphenylacetate 3- monooxygenase (ec 1.14.13.3) smallchain - escherichia coli (atcc 11105)
CONTIG450	2456431_f2_61	2314	7976	2319	773	2860	5.0(10)-298	Escherichia coli	b4354	[pn:hypothetical 77.9 kd protein in mur-tsrl intergenic region] [gn:yjiy]
CONTIG450	24632126_f2_62	2315	7977	699	233	721	2.3(10)-71	Escherichia coli	b4352	[pn:f2] [gn:yjia]
CONTIG450	34156635_f3_65	2316	7978	588	196	500	6.2(10)-48	Escherichia coli	b4363	[pn:p14 protein] [gn:yjib]
CONTIG450	3955313_f3_67	2317	7979	555	185	677	1.1(10)-66	Escherichia coli	b4362	[pn:primosomal protein i] [gn:dnad]
CONTIG450	31906558_f3_69	2318	7980	2334	778	3278	0	Escherichia coli	b4359	[pn:phosphoglycerol transferase i] [gn:mdob]
CONTIG450	35820818_f3_79	2319	7981	1140	380	1460	1.2(10)-149	Escherichia coli	Z37980	or:escherichia coli pn:homoprotocatechuate dioxygenase gn:hpac le:3605 re:4456 di:direct
CONTIG450	3956693_f3_80	2320	7982	390	130	572	1.5(10)-55	Escherichia coli	S10709	5-carboxymethyl-2- hydroxymuconate isomerase - escherichiacoli

CONTIG450	12776580_f3_82	2321	7983	1017	339	703	1.8(10)-69	Escherichia coli	b2245	[pn:hypothetical protein]
CONTIG450	6066957_f3_83	2322	7984	1365	455	1480	8.8(10)-152	Escherichia coli	Z37980	or:escherichia coli pn:hypothetical 4-hydroxyphenylacetate permease gn:hpax le:6734 re:8110 di:direct
CONTIG450	4035443_f3_84	2323	7985	942	314	1372	2.3(10)-140	Escherichia coli	Z37980	or:escherichia coli pn:regulator of the 4hpa-hydroxylase operon gn:hpaa le:8120 re:9007 di:direct
CONTIG450	24737630_f3_85	2324	7986	1686	562	2653	4.4(10)-276	Escherichia coli	B55349	4-hydroxyphenylacetate 3-monooxygenase (ec 1.14.13.3) largechain - escherichia coli (atcc 11105)
CONTIG450	3228125_c1_108	2325	7987	1704	568	141	2.1(10)-8	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr le:<1 re:588 di:direct
CONTIG450	12698757_c1_111	2326	7988	1788	596	1893	1.5(10)-195	Escherichia coli	b4355	[pn:methyl-accepting chemotaxis protein i] [gn:tsr]
CONTIG450	24901515_c2_138	2327	7989	456	152	617	2.5(10)-60	Escherichia coli	Q07095	homoprotocatechuate degradative operon repressor.
CONTIG451	5911250_f1_1	2328	7990	825	275	1103	7.7(10)-112	Escherichia coli	b3528	[pn:c4-dicarboxylate transport protein] [gn:dcta]
CONTIG451	21542930_f1_2	2329	7991	1503	501	1973	5.0(10)-204	Escherichia coli	b3527	[pn:53.1 kd protein in kdkg-dcta intergenic region precursor] [gn:yhi]
CONTIG451	25986526_f1_5	2330	7992	822	274	998	1.0(10)-100	Escherichia coli	b3525	[pn:hypothetical 29.7 kd protein in tref-kdkg intergenic region]
CONTIG451	25665877_f1_11	2331	7993	762	254	360	4.2(10)-33	Bacillus subtilis	fabG	[pn:3-oxoacyl-acyl-carrier protein reductase] [gn:ylpf]
CONTIG451	10272250_f1_12	2332	7994	687	229	481	6.4(10)-46	Escherichia coli	b3520	[pn:hypothetical transcriptional regulator in tref- kdkg intergenic region] [gn:yhib]
CONTIG451	207877_f1_21	2333	7995	2229	743	3076	0	Escherichia coli	b3498	[pn:oligopeptidase a] [gn:prlc]
CONTIG451	5328530_f1_22	2334	7996	462	154	551	2.3(10)-53	Escherichia coli	b3494	[pn:hypothetical 13.0 kd protein in pit-uspa intergenic region] [gn:yhio]
CONTIG451	5864762_f1_26	2335	7997	1287	429	1518	8.1(10)-156	Escherichia coli	b3492	[pn:hypothetical 43.8 kd protein in rhsb-pit intergenic region] [gn:yhin]
CONTIG451	7166656_f2_54	2336	7998	861	287	1222	1.8(10)-124	Escherichia coli	b3497	[pn:hypothetical protein in uspa-prlc intergenic region] [gn:yhiq]

CONTIG451	4338393_f2_60	2337	7999	852	284	286	2.8(10)-25	Thiobacillus ferrooxidans	AF032884	[de:thiobacillus ferrooxidans n-acetylglucosamine-1-phosphateuridylyltransferase (glmu) gene, partial cds; glucosamine synthase(glms)] [pn:transposition complex] [gn:tnsa]
CONTIG451	4958318_f2_61	2338	8000	945	315	292	3.2(10)-25	Thiobacillus ferrooxidans	AF032884	[de:thiobacillus ferrooxidans n-acetylglucosamine-1-phosphateuridylyltransferase (glmu) gene, partial cds; glucosamine synthase(glms) and recg (recg) genes, complete cds; and transposon tn5468,complete sequenc"] [pn:tnsc]
CONTIG451	53382_f3_70	2339	8001	2085	695	2730	3.0(10)-284	Escherichia coli	b3524	[pn:hypothetical 75.1 kd protein in tref-kdkg intergenic region]
CONTIG451	26601457_f3_95	2340	8002	1701	567	466	6.5(10)-44	Thiobacillus ferrooxidans	AF032884	[de:thiobacillus ferrooxidans n-acetylglucosamine-1-phosphateuridylyltransferase (glmu) gene, partial cds; glucosamine synthase(glms) and recg (recg) genes, complete cds; and transposon tn5468,complete"] [pn:tnsb]
CONTIG451	3157016_c1_104	2341	8003	1506	502	2144	3.7(10)-222	Escherichia coli	b3493	[pn:pita] [gn:pita]
CONTIG451	30555383_c1_109	2342	8004	1443	481	2148	1.3(10)-222	Escherichia coli	b3500	[pn:glutathione oxidoreductase] [gn:gor]
CONTIG451	3939063_c1_120	2343	8005	1332	444	1671	5.0(10)-172	Escherichia coli	b3523	[pn:hypothetical metabolite transport protein in tref-kdkg intergenic region] [gn:yhje]
CONTIG451	23714693_c2_132	2344	8006	453	151	724	1.1(10)-71	Escherichia coli	b3495	[pn:universal stress protein a] [gn:uspa]
CONTIG451	35678462_c2_140	2345	8007	1707	569	2503	3.3(10)-260	Escherichia coli	b3519	[pn:probable cytoplasmic trehalase] [gn:tref]
CONTIG451	3242338_c2_144	2346	8008	351	117	141	6.7(10)-10	Salmonella typhimurium	X67137	or:salmonella typhimurium pn:gp19 protein gn:gene 19 lc:578 re:1018 di:direct
CONTIG451	11034506_c2_148	2347	8009	675	225	643	4.2(10)-63	Escherichia coli	b3522	[pn:hypothetical 37.9 kd protein in tref-kdkg intergenic region]

CONTIG451	598951_c2_149	2348	8010	468	156	559	3.5(10)-54	Escherichia coli	b3522	[pn: hypothetical 37.9 kd protein in tref-kdkg intergenic region]
CONTIG451	24353507_c3_174	2349	8011	882	294	1353	2.5(10)-138	Escherichia coli	b3499	[pn: hypothetical 31.9 kd protein in prle-gor intergenic region] [gn:yhir]
CONTIG451	23594561_c3_182	2350	8012	573	191	156	1.8(10)-11	Bacillus subtilis	ynaD	[pn: hypothetical protein]
CONTIG451	3991556_c3_184	2351	8013	909	303	1012	3.3(10)-102	Escherichia coli	b3521	[pn: hypothetical transcriptional regulator in tref- kdkg intergenic region] [gn:yhjc]
CONTIG451	24254075_c3_191	2352	8014	990	330	1340	6.0(10)-137	Escherichia coli	b3526	[pn: 2-dehydro-3-deoxygluconokinase] [gn:kdkg]
CONTIG452	21900187_f1_9	2353	8015	318	106	115	1.1(10)-6	Pseudomonas aeruginosa	JQ0133	hypothetical 26.4k protein - pseudomonas aeruginosa
CONTIG452	11020661_f2_35	2354	8016	702	234	746	5.2(10)-74	Escherichia coli	b0396	[pn: araj protein precursor] [gn:araj]
CONTIG452	4870402_f2_51	2355	8017	909	303	314	3.2(10)-28	Escherichia coli	b3521	[pn: hypothetical transcriptional regulator in tref- kdkg intergenic region] [gn:yhjc]
CONTIG452	34648408_f2_52	2356	8018	447	149	642	5.5(10)-63	Escherichia coli	b1482	[pn: osmotically inducible protein c] [gn:osmc]
CONTIG452	14636666_f2_54	2357	8019	795	265	568	3.7(10)-55	Bacillus subtilis	ykvO	[pn: hypothetical protein]
CONTIG452	12163286_f2_62	2358	8020	378	126	107	2.3(10)-5	Xenopus laevis	P17437	skin secretory protein xp2 precursor (apeg protein).
CONTIG452	36565837_f2_68	2359	8021	1506	502	104	0.0066	Bacillus subtilis	ytpA	[pn: hypothetical protein]
CONTIG452	36429028_f2_69	2360	8022	1215	405	691	3.6(10)-68	Escherichia coli	b1163	[pn: hypothetical protein]
CONTIG452	1306533_f3_73	2361	8023	513	171	143	4.2(10)-10	Escherichia coli	b4178	[pn: hypothetical 15.6 kd protein in pura-vacb intergenic region] [gn:yjeb]
CONTIG452	35290831_c1_106	2362	8024	1536	512	947	2.7(10)-95	Escherichia coli	b1485	[pn: hypothetical protein]
CONTIG452	17053875_c1_109	2363	8025	987	329	1160	7.0(10)-118	Escherichia coli	b1483	[pn: hypothetical protein]
CONTIG452	5292305_c1_111	2364	8026	921	307	404	9.1(10)-38	Escherichia coli	b3521	[pn: hypothetical transcriptional regulator in tref- kdkg intergenic region] [gn:yhjc]

CONTIG452	14945160_c1_115	2365	8027	1785	595	2635	3.5(10)-274	Escherichia coli	b1479	[pn:nad-linked malic enzyme] [gn:sfca]
CONTIG452	34413433_c1_116	2366	8028	1716	572	455	4.9(10)-52	Bacillus subtilis	ydiF	[pn:hypothetical protein]
CONTIG452	22010303_c2_128	2367	8029	1050	350	1476	2.2(10)-151	Escherichia coli	b1486	[pn:hypothetical protein]
CONTIG452	35836461_c3_147	2368	8030	867	289	126	1.1(10)-5	Escherichia coli	b1853	[pn:hypothetical 32.0 kd protein in pyka-zwf intergenic region] [gn:yebk]
CONTIG452	16692842_c3_148	2369	8031	585	195	662	4.2(10)-65	Escherichia coli	b1488	[pn:hypothetical protein]
CONTIG452	12386275_c3_149	2370	8032	1548	516	2261	1.5(10)-234	Escherichia coli	b1487	[pn:hypothetical protein]
CONTIG452	32656630_c3_153	2371	8033	1044	348	1241	1.8(10)-126	Escherichia coli	b1484	[pn:hypothetical protein]
CONTIG452	5953808_c3_161	2372	8034	930	310	94	0.03699	Bacillus subtilis	yobT	[pn:hypothetical protein]
CONTIG452	41502_c3_163	2373	8035	267	89	307	1.7(10)-27	Escherichia coli	b1481	[pn:hypothetical protein]
CONTIG452	22464212_c3_167	2374	8036	1023	341	1349	6.7(10)-138	Escherichia coli	b1478	[pn:hypothetical protein]
CONTIG452	36125916_c3_168	2375	8037	1221	407	558	4.4(10)-54	Mycobacterium tuberculosis	Z96073	dehydrogenase, mtcy16f9.02, mtcy16f9.02, probable dehydrogenase, len
CONTIG453	22132932_f3_71	2376	8038	2112	704	1761	1.5(10)-181	Escherichia coli	b0779	[pn:excision nuclease abc subunit b] [gn:uvrb]
CONTIG453	35335183_f3_75	2377	8039	2709	903	133	6.7(10)-5	Archaeoglobus fulgidus	H69378	[pn:purine ntpase homolog]
CONTIG453	11722916_c1_80	2378	8040	441	147	293	2.5(10)-25	Rhizobium sp.	P50360	hypothetical 29.3 kd protein in region 2 of sym plasmid (no1265).
CONTIG453	2047880_c1_81	2379	8041	1050	350	1581	1.7(10)-162	Yersinia pestis	AF053945	[de:yersinia pestis plasmid ppep1, complete plasmid sequence.] [pn:transposase]
CONTIG453	5286516_c1_88	2380	8042	243	81	283	6.0(10)-25	Salmonella dublin	S22685	vacc protein - salmonella dublin virulence plasmid
CONTIG453	2932082_c1_90	2381	8043	762	254	391	2.2(10)-36	Saccharomyces cerevisiae	P40586	hypothetical 27.4 kd protein in hyr1 3'region.
CONTIG453	4726577_c1_91	2382	8044	267	89	145	2.6(10)-10	Escherichia coli	b1892	[pn:flagellar transcriptional activator flhD] [gn:flhD]

CONTIG453	10744011_c1_95	2383	8045	1113	371	1628	1.8(10)-167	Escherichia coli	b0356	[pn:alcohol-acetaldehyde dehydrogenase] [gn:adhc]
CONTIG453	33644826_c1_97	2384	8046	1362	454	91	0.53	Helicobacter pylori	HP0870	[pn:flagellar hook flge] [gn:flge]
CONTIG453	26255200_c1_98	2385	8047	372	124	203	1.8(10)-16	Haemophilus influenzae	HI0184	[pn:hypothetical protein]
CONTIG453	24306507_c2_130	2386	8048	2655	885	1136	5.4(10)-163	Bacillus subtilis	uvrA	[pn:exonuclease abc]
CONTIG453	33697188_c2_132	2387	8049	279	93	412	1.3(10)-38	Escherichia coli	b0357	[pn:hypothetical protein]
CONTIG453	22672286_c3_135	2388	8050	804	268	1260	1.8(10)-128	Yersinia pestis	AF053945	[de:yersinia pestis plasmid ppcpl, complete plasmid sequence] [pn:transposase]
CONTIG453	24025381_c3_144	2389	8051	219	73	271	1.1(10)-23	Salmonella dublin	S22686	vagD protein - salmonella dublin virulence plasmid
CONTIG453	10727336_c3_147	2390	8052	288	96	249	2.3(10)-21	Escherichia coli	b0357	[pn:hypothetical protein]
CONTIG453	19767826_c3_149	2391	8053	621	207	683	2.5(10)-67	Escherichia coli	b0355	[pn:hypothetical protein] [gn:yaim]
CONTIG454	15828957_f1_4	2392	8054	633	211	731	2.1(10)-72	Escherichia coli	b3249	[pn:rod shape-determining protein mred] [gn:mred]
CONTIG454	3984837_f1_5	2393	8055	603	201	864	1.7(10)-86	Escherichia coli	b3248	[pn:hypothetical 21.5 kd protein in cafa-mred intergenic region] [gn:ynde]
CONTIG454	24627202_f1_10	2394	8056	1446	482	2135	3.3(10)-221	Escherichia coli	b3244	[pn:tldd protein] [gn:tldd]
CONTIG454	10179131_f1_11	2395	8057	231	77	366	9.8(10)-34	Escherichia coli	b3242	[pn:hypothetical protein] [gn:yher]
CONTIG454	36042040_f1_14	2396	8058	2031	677	2286	3.3(10)-237	Escherichia coli	b3240	[pn:hypothetical 73.6 kd protein in argg-cafa intergenic region] [gn:yhcp]
CONTIG454	23614003_f1_17	2397	8059	963	321	1415	6.7(10)-145	Escherichia coli	b3236	[pn:malate dehydrogenase] [gn:mdh]
CONTIG454	13087756_f2_33	2398	8060	1020	340	1207	7.4(10)-123	Escherichia coli	b3250	[pn:rod shape-determining protein mrec] [gn:mrec]
CONTIG454	14453433_f2_35	2399	8061	1506	502	2182	3.6(10)-226	Escherichia coli	b3247	[pn:cytoplasmic axial filament protein] [gn:cafa]
CONTIG454	16026457_f2_36	2400	8062	3849	1283	3981	0	Escherichia coli	b3245	[pn:hypothetical 107.7 kd protein in argg-cafa intergenic region]

CONTIG454	30208260_f2_41	2401	8063	960	320	1415	6.7(10)-145	Escherichia coli	b3241	[pn:hypothetical 34.8 kd protein in argr-cafa intergenic region] [gn:yhcq]
CONTIG454	15647540_f3_55	2402	8064	1983	661	2669	8.8(10)-278	Escherichia coli	b3252	[pn:hypothetical 73.3 kd protein in mreB-accb intergenic region] [gn:yhda]
CONTIG454	32230311_f3_56	2403	8065	1170	390	1827	1.5(10)-188	Escherichia coli	b3251	[pn:rod shape-determining protein mreB] [gn:mreb]
CONTIG454	35282183_f3_70	2404	8066	1674	558	1376	9.1(10)-141	Escherichia coli	b2661	[pn:succinate-semialdehyde dehydrogenase] [gn:gabd]
CONTIG454	22917932_f3_71	2405	8067	315	105	302	5.9(10)-27	Escherichia coli	b3239	[pn:hypothetical protein] [gn:yhco]
CONTIG454	23650765_c1_77	2406	8068	1125	375	1305	3.1(10)-133	Escherichia coli	b3235	[pn:protease precursor] [gn:degq]
CONTIG454	16265886_c1_110	2407	8069	1062	354	1419	2.6(10)-145	Escherichia coli	b1971	[pn:hypothetical protein]
CONTIG454	14455203_c1_111	2408	8070	243	81	309	1.1(10)-27	Escherichia coli	b1972	[pn:hypothetical protein]
CONTIG454	6070136_c2_112	2409	8071	1425	475	1622	7.9(10)-167	Escherichia coli	b3234	[pn:protease precursor] [gn:degq]
CONTIG454	34244001_c2_116	2410	8072	219	73	124	4.2(10)-8	Escherichia coli	b3237	[pn:arginine repressor] [gn:argr]
CONTIG454	4144568_c2_146	2411	8073	984	328	1280	1.3(10)-130	Escherichia coli	b3253	[pn:hypothetical 34.7 kd protein in mreB-accb intergenic region] [gn:yhdh]
CONTIG454	12585313_c3_149	2412	8074	474	158	540	3.6(10)-52	Escherichia coli	b3233	[pn:hypothetical 15.2 kd protein in rplM-hhoA intergenic region] [gn:yhcb]
CONTIG454	24220842_c3_150	2413	8075	438	146	632	6.4(10)-62	Escherichia coli	b3237	[pn:arginine repressor] [gn:argr]
CONTIG454	24644052_c3_151	2414	8076	270	90	176	1.3(10)-13	Escherichia coli	b3238	[pn:hypothetical protein] [gn:yhcn]
CONTIG454	13683312_c3_155	2415	8077	537	179	164	2.5(10)-12	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:car le:59 re:580 di:direct nt:orf2
CONTIG454	32244052_c3_161	2416	8078	930	310	1440	1.5(10)-147	Escherichia coli	b3243	[pn:hypothetical protein] [gn:yhcs]
CONTIG455	23642302_f1_27	2417	8079	1731	577	2126	3.1(10)-220	Escherichia coli	b0445	[pn:hypothetical 65.0 kd protein in hupB-cof intergenic region]

CONTIG455	32228380_f1_28	2418	8080	699	233	1133	5.2(10)-115	Escherichia coli	b0444	[pn:hypothetical protein] [gn:ybax]
CONTIG455	7686_f2_62	2419	8081	1107	369	976	2.2(10)-98	Mycobacterium tuberculosis	AL022121	[de:mycobacterium tuberculosis sequence v025.] [pn:putative lyase] [gn:mtv025.032] [nt:mtv025.032,
CONTIG455	32458412_f3_76	2420	8082	1566	522	1507	1.2(10)-154	Escherichia coli	b0457	[pn:hypothetical protein] [gn:ylab]
CONTIG455	24254782_f3_85	2421	8083	1539	513	284	4.5(10)-25	Escherichia coli	b1439	[pn:hypothetical protein]
CONTIG455	36066375_f3_87	2422	8084	330	110	484	3.1(10)-46	Escherichia coli	b0454	[pn:hypothetical protein] [gn:ybaz]
CONTIG455	13751263_f3_88	2423	8085	942	314	1283	6.5(10)-131	Escherichia coli	b0452	[pn:acyl-coa thioesterase ii] [gn:tesb]
CONTIG455	31439416_c1_105	2424	8086	504	168	550	3.1(10)-53	Escherichia coli	b0443	[pn:hypothetical protein] [gn:ybaw]
CONTIG455	24500877_c1_106	2425	8087	363	121	128	1.6(10)-8	Haemophilus influenzae	1111420	[pn:hypothetical protein]
CONTIG455	3913580_c1_115	2426	8088	621	207	794	4.2(10)-79	Escherichia coli	b0447	[pn:hypothetical protein]
CONTIG455	4875126_c1_116	2427	8089	1785	595	2281	1.2(10)-236	Escherichia coli	b0448	[pn:mdla]
CONTIG455	35582912_c1_126	2428	8090	582	194	627	2.2(10)-61	Escherichia coli	b0453	[pn:hypothetical protein] [gn:ybay]
CONTIG455	29877090_c1_134	2429	8091	1122	374	279	1.1(10)-29	Haemophilus influenzae	H11635	[pn:purine nucleotide synthesis repressor protein] [gn:purf]
CONTIG455	4140_c2_140	2430	8092	2034	678	2534	1.8(10)-263	Escherichia coli	b0441	[pn:hypothetical protein] [gn:ybau]
CONTIG455	5120650_c2_148	2431	8093	2046	682	2330	7.4(10)-242	Escherichia coli	b0449	[pn:mdlb]
CONTIG455	6536566_c2_150	2432	8094	1338	446	1687	1.0(10)-173	Escherichia coli	b0451	[pn:hypothetical protein in mdl-tesb intergenic region] [gn:amtb]
CONTIG455	4509562_c2_157	2433	8095	678	226	309	1.1(10)-27	Haemophilus influenzae	H10522	[pn:sp]
CONTIG455	24078333_c2_160	2434	8096	3111	1037	3614	0	Escherichia coli	b0344	[pn:beta-galactosidase] [gn:lacz]
CONTIG455	12698806_c3_164	2435	8097	522	174	827	1.3(10)-82	Escherichia coli	b0439	[pn:lon protease] [gn:lon]
CONTIG455	33860768_c3_165	2436	8098	360	120	292	6.7(10)-26	Escherichia coli	b0440	[pn:dna-binding protein hu-beta] [gn:hupb]

CONTIG455	24344391_c3_166	2437	8099	501	167	339	7.0(10)-31	Escherichia coli	b0442	[pn:hypothetical protein] [gn:ybav]
CONTIG455	34257212_c3_168	2438	8100	381	127	130	1.0(10)-8	Haemophilus influenzae	HI1419	[pn:hypothetical protein]
CONTIG455	4470206_c3_170	2439	8101	843	281	1105	4.7(10)-112	Escherichia coli	b0446	[pn:cof protein] [gn:cof]
CONTIG455	886451_c3_177	2440	8102	375	125	540	3.6(10)-52	Escherichia coli	b0450	[pn:nitrogen regulatory protein p-ii] [gn:glk]
CONTIG456	17069787_f1_4	2441	8103	1119	373	1812	5.7(10)-187	Escherichia coli	b2806	[pn:hypothetical 41.9 kd protein in fuc-geva intergenic region] [gn:ygd]
CONTIG456	14339808_f1_12	2442	8104	462	154	381	2.5(10)-35	Escherichia coli	b2792	[pn:hypothetical protein]
CONTIG456	24726386_f1_18	2443	8105	1383	461	2148	1.3(10)-222	Escherichia coli	b2788	[pn:hypothetical protein] [gn:ygy]
CONTIG456	14704837_f1_19	2444	8106	1350	450	2115	4.5(10)-219	Escherichia coli	b2787	[pn:hypothetical protein] [gn:ygx]
CONTIG456	1440751_f1_29	2445	8107	1653	551	2559	4.0(10)-266	Escherichia coli	b2780	[pn:ctp synthase] [gn:pyrg]
CONTIG456	960000_f1_31	2446	8108	1350	450	749	2.5(10)-74	Escherichia coli	b1621	[pn:pts system, maltose and glucose-specific ii abc component] [gn:malx]
CONTIG456	24480282_f2_49	2447	8109	1389	463	2172	4.0(10)-225	Escherichia coli	b2789	[pn:hypothetical protein]
CONTIG456	35347826_f2_61	2448	8110	1566	522	1626	3.0(10)-167	Escherichia coli	b2785	[pn:hypothetical ma methyltransferase in rela-bara intergenic region] [gn:ygea]
CONTIG456	5886253_f2_62	2449	8111	2280	760	3496	0	Escherichia coli	b2784	[pn:gtp pyrophosphokinase] [gn:rela]
CONTIG456	16208337_f2_66	2450	8112	1371	457	1985	2.7(10)-205	Escherichia coli	b2779	[pn:lase] [gn:eno]
CONTIG456	22147011_f3_71	2451	8113	936	312	1509	7.4(10)-155	Escherichia coli	b2808	[pn:regulatory protein for glycine cleavage pathway] [gn:geva]
CONTIG456	15868766_f3_72	2452	8114	435	145	613	6.5(10)-60	Escherichia coli	b2807	[pn:hypothetical 14.3 kd protein in fuc-geva intergenic region] [gn:ygd]
CONTIG456	33750181_f3_83	2453	8115	606	202	679	6.7(10)-67	Escherichia coli	b2793	[pn:syd] [gn:syd]
CONTIG456	14880066_f3_85	2454	8116	792	264	1145	2.7(10)-116	Escherichia coli	b2791	[pn:hypothetical protein] [gn:yqcb]

CONTIG456	22870800_f3_86	2455	8117	465	155	622	7.2(10)-61	Escherichia coli	b2790	[pn:hypothetical protein]
CONTIG456	3933193_f3_89	2456	8118	1155	385	1206	9.5(10)-123	Escherichia coli	b3124	[pn:hypothetical 42.1 kd protein in rnpb-soha intergenic region] [gn:yhad]
CONTIG456	16145293_f3_99	2457	8119	834	278	1014	2.1(10)-102	Escherichia coli	b2781	[pn:mazg protein] [gn:mazg]
CONTIG456	563568_c1_137	2458	8120	1374	458	2203	2.1(10)-228	Escherichia coli	b2795	[pn:hypothetical protein in sdac 5'''region] [gn:ygdh]
CONTIG456	4298457_c1_138	2459	8121	1371	457	1818	1.3(10)-187	Escherichia coli	b2796	[pn:putative serine transporter] [gn:sdac]
CONTIG456	34664182_c1_140	2460	8122	774	258	1130	1.1(10)-114	Escherichia coli	b2798	[pn:potential 5'''-3''' nuclease] [gn:exo]
CONTIG456	4563193_c2_147	2461	8123	834	278	323	3.5(10)-29	Haemophilus influenzae	H10143	[pn:gb]
CONTIG456	19619037_c2_175	2462	8124	846	282	1306	2.3(10)-133	Escherichia coli	b2794	[pn:hypothetical protein] [gn:yqcd]
CONTIG456	13707307_c3_188	2463	8125	1299	433	200	3.0(10)-13	Schizosaccharomyces pombe	L37084	or: schizosaccharomyces pombe pn:phosphopyruvate hydratase ec.4.2.1.11 le:2 re:1342 di:complement sr:schizosaccharomyces pombe cdna to mma
CONTIG456	25831336_c3_191	2464	8126	1398	466	175	5.2(10)-12	Escherichia coli	A30374	hypothetical 77k protein (spot 3' region) - escherichia coli
CONTIG456	4379716_c3_195	2465	8127	2769	923	3912	0	Escherichia coli	b2786	[pn:sensor protein bara] [gn:bara]
CONTIG456	32314042_c3_212	2466	8128	1383	461	2082	1.3(10)-215	Escherichia coli	b2797	[pn:l-serine dehydratase 2] [gn:sdab]
CONTIG457	47891_f1_26	2467	8129	501	167	597	3.2(10)-58	Escherichia coli	b3355	[pn:phosphoribulokinase] [gn:prkb]
CONTIG457	35792657_f1_36	2468	8130	822	274	262	1.0(10)-22	Escherichia coli	U82664	or: escherichia coli le:133380 re:134066 di:direct nt-hypothetical protein
CONTIG457	26759702_f2_37	2469	8131	222	74	321	5.7(10)-29	Escherichia coli	b3348	[pn:slyx protein] [gn:slyx]
CONTIG457	24412918_f2_38	2470	8132	654	218	539	4.5(10)-52	Escherichia coli	B49988	hypothetical protein 159 - escherichia coli

CONTIG457	3947187_f2_64	2471	8133	222	74	318	1.2(10)-28	Escherichia coli	b3354	[pn:hypothetical 8.5 kd protein in kifb-prkb intergenic region]
CONTIG457	568755_f2_65	2472	8134	531	177	653	3.7(10)-64	Escherichia coli	b3355	[pn:phosphoribulokinase] [gn:prkb]
CONTIG457	7067711_f2_68	2473	8135	639	213	1070	2.5(10)-108	Escherichia coli	b3357	[pn:cyclic amp receptor protein] [gn:crp]
CONTIG457	24308275_f2_69	2474	8136	2145	715	2846	1.6(10)-296	Escherichia coli	b3358	[pn:hypothetical 79.5 kd protein in crp-argd intergenic region] [gn:yhfk]
CONTIG457	4484686_f3_78	2475	8137	1938	646	2854	2.2(10)-297	Escherichia coli	b3352	[pn:hypothetical abc transporter in kifb-prkb intergenic region]
CONTIG457	3466041_f3_79	2476	8138	948	316	1171	4.9(10)-119	Klebsiella pneumoniae	U95087	[PN:MdcR] [GN:mdeR] [FN:regulates expression of malonate decarboxylase] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdcA,mdcB,mdcC,mdcD,mdcE,mdcF,mdcG,mdcH,mdcR) genes, completecds.] [NT:transcriptional regul]
CONTIG457	34103250_f3_91	2477	8139	1050	350	1317	1.6(10)-134	Escherichia coli	b3353	[pn:hypothetical 38.5 kd protein in kifb-prkb intergenic region]
CONTIG457	132825_f3_92	2478	8140	318	106	137	9.3(10)-9	Escherichia coli	U18997	or:escherichia coli lc-265033 re:266106 direct nt:orf_0357; codon usage statistics poor where o72
CONTIG457	21678790_c1_100	2479	8141	573	191	737	4.7(10)-73	Escherichia coli	b3363	[pn:peptidyl-prolyl cis-trans isomerase a] [gn:ppia]
CONTIG457	21925080_c1_101	2480	8142	690	230	542	2.2(10)-52	Escherichia coli	b3361	[pn:cell filamentation protein] [gn:fic]
CONTIG457	16933387_c1_102	2481	8143	594	198	804	3.7(10)-80	Escherichia coli	b3360	[pn:para-aminobenzoate synthetase] [gn:paba]
CONTIG457	21485675_c1_103	2482	8144	1266	422	1917	4.2(10)-198	Escherichia coli	b3359	[pn:acetylornitine delta-aminotransferase] [gn:argd]
CONTIG457	22689078_c1_106	2483	8145	411	137	641	7.0(10)-63	Escherichia coli	b3356	[pn:hypothetical protein] [gn:yhfa]

CONTIG457	26019656_c1_111	2484	8146	885	295	985	2.5(10)-99	Klebsiella pneumoniae	U95087	[PN:MdcB] [GN:mdeB] [FN:involved in biosynthesis of the prosthetic] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdeA,mdeB, mdeC, mdeD, mdeE, mdeF, mdeG, mdeH, mdeR) genes, completecds.] [NT:similar to CtiG proteins]
CONTIG457	3954838_c1_112	2485	8147	309	103	366	9 8(10)-34	Klebsiella pneumoniae	U95087	[PN:MdcC] [GN:mdeC] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdeA,mdeB, mdeC, mdeD, mdeE, mdeF, mdeG, mdeH, mdeR) genes, completecds.] [NT:acyl carrier protein; delta subunit of malonate] [LE:2803] [RE:3102] [DI:1]
CONTIG457	29297917_c1_113	2486	8148	828	276	1026	1.1(10)-103	Klebsiella pneumoniae	U95087	[PN:MdcE] [GN:mdeE] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdeA,mdeB, mdeC, mdeD, mdeE, mdeF, mdeG, mdeH, mdeR) genes, completecds.] [NT:decarboxylase subunit; gamma subunit of malonate] [LE:3928] [RE:4728] [DI:1]
CONTIG457	19650250_c1_114	2487	8149	963	321	1138	1 5(10)-115	Klebsiella pneumoniae	U95087	[PN:MdcF] [GN:mdeF] [FN:putative malonate transporter] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdeA,mdeB, mdeC, mdeD, mdeE, mdeF, mdeG, mdeH, mdeR) genes, completecds.] [NT:encodes ten hydrophobic domains] [LE:4]
CONTIG457	35832883_c1_122	2488	8150	1950	650	2271	1.3(10)-235	Escherichia coli	b3350	[pn:glutathione-regulated potassium-efflux system protein] [gn:kefB]

CONTIG457	1449027_c2_138	2489	8151	1671	557	2387	4.2(10)-269	Klebsiella pneumoniae	U95087	[PN:MdcA] [GN:mdeA] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdcA,mdcB, mdcC, mdcD, mdcE, mdcF, mdcG, mdcH, mdcR) genes, completecds.] [NT:acyl carrier protein transferase; alpha subunit of] [LE:288] [RE:1943] [D
CONTIG457	25650277_c2_140	2490	8152	837	279	1180	5.4(10)-120	Klebsiella pneumoniae	U95087	[PN:MdcD] [GN:mdeD] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdcA,mdcB, mdcC, mdcD, mdcE, mdcF, mdcG, mdcH, mdcR) genes, completecds.] [NT:decarboxylase subunit; beta subunit of malonate] [LE:3095] [RE:3928] [DI:
CONTIG457	10444826_c2_142	2491	8153	1059	353	1145	2.7(10)-116	Klebsiella pneumoniae	U56096	or:klebsiella pneumoniae pn mdcg gn.mdcg le:6354 re:7337 di:direct nt:similar to malonyl coa-acyl carrier protein
CONTIG457	2625166_c2_147	2492	8154	792	264	330	6.4(10)-30	Pseudomonas aeruginosa	JQ0133	hypothetical 26.4k protein - pseudomonas aeruginosa
CONTIG457	14960906_c2_148	2493	8155	597	199	882	2.0(10)-88	Escherichia coli	b3351	pn:hypothetical nadph oxidoreductase in kifb-prkb intergenic region] [gn:yer]
CONTIG457	14461081_c3_160	2494	8156	564	188	537	7.4(10)-52	Erwinia chrysanthemi	X89443	[GN:ORF3] [DE:E.chrysanthemi DNA for crp gene.] [LE:1200] [RE:1874] [DI:complement]
CONTIG457	3928590_c3_161	2495	8157	198	66	145	2.6(10)-10	Erwinia chrysanthemi	X89443	[GN:ORF3] [DE:E.chrysanthemi DNA for crp gene.] [LE:1200] [RE:1874] [DI:complement]
CONTIG457	15752042_c3_173	2496	8158	696	232	643	4.2(10)-63	Klebsiella pneumoniae	U95087	[PN:MdcG] [GN:mdeG] [FN:involved in formation of the holo-acyl carrier] [DE:Klebsiella pneumoniae malonate decarboxylase gene cluster (mdcA,mdcB, mdcC, mdcD, mdcE, mdcF, mdcG, mdcH, mdcR) genes, completecds.] [LE:5828] [RE:6445] [DI:d

CONTIG457	33984378_c3_186	2497	8159	672	224	742	1.3(10)-73	Escherichia coli	b3349	[pn:probable flkbp-type peptidyl-prolyl cis-trans isomerase] [gn:slyd]
CONTIG458	36150466_f1_9	2498	8160	423	141	320	7.2(10)-29	Escherichia coli	b1926	[pn:flagellar protein flit] [gn:flit]
CONTIG458	12601516_f1_16	2499	8161	1713	571	1997	1.3(10)-206	Escherichia coli	b1938	[pn:flagellar basal-body m-ring protein] [gn:flif]
CONTIG458	2847202_f1_19	2500	8162	1215	405	430	1.0(10)-49	Escherichia coli	b1943	[pn:hook-length control protein] [gn:flif]
CONTIG458	13933302_f1_22	2501	8163	441	147	267	3.0(10)-23	Escherichia coli	b1947	[pn:flagellar protein flio] [gn:flio]
CONTIG458	12362590_f1_24	2502	8164	387	129	292	6.7(10)-26	Escherichia coli	b1949	[pn:flagellar biosynthetic protein flit] [gn:flit]
CONTIG458	3166591_f1_25	2503	8165	792	264	919	2.5(10)-92	Escherichia coli	b1950	[pn:flagellar biosynthetic protein flir] [gn:flir]
CONTIG458	4423218_f1_26	2504	8166	633	211	916	5.0(10)-92	Escherichia coli	b1951	[pn:colanic acid capsular biosynthesis activation protein a] [gn:rcsa]
CONTIG458	3962502_f1_29	2505	8167	927	309	821	6.0(10)-82	Escherichia coli	b1955	[pn:hypothetical protein]
CONTIG458	4100318_f2_42	2506	8168	1422	474	1613	7.0(10)-166	Escherichia coli	b1924	[pn:flagellar hook associated protein 2] [gn:flid]
CONTIG458	33631457_f2_43	2507	8169	438	146	481	6.4(10)-46	Escherichia coli	b1925	[pn:flagellar protein flis] [gn:flis]
CONTIG458	911533_f2_51	2508	8170	1077	359	1487	1.6(10)-152	Escherichia coli	b1939	[pn:flagellar motor switch protein flig] [gn:flig]
CONTIG458	35242718_f2_53	2509	8171	1443	481	2199	5.5(10)-228	Escherichia coli	b1941	[pn:flagellum-specific atp synthase] [gn:flit]
CONTIG458	34620911_f2_54	2510	8172	465	155	635	3.1(10)-62	Escherichia coli	b1942	[pn:flagellar flit protein] [gn:flit]
CONTIG458	35727283_f2_56	2511	8173	528	176	552	1.8(10)-53	Escherichia coli	b1944	[pn:flit protein] [gn:flit]
CONTIG458	22007193_f2_57	2512	8174	426	142	633	5.0(10)-62	Escherichia coli	b1946	[pn:flagellar motor switch protein flin] [gn:flin]
CONTIG458	10015706_f3_74	2513	8175	1560	520	2350	5.5(10)-244	Escherichia coli	b1927	[pn:cytoplasmic alpha-amylase] [gn:amya]
CONTIG458	26694825_f3_78	2514	8176	729	243	608	7.0(10)-71	Escherichia coli	b1940	[pn:flagellar assembly protein flih] [gn:flih]
CONTIG458	2535457_f3_82	2515	8177	1068	356	1634	4.2(10)-168	Escherichia coli	b1945	[pn:cg site no. 774] [gn:flim]

CONTIG458	12397666_f3_84	2516	8178	804	268	730	2.6(10)-72	Escherichia coli	b1948	[pn:flagellar biosynthetic protein flip] [gn:flip]
CONTIG458	32306326_f3_87	2517	8179	258	86	272	9.0(10)-24	Escherichia coli	b1953	[pn:hypothetical protein]
CONTIG458	29939465_c1_93	2518	8180	348	116	306	2.2(10)-27	Escherichia coli	b1952	[pn:dsrb protein] [gn:dsrb]
CONTIG458	43322291_c1_105	2519	8181	309	103	131	7.7(10)-9	Bacillus subtilis	S14505	hypothetical protein 12 (flaa operon) - bacillus subtilis
CONTIG458	21910312_c1_112	2520	8182	336	112	406	5.7(10)-38	Escherichia coli	b1937	[pn:flagellar hook-basal body complex protein flie] [gn:flie]
CONTIG458	4006355_c1_113	2521	8183	489	163	486	1.8(10)-46	Escherichia coli	b1928	[pn:hypothetical 15.0 kd protein in amyA-flie intergenic region] [gn:yedd]
CONTIG458	9800156_c1_123	2522	8184	810	270	1133	5.2(10)-115	Escherichia coli	b1922	[pn:ma polymerase sigma transcription factor for flagellar operon] [gn:flia]
CONTIG458	6928936_c1_124	2523	8185	567	189	718	4.9(10)-71	Escherichia coli	b1921	[pn:fliz protein] [gn:fliz]
CONTIG458	20837_c1_125	2524	8186	1059	353	1369	5.0(10)-140	Escherichia coli	b1919	[pn:hypothetical protein]
CONTIG458	33491312_c1_126	2525	8187	690	230	966	2.6(10)-97	Escherichia coli	b1918	[pn:yecv]
CONTIG458	33991554_c2_129	2526	8188	509	169	528	6.7(10)-51	Escherichia coli	b1956	[pn:hypothetical protein]
CONTIG458	24507182_c3_179	2527	8189	1728	576	2023	2.5(10)-209	Escherichia coli	U47614	or:escherichia coli pn:flagellin gn:flie lc:1 re:1758 di:direct
CONTIG458	32692516_c3_181	2528	8190	855	285	1110	1.3(10)-112	Escherichia coli	b1920	[pn:flty protein precursor] [gn:flty]
CONTIG458	34414030_c3_184	2529	8191	759	253	1160	7.0(10)-118	Escherichia coli	b1917	[pn:hypothetical protein] [gn:yecv]
CONTIG459	3239041_f1_4	2530	8192	444	148	141	6.7(10)-10	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr lc:59 re:580 di:direct nt:orf2
CONTIG459	26735180_f1_7	2531	8193	933	311	1015	1.7(10)-102	Haemophilus influenzae	H10362	[pn:adhesin b precursor] [gn:fima]
CONTIG459	24422707_f1_10	2532	8194	1167	389	635	3.1(10)-62	Haemophilus influenzae	I110359	[pn:gb]
CONTIG459	13163556_f1_12	2533	8195	1380	460	1480	8.8(10)-152	Escherichia coli	b0585	[pn:enterochelin esterase] [gn:fcs]

CONTIG459	781658_f1_13	2534	8196	3885	1295	4972	0	Escherichia coli	b0586	[pn:enterobactin synthetase component f] [gn:entf]
CONTIG459	21505208_f2_35	2535	8197	954	318	669	7.5(10)-66	Haemophilus influenzae	H10360	[pn:hydrophobic membrane protein]
CONTIG459	33875656_f2_42	2536	8198	249	83	262	1.0(10)-22	Escherichia coli	B31958	hypothetical 8k protein (fes 3' region) - escherichia coli
CONTIG459	1425657_f3_61	2537	8199	1521	507	90	0.12	Azospirillum brasilense	X70360	orazospirillum brasilense gn:car
CONTIG459	5316943_f3_62	2538	8200	2043	681	3181	0	Escherichia coli	b0314	le:<1 re:588 di:direct
CONTIG459	20318790_f3_63	2539	8201	348	116	114	5.0(10)-7	Escherichia coli	b3555	[pn:high-affinity choline transport protein] [gn:betf]
CONTIG459	12370787_f3_66	2540	8202	948	316	819	9.6(10)-82	Haemophilus influenzae	H10361	[pn:hypothetical 11.0 kd protein in bise-cspa intergenic region]
CONTIG459	6539591_f3_81	2541	8203	354	118	91	0.00129	Mus musculus	P21952	[pn:iii dicitrate transport atp-binding protein fecf] [gn:fece]
CONTIG459	679507_f3_87	2542	8204	1263	421	1338	9.8(10)-137	Escherichia coli	b0591	octamer-binding transcription factor 6 (oct-6) (pou-domain transcription factor scip).
CONTIG459	10554188_c1_91	2543	8205	996	332	1279	1.7(10)-130	Escherichia coli	b0592	[pn:hypothetical membrane protein p43] [gn:ybda]
CONTIG459	31848911_c1_95	2544	8206	1320	440	1102	1.0(10)-111	Escherichia coli	b0589	[pn:ferrienterobactin-binding periplasmic protein precursor] [gn:fepb]
CONTIG459	19538413_c1_115	2545	8207	663	221	911	1.7(10)-91	Escherichia coli	b0313	[pn:ferric enterobactin transport protein fepg] [gn:fepg]
CONTIG459	5267181_c2_127	2546	8208	1059	353	1010	5.5(10)-102	Escherichia coli	b0590	[pn:regulatory protein beti] [gn:beti]
CONTIG459	29979075_c2_146	2547	8209	1593	531	2240	2.6(10)-232	Escherichia coli	b0312	[pn:ferric enterobactin transport protein fepd] [gn:fepd]
CONTIG459	16970218_c3_156	2548	8210	720	240	275	4.2(10)-24	Escherichia coli	P21500	[pn:betaine aldehyde dehydrogenase] [gn:betb]
CONTIG459	16270216_c3_161	2549	8211	978	326	1127	2.2(10)-114	Escherichia coli	b0588	very hypothetical 18.0 kd protein in fepb 3'region.
CONTIG459								Escherichia coli		[pn:ferric enterobactin transport atp-binding protein fepc] [gn:fepc]

CONTIG459	16219582_c3_162	2550	8212	327	109	92	0.0011	Nicotiana alata	U88587	[de:nicotiana alata 120 kda style glycoprotein (naprp5) mma, completecds.] [pn:120 kda style glycoprotein] [gn:naprp5] [nt:style-specific protein possessing features of]
CONTIG459	24254052_c3_172	2551	8213	2265	755	2862	3.1(10)-298	Escherichia coli	b0584	[pn:ferrienterobactin receptor precursor] [gn:fcpa]
CONTIG459	12134390_c3_173	2552	8214	762	254	465	3.2(10)-44	Escherichia coli	b0583	[pn:enterobactin synthetase component d] [gn:cntd]
CONTIG459	33678892_c3_184	2553	8215	1722	574	2774	6.5(10)-289	Escherichia coli	b0311	[pn:choline dehydrogenase] [gn:beta]
CONTIG46	25397792_f2_2	2554	8216	435	145	462	6.5(10)-44	Escherichia coli	b0814	[pn:outer membrane protein x precursor] [gn:ompx]
CONTIG460	4392308_f1_11	2555	8217	531	177	624	4.5(10)-61	Escherichia coli	b3995	[pn:hypothetical protein] [gn:yjae]
CONTIG460	13759633_f1_12	2556	8218	1899	633	3132	0	Escherichia coli	b3994	[pn:thic protein] [gn:thic]
CONTIG460	32661541_f1_14	2557	8219	945	315	799	1.3(10)-79	Escherichia coli	b3992	[pn:thif]
CONTIG460	35267665_f1_19	2558	8220	357	119	189	5.5(10)-15	Bacillus subtilis	licA	[pn:phosphotransferase system] [gn:celc]
CONTIG460	16510407_f2_52	2559	8221	237	79	173	2.7(10)-13	Escherichia coli	S77700	[PN:thiG] protein]
CONTIG460	13073963_f2_53	2560	8222	1800	600	1706	9.9(10)-176	Escherichia coli	b3990	[pn:thih protein] [gn:thih]
CONTIG460	11019027_f2_54	2561	8223	1656	552	245	3.8(10)-20	Escherichia coli	b1535	[pn:ydeh]
CONTIG460	24256925_f2_55	2562	8224	342	114	219	3.7(10)-18	Bacillus subtilis	ydhM	[pn:hypothetical protein]
CONTIG460	10196957_f3_65	2563	8225	1734	578	2535	1.3(10)-263	Escherichia coli	b4006	[pn:phosphoribosylaminoimidazolec arboxamide formyltransferase and imp cyclohydrolase]
CONTIG460	22869525_f3_66	2564	8226	1308	436	2030	4.5(10)-210	Escherichia coli	b4005	[pn:phosphoribosylglycineamide synthetase] [gn:purd]
CONTIG460	35339517_f3_74	2565	8227	717	239	899	3.2(10)-90	Escherichia coli	b3993	[pn:thie protein] [gn:thie]
CONTIG460	32245792_f3_77	2566	8228	885	295	1226	7.2(10)-125	Escherichia coli	b3991	[pn:thig protein] [gn:thig]

CONTIG460	24647902_c1_92	2567	8229	4167	1389	6740	0	Escherichia coli	b3987	[pn:dna-directed rna polymerase, beta-subunit] [gn:rpob]
CONTIG460	31291250_c1_112	2568	8230	612	204	886	7.7(10)-89	Escherichia coli	b3999	[pn:hypothetical 22.6 kd protein in heme-hupa intergenic region] [gn:yjag]
CONTIG460	24025251_c1_113	2569	8231	276	92	424	7.0(10)-40	Escherichia coli	b4000	[pn:histone-like dna-binding protein hu-alpha] [gn:hupa]
CONTIG460	16525791_c2_126	2570	8232	4266	1422	6482	0	Escherichia coli	b3988	[pn:dna-directed rna polymerase, beta"-subunit] [gn:rpoc]
CONTIG460	16219716_c2_140	2571	8233	1092	364	1701	3.2(10)-175	Escherichia coli	b3997	[pn:uroporphyrinogen decarboxylase] [gn:heme]
CONTIG460	3962943_c2_141	2572	8234	681	227	1077	4.4(10)-109	Escherichia coli	b3998	[pn:hypothetical 24.9 kd protein in heme-hupa intergenic region] [gn:yjaf]
CONTIG460	13792203_c3_147	2573	8235	258	86	382	2.0(10)-35	Escherichia coli	b3985	[pn:50s ribosomal subunit protein 110] [gn:rpl]
CONTIG460	14094452_c3_148	2574	8236	366	122	372	2.2(10)-34	Escherichia coli	b3986	[pn:50s ribosomal subunit protein 17/112] [gn:rpl]
CONTIG460	33492292_c3_162	2575	8237	795	265	1160	7.0(10)-118	Escherichia coli	b3996	[pn:hypothetical 29.8 kd protein in thic-heme intergenic region] [gn:yjad]
CONTIG460	6508428_c3_168	2576	8238	708	236	906	5.9(10)-91	Escherichia coli	b4001	[pn:hypothetical 26.3 kd protein in hupa-hydh intergenic region] [gn:yjah]
CONTIG461	36428933_f1_16	2577	8239	897	299	944	5.5(10)-95	Escherichia coli	b0826	[pn:molybdopterin biosynthesis moeb protein] [gn:moeb]
CONTIG461	24120405_f1_19	2578	8240	915	305	1322	4.7(10)-135	Escherichia coli	b0824	[pn:hypothetical protein] [gn:yjig]
CONTIG461	26041332_f1_31	2579	8241	2403	801	560	2.7(10)-52	Saccharomyces cerevisiae	YBR229C	[pn:glucosidase ii, catalytic subunit] [gn:rot2]
CONTIG461	24103381_f2_39	2580	8242	1329	443	2083	1.1(10)-215	Escherichia coli	b0835	[pn:hypothetical protein] [gn:yjig]
CONTIG461	32229531_f2_40	2581	8243	555	185	101	0.00072	Streptococcus pneumoniae	L29323	or:streptococcus pneumoniae pn:methyl transferase lc:508 re:1125 di:complement sr:transposon tn5252 dna; and streptococcus pneumoniae (strain sp1000 nt:member of the mtr gene cluster; putative

CONTIG461	19633331_f2_50	2582	8244	1173	391	1531	3.5(10)-157	Escherichia coli	b0823	[pn:hypothetical protein]
CONTIG461	11845627_f2_52	2583	8245	879	293	1168	1.0(10)-118	Escherichia coli	b0822	[pn:hypothetical protein]
CONTIG461	2540786_f2_57	2584	8246	1347	449	923	9.3(10)-93	Escherichia coli	b3093	[pn:hexuronate transporter] [gn:exut]
CONTIG461	24620452_f2_61	2585	8247	1236	412	161	7.7(10)-10	Pseudomonas aeruginosa	JQ0133	hypothetical 26.4k protein - pseudomonas aeruginosa
CONTIG461	287575_f3_64	2586	8248	690	230	837	1.2(10)-83	Escherichia coli	b0838	[pn:hypothetical protein]
CONTIG461	9770206_f3_77	2587	8249	1287	429	1701	3.2(10)-175	Escherichia coli	b0827	[pn:molybdopterin biosynthesis moea protein] [gn:moea]
CONTIG461	16101557_f3_81	2588	8250	1455	485	2307	2.0(10)-239	Escherichia coli	b0823	[pn:hypothetical protein]
CONTIG461	2734432_f3_82	2589	8251	1293	431	1983	4.4(10)-205	Escherichia coli	b0821	[pn:hypothetical protein]
CONTIG461	22949052_c1_113	2590	8252	1887	629	2443	7.9(10)-254	Escherichia coli	b0829	[pn:hypothetical protein]
CONTIG461	16832768_c1_118	2591	8253	414	138	358	6.9(10)-33	Escherichia coli	b0836	[pn:hypothetical protein]
CONTIG461	23573328_c2_137	2592	8254	690	230	955	3.7(10)-96	Escherichia coli	b0825	[pn:hypothetical protein]
CONTIG461	34414165_c2_142	2593	8255	945	315	1234	1.0(10)-125	Escherichia coli	b0828	[pn:hypothetical protein in moea-grxa intergenic region] [gn:ybik]
CONTIG461	23446041_c2_147	2594	8256	942	314	1292	7.2(10)-132	Escherichia coli	b0831	[pn:hypothetical protein]
CONTIG461	22146880_c2_151	2595	8257	1152	384	1539	4.9(10)-158	Escherichia coli	b0837	[pn:hypothetical protein]
CONTIG461	13704165_c2_153	2596	8258	345	115	248	5.9(10)-21	Escherichia coli	b0839	[pn:penicillin-binding protein 6 precursor] [gn:dacc]
CONTIG461	19583290_c3_154	2597	8259	1632	544	2615	4.7(10)-272	Escherichia coli	b0820	[pn:hypothetical protein]
CONTIG461	20179036_c3_164	2598	8260	1125	375	244	8.5(10)-20	Escherichia coli	b3934	[pn:transcriptional repressor cytr] [gn:cytr]
CONTIG461	31730393_c3_180	2599	8261	1623	541	2250	2.2(10)-233	Escherichia coli	b0830	[pn:hypothetical protein]
CONTIG461	30511340_c3_182	2600	8262	963	321	1247	4.2(10)-127	Escherichia coli	b0832	[pn:hypothetical protein]

CONTIG462	15132125_f1_2	2601	8263	828	276	907	4.5(10)-91	Escherichia coli	b1859	[pn:hypothetical 27.8 kd protein in msbb-ruvb intergenic region] [gn:yebl]
CONTIG462	24330036_f1_10	2602	8264	300	100	325	2.2(10)-29	Salmonella typhimurium	Q56031	virulence protein msga.
CONTIG462	14879752_f2_33	2603	8265	762	254	1110	1.3(10)-112	Escherichia coli	b1858	[pn:hypothetical protein] [gn:yeblm]
CONTIG462	21677187_f3_66	2604	8266	594	198	794	4.2(10)-79	Escherichia coli	b1867	[pn:hypothetical 21.8 kd protein in asps 5'''region] [gn:yeed]
CONTIG462	35604677_f3_68	2605	8267	822	274	155	7.7(10)-10	Bacteriophage M1	P08231	tail fiber protein gp37 (fragment).
CONTIG462	36125431_f3_71	2606	8268	216	72	93	8.3(10)-5	Bacteriophage phi-80	P17651	adsorption-inhibiting cor protein.
CONTIG462	22163441_c1_92	2607	8269	396	132	156	1.8(10)-11	Bacteriophage lambda	P03737	minor tail protein m.
CONTIG462	6062568_c1_94	2608	8270	597	199	198	6.2(10)-16	Yersinia pestis	AF053947	[dc:yersinia pestis plasmid pmt1, complete plasmid sequence] [pn:unknown]
CONTIG462	34574067_c1_103	2609	8271	465	155	685	1.5(10)-67	Escherichia coli	b1865	[pn:dtp pyrophosphohydrolase] [gn:ntpa]
CONTIG462	5208563_c1_104	2610	8272	768	256	1208	5.7(10)-123	Escherichia coli	b1864	[pn:hypothetical 26.4 kd protein in ruvc-asps intergenic region] [gn:yebl]
CONTIG462	24430416_c1_106	2611	8273	870	290	810	8.6(10)-81	Escherichia coli	b1861	[pn:holliday junction dna helicase ruva] [gn:ruva]
CONTIG462	116702_c2_110	2612	8274	3492	1164	228	8.5(10)-18	Salmonella typhimurium	AF007380	[PN:lambdaphage H tail component homolog] [DE:Salmonella typhimurium lambda phage K tail component homolog gene,partial cds, lambda phage L tail component homolog, copper-zincsuperoxide dismutase (sodC), attachment and invasion prote
CONTIG462	1063557_c2_111	2613	8275	762	254	434	6.0(10)-41	Coxiella burnetii	Y15898	[de:coxiella burnetii plasmid qprs dna] [pn:hypothetical protein] [gn:orf 248]

CONTIG462	26966_c2_113	2614	8276	3873	1291	1007	4.4(10)-101	Yersinia pestis	AF053947	[de:yersinia pestis plasmid pmt1, complete plasmid sequence.] [pn:phage lambda host specific protein j] [pn:dna-invertase pin] [gn:pin]
CONTIG462	33828125_c2_120	2615	8277	606	202	736	6.0(10)-73	Escherichia coli	b1158	
CONTIG462	33752027_c2_125	2616	8278	543	181	750	2.0(10)-74	Escherichia coli	b1863	[pn:crossover junction endodeoxyribonuclease ruvc] [gn:ruvc]
CONTIG462	31875053_c2_129	2617	8279	477	159	442	8.6(10)-42	Escherichia coli	b1857	[pn:31.1 kd protein in msbb-ruvb intergenic region] [gn:yeb1]
CONTIG462	3393908_c3_137	2618	8280	855	285	319	9.4(10)-29	Yersinia pestis	AF053947	[de:yersinia pestis plasmid pmt1, complete plasmid sequence.] [pn:phage lambda minor tail protein l homolog]
CONTIG462	22541631_c3_148	2619	8281	1821	607	2868	7.2(10)-299	Escherichia coli	b1866	[pn:aspartyl-tRNA synthetase] [gn:asps]
CONTIG462	25431592_c3_149	2620	8282	1014	338	1623	6.2(10)-167	Escherichia coli	b1860	[pn:holliday junction dna helicase ruvb] [gn:ruvb]
CONTIG463	32605317_fl_1	2621	8283	591	197	428	2.6(10)-40	Shigella flexneri	P20102	mercuric resistance protein merd
CONTIG463	4788505_fl_3	2622	8284	1323	441	1941	1.2(10)-200	Pseudomonas aeruginosa	U49101	or:pseudomonas aeruginosa pn:tnia gn:tnia lc:6735 re:8450
CONTIG463	13162887_fl_4	2623	8285	495	165	675	1.8(10)-66	Klebsiella pneumoniae	S32177	transposase - klebsiella pneumoniae
CONTIG463	12111286_fl_9	2624	8286	1563	521	2589	2.7(10)-269	Pseudomonas aeruginosa	Q57541	transposase for insertion sequences is1326/is1353.
CONTIG463	24644811_fl_15	2625	8287	1020	340	1583	1.1(10)-162	Corynebacterium glutamicum	Y14748	[de:corynebacterium glutamicum plasmid peg4 integron (neg) sequence.] [gn:int]
CONTIG463	26614682_f2_25	2626	8288	510	170	810	8.6(10)-81	Escherichia coli	L29404	or:escherichia coli pn:mercuric reductase gn:mcra lc:<1 re:663 di:direct sr:escherichia coli (strain dh1) dna nt:putative
CONTIG463	16141561_f2_27	2627	8289	927	309	1060	2.7(10)-107	Escherichia coli	L29404	or:escherichia coli lc:1273 re:1980 di:direct sr:escherichia coli (strain dh1) dna nt:urf2; putative

CONTIG463	11891882_f2_29	2628	8290	738	246	1268	2.6(10)-129	Salmonella ordonez	S34451	hypothetical protein (insertion sequence is261) - salmonellaordonez plasmid pip173
CONTIG463	24500431_f2_32	2629	8291	276	92	269	7.2(10)-23	Klebsiella pneumoniae	S32179	hypothetical protein 6 - klebsiella pneumoniae
CONTIG463	30494567_f2_37	2630	8292	204	68	111	5.7(10)-6	Ralstonia eutropha	D64144	or:ralstonia eutropha le:777 re:1793 di:direct sr:alcaligenes eutrophus (strain:nh9) plasmid:pent91 dna nt:orfa2
CONTIG463	4401693_f2_39	2631	8293	795	265	1327	1.3(10)-135	Insertion sequence IS1326	U38187	or:insertion sequence is1326 pn:istb le:1618 re:2403 di:direct nt:contains ntp binding domain motifs
CONTIG463	2838312_f2_44	2632	8294	348	116	258	2.7(10)-22	Citrobacter freundii	Z54241	or:citrobacter freundii pn:dna integrase gn:nt le:<1 re:285 di:complement
CONTIG463	21667626_f2_49	2633	8295	3024	1008	4907	0	Escherichia coli	P13694	transposase for transposon tn3926.
CONTIG463	135818_f2_50	2634	8296	1032	344	1554	1.3(10)-159	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn:tnpa gn:tnpa le:10303 re:11307 di:complement
CONTIG463	25683166_f3_52	2635	8297	561	187	326	1.7(10)-29	Escherichia coli	L29404	or:escherichia coli le:1040 re:1276 di:direct sr:escherichia coli (strain dh1) dna nt:orf1; putative
CONTIG463	16462943_f3_57	2636	8298	873	291	1197	8.5(10)-122	Pseudomonas aeruginosa	U49101	or:pseudomonas aeruginosa pn:tnbdelta1 gn:tnbdelta1 le:5872 re:6732 di:complement nt:truncated version of tnib found in tn402, embl
CONTIG463	9929075_f3_70	2637	8299	618	206	838	9.4(10)-84	Enterobacter cloacae	Y09025	resolvase family recombinase, tnpr,
CONTIG463	35629583_c1_84	2638	8300	435	145	708	5.5(10)-70	Escherichia coli	P10017	hypothetical 14.4 kd protein (orf1).
CONTIG463	12398261_c1_85	2639	8301	447	149	667	1.2(10)-65	Escherichia coli	P10018	hypothetical 14.7 kd protein (orf2).
CONTIG463	3416040_c1_87	2640	8302	930	310	1401	2.1(10)-143	Mycobacterium fortuitum	S10928	dihydropteroate synthase (ec 2.5.1.15) - mycobacteriumfortuitum transposon tn610
CONTIG463	10415891_c2_110	2641	8303	733	251	1335	2.0(10)-136	unidentified bacterium	X04555	or:unidentified bacterium sp:p10019 le:1080 re:1829 di:direct nt:aad(2) (aa 1-249)

CONTIG463	4723833_c2_111	2642	8304	387	129	581	1.6(10)-56	Plasmid pDGO100	L06418	or:plasmid pdgo100 pn:quaternary ammonium compound-resistance protein gn:suli lc:1986 re:2333 di:direct sr:plasmid pdgo100 (clone: integron in7) dna nt:orf4; putative
CONTIG463	7050966_c2_113	2643	8305	603	201	889	3.7(10)-89	Pseudomonas aeruginosa	U12338	or:pseudomonas aeruginosa pn:unknown lc:6192 re:6692 di:direct nt:orf5
CONTIG463	36520917_c2_123	2644	8306	411	137	151	5.9(10)-11	Xanthomonas sp.	S32799	hypothetical protein l - xanthomonas sp. transposon tn5053(fragment)
CONTIG463	33332337_c2_124	2645	8307	204	68	187	9.0(10)-15	Xanthomonas sp.	S32799	hypothetical protein l - xanthomonas sp. transposon tn5053(fragment)
CONTIG463	10582283_c2_125	2646	8308	210	70	94	0.00013	Xanthomonas sp.	S32799	hypothetical protein l - xanthomonas sp. transposon tn5053(fragment)
CONTIG463	26660405_c2_128	2647	8309	477	159	90	0.00519	Mycobacteriu m tuberculosis	AL009198	[dc:mycobacterium tuberculosis sequence v004.] [pn:pgrs-family protein] [gn:mtv004.01c] [nt:mtv004.01c, member of the m. tuberculosis pgrs]
CONTIG463	10970768_c3_130	2648	8310	411	137	374	1.3(10)-34	Escherichia coli	b2669	[pn:dna-binding protein spa] [gn:spa]
CONTIG463	9931525_c3_151	2649	8311	1548	516	1540	3.7(10)-158	Insertion sequence IS1353	U40482	or:insertion sequence is1353 lc:671 re:1585 di:direct nt:orf; possible alternate start site at nt 686
CONTIG463	21666540_c3_154	2650	8312	714	238	1128	1.8(10)-114	Transposon Tn1525	M12900	or:transposon tn1525 gn:p12 lc:996 re:>1721 di:direct sr:transposon tn1525 dna nt:putative
CONTIG464	4333406_f1_3	2651	8313	1233	411	94	0.33	Gallus gallus	D88828	[dc:gallus gallus mrna for chicken rabaptin-5, complete cds.] [pn:chicken rabaptin-5]
CONTIG464	4329843_f1_4	2652	8314	651	217	991	5.7(10)-100	Plasmid R478	U49054	or:plasmid r478 pn:terx gn:terx lc:1800 re:2441 di:direct nt:shows similarity to r478 terz. terd. and tere
CONTIG464	3912918_f2_16	2653	8315	1152	384	873	1.8(10)-87	Serratia marcescens	U59239	or:serratia marcescens lc:820 re:1413 di:complement nt:orf3
CONTIG464	568791_f2_29	2654	8316	186	62	279	1.6(10)-24	Escherichia coli	b3503	[pn:arsenate reductase] [gn:arsc]
CONTIG464	30157255_f2_31	2655	8317	279	93	99	0.00012	Escherichia coli	U95365	transposase, is5b,

CONTIG464	26770126_f3_35	2656	8318	1191	397	810	8.6(10)-81	Serratia marcescens	U59239	or:serratia marcescens le:<1 re:715 di:complement nt:orf4
CONTIG464	33402312_f3_36	2657	8319	1035	345	100	0.01499	Haemophilus influenzae	HI0023	[pn:citrate lyase beta chain] [gn:cite]
CONTIG464	12297782_f3_37	2658	8320	501	167	666	1.6(10)-65	Plasmid R478	U49054	or:plasmid r478 pn:terw gn:terw le:205 re:672 di:direct
CONTIG464	2140678_f3_38	2659	8321	747	249	944	5.5(10)-95	Plasmid R478	U49054	or:plasmid r478 pn:tery gn:tery le:1184 re:1777 di:direct
CONTIG464	4956283_f3_39	2660	8322	687	229	373	1.8(10)-34	Plasmid R478	U49054	or:plasmid r478 pn:tery gn:tery le:1184 re:1777 di:direct
CONTIG464	34194711_f3_40	2661	8323	1125	375	195	4.2(10)-15	Escherichia coli	b2073	[pn:hypothetical protein]
CONTIG464	672833_f3_43	2662	8324	1590	530	114	0.0014	Saccharomyces cerevisiae	YKL166C	[pn:camp-dependent protein kinase 3, catalytic chain] [gn:tpk3]
CONTIG464	4339135_f3_47	2663	8325	1026	342	1684	2.1(10)-173	Escherichia coli	b1370	[pn:insertion element is5 hypothetical protein] [gn:yi52_5]
CONTIG464	35212692_c1_54	2664	8326	1236	412	679	6.7(10)-67	Escherichia coli	b1650	[pn:hypothetical protein] [gn:nema]
CONTIG464	10563465_c1_59	2665	8327	420	140	102	9.3(10)-6	Escherichia coli	b2861	[pn:insertion element is2 hypothetical 13.4 kd protein]
CONTIG464	24783465_c2_79	2666	8328	786	262	315	2.5(10)-28	Bacillus subtilis	ykvO	[pn:hypothetical protein]
CONTIG464	21773383_c2_82	2667	8329	300	100	446	3.2(10)-42	Escherichia coli	D90774	or:escherichia coli gn:is5 le:13994 re:14362 di:direct sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:orf_id:o263#20; similar to [swissprot accession]
CONTIG464	22458580_c2_83	2668	8330	384	128	490	7.0(10)-47	Escherichia coli	b1371	[pn:hypothetical protein]
CONTIG464	3940943_c3_106	2669	8331	711	237	90	0.05299	Pseudomonas syringae	AF036929	[de:pseudomonas syringae disulfide oxidoreductase (dsba) gene, completecds.] [pn:disulfide oxidoreductase] [gn:dsba] [nt:dsba]
CONTIG464	10411407_c3_108	2670	8332	483	161	298	1.6(10)-26	Rhizobium sp.	S34667	hypothetical protein 140 - rhizobium sp
CONTIG464	25572937_c3_109	2671	8333	1623	541	759	2.2(10)-75	Rhizobium sp.	P50360	hypothetical 29.3 kd protein in region 2 of sym plasmid (no1265).
CONTIG465	22837807_f1_36	2672	8334	828	276	1294	4.5(10)-132	Escherichia coli	b0166	[pn:2,3,4,5-tetrahydropyridine-2-carboxylate n- succinyltransferase]

CONTIG465	35971925_f1_37	2673	8335	423	141	640	9.0(10)-63	Escherichia coli	b0163	[pn:hypothetical 15.1 kd protein in htra-dapd intergenic region] [gn:yaeh]
CONTIG465	34256578_f2_78	2674	8336	2742	914	4041	0	Escherichia coli	b0167	[pn:uridylyltransferase] [gn:glnd]
CONTIG465	33407706_f2_87	2675	8337	747	249	1114	5.2(10)-113	Escherichia coli	b0159	[pn:pfs protein] [gn:pfs]
CONTIG465	13067707_f2_89	2676	8338	723	241	886	7.7(10)-89	Escherichia coli	b0157	[pn:hypothetical protein in heml-pfs intergenic region] [gn:yads]
CONTIG465	24470635_f3_124	2677	8339	831	277	1239	3.0(10)-126	Escherichia coli	b0168	[pn:methionine aminopeptidase] [gn:map]
CONTIG465	12698840_f3_131	2678	8340	840	280	1023	2.2(10)-103	Escherichia coli	b0158	[pn:hypothetical 29.4 kd protein in heml-pfs intergenic region] [gn:yadt]
CONTIG465	35625650_c1_134	2679	8341	360	120	403	1.2(10)-37	Escherichia coli	b0155	[pn:hypothetical protein in heml-pfs intergenic region] [gn:yadq]
CONTIG465	22773593_c1_141	2680	8342	1545	515	2268	2.7(10)-235	Escherichia coli	b0160	[pn:deoxyguanosinetriphosphate triphosphohydrolase] [gn:dgt]
CONTIG465	25476662_c1_142	2681	8343	1491	497	1973	5.0(10)-204	Escherichia coli	b0161	[pn:heat shock protein htra] [gn:htra]
CONTIG465	26735086_c1_151	2682	8344	648	216	651	6.2(10)-64	Escherichia coli	b0171	[pn:uridine 5'''-monophosphate kinase] [gn:pyrh]
CONTIG465	9776338_c1_152	2683	8345	582	194	769	1.8(10)-76	Escherichia coli	b0172	[pn:ribosome recycling factor] [gn:frf]
CONTIG465	31797711_c1_154	2684	8346	1428	476	1850	5.4(10)-191	Escherichia coli	b0176	[pn:hypothetical protein in cdsa 3'''region] [gn:yael]
CONTIG465	31445208_c1_155	2685	8347	585	195	689	5.7(10)-68	Escherichia coli	b0180	[pn:3r-hydroxymyristol acyl carrier protein dehydrase] [gn:fabz]
CONTIG465	25431660_c1_156	2686	8348	792	264	1258	2.8(10)-128	Escherichia coli	b0181	[pn:udp-n-acetylglucosamine o-acyltransferase] [gn:lpax]
CONTIG465	26822803_c1_159	2687	8349	3501	1167	5547	0	Escherichia coli	b0184	[pn:dna polymerase iii, alpha chain] [gn:dnae]
CONTIG465	13870910_c1_160	2688	8350	972	324	1391	2.3(10)-142	Escherichia coli	b0185	[pn:acetyl-coenzyme a carboxylase carboxyl transferase subunit alpha] [gn:acea]
CONTIG465	20885086_c2_163	2689	8351	372	124	480	8.0(10)-46	Escherichia coli	b0156	[pn:hypothetical 12.1 kd protein in heml-pfs intergenic region] [gn:yadr]
CONTIG465	32074135_c2_177	2690	8352	777	259	1210	3.6(10)-123	Escherichia coli	b0169	[pn:30s ribosomal protein s2] [gn:rpsb]

CONTIG465	22011677_c2_178	2691	8353	936	312	1253	9.9(10)-128	Escherichia coli	b0170	[pn:elongation factor ts] [gn:tsf]
CONTIG465	12985030_c2_179	2692	8354	330	110	438	2.2(10)-41	Escherichia coli	b0171	[pn:uridine 5'-monophosphate kinase] [gn:pyrh]
CONTIG465	3958312_c2_181	2693	8355	768	256	1206	9.5(10)-123	Escherichia coli	b0174	[pn:hypothetical protein] [gn:yaes]
CONTIG465	24634376_c2_182	2694	8356	861	287	1074	9.1(10)-109	Escherichia coli	b0175	[pn:phosphatidate cytidyltransferase] [gn:cdsa]
CONTIG465	4554813_c2_184	2695	8357	1449	483	2171	5.2(10)-225	Escherichia coli	b0177	[pn:hypothetical protein] [gn:yaet]
CONTIG465	25441525_c2_185	2696	8358	1002	334	1484	3.2(10)-152	Escherichia coli	b0177	[pn:hypothetical protein] [gn:yaet]
CONTIG465	2595412_c2_186	2697	8359	561	187	605	4.5(10)-59	Escherichia coli	b0178	[pn:histone-like protein hlp-1 precursor] [gn:hlpa]
CONTIG465	9869053_c2_187	2698	8360	1029	343	1513	2.7(10)-155	Escherichia coli	b0179	[pn:udp-3-o-3-hydroxymyristoyl glucosamine n-acyltransferase] [gn:lpdx]
CONTIG465	31927308_c2_189	2699	8361	630	210	927	3.5(10)-93	Escherichia coli	b0183	[pn:ribonuclease hii] [gn:mhb]
CONTIG465	4494032_c2_193	2700	8362	2136	712	3424	0	Escherichia coli	b0186	[pn:lysine decarboxylase] [gn:ldcc]
CONTIG465	14664812_c2_194	2701	8363	402	134	538	5.7(10)-52	Escherichia coli	b0187	[pn:hypothetical protein]
CONTIG465	12114076_c3_202	2702	8364	1200	400	1846	1.3(10)-190	Escherichia coli	b0162	[pn:hypothetical 44.3 kd protein in htra-dapd intergenic region] [gn:yaeg]
CONTIG465	33603957_c3_210	2703	8365	1272	424	1767	3.3(10)-182	Escherichia coli	b0173	[pn:hypothetical protein in fr 3' region] [gn:yaem]
CONTIG465	12300082_c3_219	2704	8366	1176	392	1661	5.7(10)-171	Escherichia coli	b0182	[pn:lipid-a-disaccharide synthase] [gn:lpzb]
CONTIG465	14875750_c3_225	2705	8367	1077	359	1052	2.0(10)-106	Escherichia coli	b0188	[pn:cell cycle protein mesj] [gn:mesj]
CONTIG466	4792812_fl_1	2706	8368	273	91	426	4.2(10)-40	Escherichia coli	b3704	[pn:rnase p, protein component] [gn:rnpa]
CONTIG466	25676928_fl_2	2707	8369	1137	379	1798	1.8(10)-185	Escherichia coli	b3705	[pn:60 kd protein] [gn:yide]
CONTIG466	14586582_fl_3	2708	8370	1377	459	2050	3.5(10)-212	Escherichia coli	b3706	[pn:50 kd protein] [gn:thdf]

CONTIG466	4697650_f1_4	2709	8371	1287	429	1260	1.8(10)-128	Escherichia coli	b3710	[pn:hypothetical 41.5 kd protein in tnab 3'''region] [gn:yidy]
CONTIG466	14954081_f1_5	2710	8372	777	259	802	6.2(10)-80	Escherichia coli	b3712	[pn:hypothetical 28.0 kd protein in tnab-bglb intergenic region]
CONTIG466	36503530_f1_6	2711	8373	603	201	867	8.0(10)-87	Escherichia coli	b3713	[pn:hypothetical protein] [gn:yief]
CONTIG466	14729535_f2_30	2712	8374	606	202	629	1.3(10)-61	Escherichia coli	b3705	[pn:60 kd protein] [gn:yidc]
CONTIG466	12601081_f2_33	2713	8375	306	102	178	4.7(10)-13	Escherichia coli	A38160	thdF protein - escherichia coli (fragment)
CONTIG466	16454200_f2_36	2714	8376	1029	343	1163	3.3(10)-118	Escherichia coli	b3711	[pn:hypothetical transcriptional regulator in tnab- bglb intergenic region] [gn:yidz]
CONTIG466	2036331_f3_68	2715	8377	288	96	236	5.7(10)-20	Haemophilus influenzae	I111000	[pn:hypothetical protein]
CONTIG466	20317500_f3_74	2716	8378	741	247	1004	2.3(10)-101	Escherichia coli	b3715	[pn:hypothetical protein] [gn:yieh]
CONTIG466	34587752_c1_100	2717	8379	594	198	198	6.2(10)-16	Escherichia coli	b0530	[pn:hypothetical protein] [gn:sfma]
CONTIG466	15759625_c1_107	2718	8380	963	321	1357	9.5(10)-139	Escherichia coli	b3727	[pn:phosphate transport system permease protein pstc] [gn:pstc]
CONTIG466	20573253_c1_109	2719	8381	831	277	1170	6.2(10)-119	Escherichia coli	b3724	[pn:peripheral membrane protein u] [gn:phou]
CONTIG466	28557318_c2_126	2720	8382	399	133	598	2.5(10)-58	Escherichia coli	b3738	[pn:atp synthase f0 subunit a] [gn:atpb]
CONTIG466	34647257_c2_127	2721	8383	555	185	782	8.0(10)-78	Escherichia coli	b3735	[pn:atp synthase f1 delta subunit] [gn:atph]
CONTIG466	34614218_c2_128	2722	8384	1554	518	2381	2.8(10)-247	Escherichia coli	b3734	[pn:atp synthase f1 alpha subunit] [gn:atpa]
CONTIG466	35831955_c2_129	2723	8385	915	305	1381	2.7(10)-141	Escherichia coli	b3733	[pn:atp synthase f1 gamma subunit] [gn:atpg]
CONTIG466	25682955_c2_130	2724	8386	432	144	661	5.4(10)-65	Escherichia coli	b3731	[pn:atp synthase f1 epsilon subunit] [gn:atpc]
CONTIG466	22843762_c2_131	2725	8387	1425	475	2082	1.3(10)-215	Escherichia coli	b3730	[pn:udp-n-acetylglucosamine pyrophosphorylase] [gn:glml]
CONTIG466	4102305_c2_132	2726	8388	1845	615	2868	7.2(10)-299	Escherichia coli	b3729	[pn:glutamine amidotransferase]
CONTIG466	11142193_c2_139	2727	8389	786	262	1220	3.1(10)-124	Escherichia coli	b3725	[pn:phosphate transport atp-binding protein pstb] [gn:pslb]

CONTIG466	25989638_c2_141	2728	8390	1377	459	1938	2.6(10)-200	Escherichia coli	b3714	[pn: hypothetical 46.9 kd protein in tnaB-bglB intergenic region]
CONTIG466	10659431_c2_147	2729	8391	480	160	90	0.11	Saccharomyces cerevisiae	YNR044W	[pn: a-agglutinin anchor subunit] [gn: aga1]
CONTIG466	26585912_c3_150	2730	8392	258	86	130	1.0(10)-8	Haemophilus influenzae	HI0484	[pn: atp synthase c chain] [gn: atpe]
CONTIG466	13082037_c3_151	2731	8393	507	169	601	1.2(10)-58	Escherichia coli	b3736	[pn: atp synthase f0 subunit b] [gn: atpf]
CONTIG466	29964050_c3_155	2732	8394	1506	502	2132	7.0(10)-221	Escherichia coli	b3732	[pn: atp synthase f1 beta subunit] [gn: atpd]
CONTIG466	5313943_c3_158	2733	8395	696	232	348	7.9(10)-32	Escherichia coli	b3143	[pn: hypothetical 25.7 kd fimbrial chaperone in agaI-mtr intergeni] [gn: yrai]
CONTIG466	35370308_c3_159	2734	8396	2538	846	1405	7.7(10)-144	Escherichia coli	b0532	[pn: hypothetical protein] [gn: sfmd]
CONTIG466	5267193_c3_160	2735	8397	1086	362	177	3.2(10)-11	Escherichia coli	b0941	[pn: hypothetical protein]
CONTIG466	19572182_c3_161	2736	8398	1074	358	1554	1.3(10)-159	Escherichia coli	b3728	[pn: periplasmic phosphate-binding protein] [gn: pstS]
CONTIG466	36617687_c3_164	2737	8399	909	303	1153	3.8(10)-117	Escherichia coli	b3726	[pn: phosphate transport system permease protein pstA] [gn: pstA]
CONTIG467	1275005_f1_42	2738	8400	303	101	91	0.005	Saccharomyces cerevisiae	YIR019C	[pn: extracellular alpha-1,4-glucan glucosidase] [gn: stA]
CONTIG467	33461682_c1_117	2739	8401	2181	727	446	7.5(10)-42	Bacillus subtilis	yknV	[pn: hypothetical protein]
CONTIG467	6835407_c2_118	2740	8402	18048	6016	2534	3.1(10)-269	Synechocystis sp.	S76109	[PN: hypothetical protein] [OR: Synechocystis sp.] [SR: PCC 6803, PCC 6803] [SR: PCC 6803,] cyad protein.
CONTIG467	35742257_c3_137	2741	8403	1197	399	360	4.2(10)-33	Bordetella pertussis	P11091	
CONTIG467	6054666_c3_139	2742	8404	783	261	143	1.8(10)-7	Klebsiella pneumoniae	L23111	or: klebsiella pneumoniae pn: fimbrial adhesin gn: fmk le: 1139 re: 2380 di: direct sr: klebsiella pneumoniae
CONTIG468	5133412_f1_2	2743	8405	330	110	391	2.2(10)-36	Escherichia coli	b0379	[pn: hypothetical protein]
CONTIG468	20397016_f1_8	2744	8406	1335	445	1652	5.2(10)-170	Escherichia coli	b0376	[pn: yaiH]

CONTIG468	33212805_f1_13	2745	8407	1728	576	299	4.7(10)-26	Prevotella melaninogenica	U27587	or:prevotella melaninogenica pn:hemolysin a gn:hly lc:188 re:1186 di:direct nt:zymogram analysis confirms the hemolytic glycoprotein x precursor.
CONTIG468	24477091_f1_21	2746	8408	876	292	95	0.14999	Equine herpesvirus 1	P28968	[pn:membrane protein]
CONTIG468	3986527_f1_23	2747	8409	1155	385	183	6.0(10)-12	Helicobacter pylori	HP0567	[pn:hypothetical 41.5 kd protein in psf-proc intergenic region] [gn:yaic]
CONTIG468	21878332_f1_24	2748	8410	1821	607	279	1.0(10)-23	Escherichia coli	b0385	[pn:hypothetical 27.4 kd protein in fec-fimb intergenic region]
CONTIG468	16025932_f1_26	2749	8411	789	263	1178	8.8(10)-120	Escherichia coli	b4306	[pn:d-alanine] [gn:ddla]
CONTIG468	20432_f2_36	2750	8412	1221	407	1549	4.2(10)-159	Escherichia coli	b0381	[pn:delta-aminolevulinic acid dehydratase] [gn:hemb]
CONTIG468	4460882_f2_43	2751	8413	1095	365	1513	2.7(10)-155	Escherichia coli	b0369	[pn:hypothetical protein] [gn:ycr]
CONTIG468	21537927_f2_59	2752	8414	1959	653	644	3.3(10)-63	Escherichia coli	b1285	or:mitochondrion podospira anserina lc:44740 re:45549 di:complement sr:podospira anserina nt:orf16; no atg start codon; author-
CONTIG468	864080_f2_64	2753	8415	183	61	129	3.6(10)-8	Podospira anserina	X55026	or:escherichia coli lc:102767 re:103075 di:complement nt:hypothetical protein
CONTIG468	26830152_f2_65	2754	8416	444	148	446	3.2(10)-42	Escherichia coli	U70214	or:escherichia coli lc:102415 re:102852 di:complement nt:hypothetical protein
CONTIG468	12915832_f3_107	2755	8417	423	141	676	1.3(10)-66	Escherichia coli	U70214	[pn:hypothetical protein]
CONTIG468	32227262_c1_109	2756	8418	522	174	703	1.8(10)-69	Escherichia coli	b0257	[pn:hypothetical 43.2 kd protein in per-argf intergenic region] [gn:ykfc]
CONTIG468	5078942_c1_111	2757	8419	1530	510	1823	3.8(10)-188	Escherichia coli	b0258	[pn:hypothetical protein]
CONTIG468	14880168_c1_112	2758	8420	210	70	100	1.5(10)-5	Escherichia coli	b4286	[pn:hypothetical protein]
CONTIG468	35267890_c1_131	2759	8421	957	319	1238	3.8(10)-126	Escherichia coli	b0368	[pn:hypothetical protein] [gn:taud]
CONTIG468	2931593_c1_138	2760	8422	432	144	549	4.0(10)-53	Escherichia coli	b0374	[pn:hypothetical protein] [gn:yaui]

CONTIG468	36148311_c1_142	2761	8423	1239	413	1814	3.5(10)-187	Escherichia coli	b0377	[pn:sbma protein] [gn:sbma]
CONTIG468	15664812_c1_143	2762	8424	1110	370	1475	3.0(10)-151	Escherichia coli	b0378	[pn:hypothetical protein] [gn:yaiv]
CONTIG468	16532656_c2_149	2763	8425	396	132	404	9.1(10)-38	Escherichia coli	b0255	[pn:hypothetical protein]
CONTIG468	32066327_c2_160	2764	8426	1425	475	2146	2.2(10)-222	Escherichia coli	b0260	[pn:hypothetical 51.5 kd transport protein in per-argf intergenic region] [gn:ykfd]
CONTIG468	3191_c2_161	2765	8427	1038	346	1487	1.6(10)-152	Escherichia coli	b0365	[pn:hypothetical protein]
CONTIG468	36229058_c2_164	2766	8428	846	282	793	5.5(10)-79	Escherichia coli	b0367	[pn:hypothetical protein] [gn:tauc]
CONTIG468	585340_c2_170	2767	8429	2391	797	996	1.7(10)-100	Escherichia coli	b0374	[pn:hypothetical protein] [gn:yaui]
CONTIG468	30136001_c2_171	2768	8430	639	213	510	5.4(10)-49	Escherichia coli	b0375	[pn:hypothetical protein] [gn:yaiv]
CONTIG468	16176655_c3_178	2769	8431	507	169	797	2.1(10)-79	Escherichia coli	Y07545	[de:coli plasmid p0157 dna, 5'-region of the ehcc-hemolysin operon,] [gn:ori5]
CONTIG468	31803342_c3_179	2770	8432	276	92	93	0.00063	Xenopus laevis	S31719	proline-rich protein - african clawed frog
CONTIG468	34645806_c3_189	2771	8433	951	317	1268	2.6(10)-129	Escherichia coli	b0261	[pn:hypothetical 33.4 kd protein in per-argf intergenic region]
CONTIG468	17089012_c3_191	2772	8434	783	261	1139	1.2(10)-115	Escherichia coli	b0366	[pn:hypothetical protein] [gn:taub]
CONTIG468	267338_c3_202	2773	8435	252	84	297	2.0(10)-26	Escherichia coli	b0380	[pn:hypothetical protein]
CONTIG468	25910005_c3_206	2774	8436	672	224	524	1.8(10)-50	Escherichia coli	b1053	[pn:hypothetical 43.9 kd protein in msyb-htrb intergenic region] [gn:ycee]
CONTIG469	25992268_f1_1	2775	8437	1167	389	1708	6.0(10)-176	Escherichia coli	b4375	[pn:peptide-chain-release factor 3] [gn:prfc]
CONTIG469	24632962_f1_10	2776	8438	732	244	1185	1.6(10)-120	Escherichia coli	b4384	[pn:purine-nucleoside phosphorylase] [gn:dcod]
CONTIG469	24744157_f1_18	2777	8439	1389	463	2188	8.3(10)-227	Escherichia coli	b4389	[pn:sms protein] [gn:rada]
CONTIG469	1206557_f1_22	2778	8440	906	302	332	3.8(10)-30	Escherichia coli	b3243	[pn:hypothetical protein] [gn:yhes]

CONTIG469	34478458_f1_27	2779	8441	414	138	423	8.9(10)-40	Escherichia coli	b4393	[pn:trpr] [gn:trpr]
CONTIG469	19729541_f1_28	2780	8442	432	144	192	2.7(10)-15	Escherichia coli	J01715	or:escherichia coli le:765 re:1178 di:direct sr:escherichia coli dna [1],[2] and mrna [2]
CONTIG469	34179716_f1_29	2781	8443	571	191	775	4.5(10)-77	Escherichia coli	b4395	[pn:probable phosphoglycerate mutase 2] [gn:gpmB]
CONTIG469	22460465_f2_30	2782	8444	642	214	726	7.0(10)-72	Escherichia coli	b4376	[pn:periplasmic protein] [gn:osmy]
CONTIG469	35242941_f2_32	2783	8445	327	109	292	6.7(10)-26	Escherichia coli	P39408	hypothetical 28.9 kd protein in osmy-deoc intergenic region.
CONTIG469	1353888_f2_33	2784	8446	468	156	666	1.6(10)-65	Escherichia coli	b4378	[pn:yjiv]
CONTIG469	14730178_f2_39	2785	8447	1239	413	2087	4.2(10)-216	Escherichia coli	b4383	[pn:phosphopentomutase] [gn:deob]
CONTIG469	3381262_f2_48	2786	8448	1071	357	1457	2.3(10)-149	Escherichia coli	b4388	[pn:phosphoserine phosphatase] [gn:serb]
CONTIG469	14588437_f2_51	2787	8449	1770	590	115	0.0004	Pseudomonas aeruginosa	JQ0133	hypothetical 26.4k protein - pseudomonas aeruginosa
CONTIG469	36428938_f3_59	2788	8450	1113	371	1490	7.5(10)-153	Escherichia coli	b4377	[pn:hypothetical 39.8 kd protein in osmy-deoc intergenic region] [gn:yju]
CONTIG469	23476055_f3_65	2789	8451	948	316	1135	3.2(10)-115	Escherichia coli	b4381	[pn:deoxyribose-phosphate aldolase] [gn:deoc]
CONTIG469	12898503_f3_66	2790	8452	1422	474	2050	3.5(10)-212	Escherichia coli	b4382	[pn:thymidine phosphorylase] [gn:deoa]
CONTIG469	16303762_f3_77	2791	8453	258	86	95	0.00129	Nephila clavipes	AF027735	[de:nephila clavipes minor ampullate silk protein misp1 mrna, partial cds.] [pn:minor ampullate silk protein misp1]
CONTIG469	10634625_f3_78	2792	8454	1236	412	1967	2.2(10)-203	Escherichia coli	b4390	[pn:transcriptional regulator nadr] [gn:nadr]
CONTIG469	15036641_f3_84	2793	8455	1983	661	3026	0	Escherichia coli	b4392	[pn:soluble lytic transglycosylase] [gn:slt]
CONTIG469	1011_c1_87	2794	8456	567	189	644	3.3(10)-63	Escherichia coli	b4394	[pn:hypothetical 18.6 kd protein in trpr-gpmB intergenic region]
CONTIG469	23849007_c1_97	2795	8457	1041	347	192	3.5(10)-13	Escherichia coli	b4051	[pn:quinone oxidoreductase] [gn:qor]

CONTIG469	5094427_c2_141	2796	8458	321	107	133	6.2(10)-9	Escherichia coli	b3215	[pn:hypothetical 25.3 kd fimbrial chaperone in glrf- nant intergenic region] [gn:yhea]
CONTIG469	32673426_c2_148	2797	8459	1629	543	2363	2.3(10)-245	Escherichia coli	b4380	[pn:hypothetical 58.0 kd protein in osmy-deoc intergenic region]
CONTIG469	32285036_c3_161	2798	8460	1764	588	2632	7.4(10)-274	Escherichia coli	b4391	[pn:abc transporter in nadr-slt intergenic region] [gn:yjik]
CONTIG469	33865627_c3_169	2799	8461	663	221	788	1.8(10)-78	Escherichia coli	b4387	[pn:smp protein precursor] [gn:smp]
CONTIG469	5339642_c3_170	2800	8462	1050	350	1653	4.0(10)-170	Escherichia coli	b4386	[pn:lipoate-protein ligase a] [gn:lpla]
CONTIG469	5193818_c3_171	2801	8463	696	232	223	1.3(10)-18	Escherichia coli	b3219	[pn:hypothetical protein] [gn:yhef]
CONTIG469	4804068_c3_172	2802	8464	699	233	252	1.2(10)-21	Escherichia coli	b3219	[pn:hypothetical protein] [gn:yhef]
CONTIG469	33790903_c3_181	2803	8465	864	288	1010	5.5(10)-102	Escherichia coli	b4379	[pn:hypothetical 31.5 kd protein in osmy-deoc intergenic region] [gn:yjiw]
CONTIG47	23814591_f2_2	2804	8466	315	105	395	8.3(10)-37	Escherichia coli	b1183	[pn:umud protein] [gn:umud]
CONTIG470	19714505_f1_5	2805	8467	570	190	355	1.3(10)-32	Escherichia coli	b0892	[pn:hypothetical protein in sers 5'''region] [gn:ycaj]
CONTIG470	24640653_f1_8	2806	8468	2451	817	3753	0	Escherichia coli	b0894	[pn:anaerobic dimethyl sulfoxide reductase chain a precursor] [gn:dmsa]
CONTIG470	14181530_f1_10	2807	8469	1152	384	1451	1.0(10)-148	Escherichia coli	b0898	[pn:hypothetical protein in dmsc 3'''region] [gn:ycad]
CONTIG470	10572341_f1_20	2808	8470	768	256	838	9.4(10)-84	Escherichia coli	b0906	[pn:hypothetical protein] [gn:ycap]
CONTIG470	16836093_f1_21	2809	8471	1095	365	1718	5.2(10)-177	Escherichia coli	b0907	[pn:phosphoserine aminotransferase] [gn:serc]
CONTIG470	32422910_f2_33	2810	8472	468	156	708	5.5(10)-70	Escherichia coli	b0889	[pn:leucine-responsive regulatory protein] [gn:lrp]
CONTIG470	33882161_f2_34	2811	8473	3705	1235	2299	0	Escherichia coli	b0890	[pn:cell division protein flsk] [gn:fsk]
CONTIG470	14572206_f2_41	2812	8474	621	207	1113	6.7(10)-113	Escherichia coli	b0895	[pn:anaerobic dimethyl sulfoxide reductase chain b] [gn:dmsb]
CONTIG470	9802290_f2_49	2813	8475	495	165	443	6.7(10)-42	Escherichia coli	b0910	[pn:cytidylate kinase] [gn:cmk]

CONTIG470	3297258_f2_50	2814	8476	327	109	469	1.2(10)-44	Escherichia coli	b0912	[pn:integration host factor beta-subunit] [gn:himd]
CONTIG470	31304137_f2_55	2815	8477	993	331	1183	2.6(10)-120	Escherichia coli	b0915	[pn:hypothetical 35.6 kd protein in msba-kdsb intergenic region] [gn:ycab]
CONTIG470	14072667_f2_57	2816	8478	780	260	1130	1.1(10)-114	Escherichia coli	b0918	[pn:3-deoxy-manno-octulosonate cytidyltransferase] [gn:kdsb]
CONTIG470	4803443_f3_63	2817	8479	624	208	923	9.3(10)-93	Escherichia coli	b0891	[pn:outer membrane lipoprotein carrier protein precursor] [gn:lola]
CONTIG470	2536578_f3_64	2818	8480	1182	394	1760	1.8(10)-181	Escherichia coli	b0892	[pn:hypothetical protein in sers 5'''region] [gn:ycay]
CONTIG470	22845400_f3_65	2819	8481	1314	438	2080	2.2(10)-215	Escherichia coli	b0893	[pn:seryl-tma synthetase] [gn:sers]
CONTIG470	14473425_f3_68	2820	8482	936	312	1206	9.5(10)-123	Escherichia coli	b0896	[pn:anaerobic dimethyl sulfoxide reductase chain c] [gn:dmse]
CONTIG470	275088_f3_76	2821	8483	1296	432	1752	1.3(10)-180	Escherichia coli	b0908	[pn:3-phosphoshikimate 1-carboxyvinyltransferase] [gn:aroa]
CONTIG470	36526905_f3_77	2822	8484	444	148	564	1.0(10)-54	Escherichia coli	b0910	[pn:cytidylate kinase] [gn:cmk]
CONTIG470	4490692_f3_78	2823	8485	1683	561	2321	6.7(10)-241	Escherichia coli	b0911	[pn:30s ribosomal protein s1] [gn:rpsa]
CONTIG470	7244037_f3_80	2824	8486	2280	760	2325	2.5(10)-241	Escherichia coli	b0913	[pn:hypothetical protein in msba 5'''region] [gn:ycal]
CONTIG470	25970202_f3_81	2825	8487	1749	583	2574	1.0(10)-267	Escherichia coli	b0914	[pn:probable transport atp-binding protein msba] [gn:msba]
CONTIG470	24507201_f3_82	2826	8488	1245	415	1670	6.4(10)-172	Escherichia coli	b0916	[pn:hypothetical protein]
CONTIG470	6058562_f3_83	2827	8489	228	76	264	6.2(10)-23	Escherichia coli	b0917	[pn:hypothetical protein]
CONTIG470	26595130_f3_85	2828	8490	900	300	1423	9.5(10)-146	Escherichia coli	b0919	[pn:hypothetical protein]
CONTIG470	30363283_c1_105	2829	8491	777	259	1312	5.5(10)-134	Escherichia coli	b0902	[pn:pyruvate formate-lyase 1 activating enzyme] [gn:pfla]
CONTIG470	36621094_c2_127	2830	8492	302	100	403	1.2(10)-37	Escherichia coli	b0920	[pn:hypothetical protein in kdsb-kicb intergenic region] [gn:ycbc]
CONTIG470	24084592_c2_148	2831	8493	1968	656	2744	1.0(10)-285	Escherichia coli	b0905	[pn:hypothetical protein] [gn:ycac]
CONTIG470	22376412_c2_149	2832	8494	969	323	1304	3.8(10)-133	Escherichia coli	b0904	[pn:probable formate transporter] [gn:foca]

CONTIG470	30736688_c2_150	2833	8495	2298	766	3671	0	Escherichia coli	b0903	[pn:formate acetyltransferase I] [gn:pflb]
CONTIG470	15100141_c2_165	2834	8496	318	106	94	0.00052	Caenorhabditis elegans	Z74033	or:caenorhabditis elegans pn.f38b7.3 le:join(22734 re:22880,22931 di:direct nt:cdna est yk117e9.5 comes from this gene; cdna est
CONTIG471	1992161_fl_6	2835	8497	1689	563	1476	2.2(10)-151	Escherichia coli	b3767	[pn:acetohydroxy acid synthase ii, large subunit] [gn:ilvg_1]
CONTIG471	4147812_fl_10	2836	8498	186	62	92	0.0016	Escherichia coli	M32253	or:escherichia coli gn:ilvd le:3652 re:5499 di:direct sr:escherichia coli (strain k-12) dna
CONTIG471	32145043_f2_26	2837	8499	222	74	235	7.5(10)-20	synthetic construct	M15619	or:artificial sequence le:29 re:>232 di direct sr:e.coli (strain se5000) synthetic dna, clone pkb1 nt:orf16-lacZ fusion protein
CONTIG471	31662801_f2_30	2838	8500	390	130	551	2.3(10)-53	Escherichia coli	b3764	[pn:hypothetical 13.1 kd protein in pssr-ilvl intergenic region] [gn:yife]
CONTIG471	3417882_f2_38	2839	8501	1560	520	2459	1.6(10)-255	Escherichia coli	b3772	[pn threonine dehydratase biosynthetic] [gn:ilva]
CONTIG471	22444682_f2_41	2840	8502	1503	501	2319	1.1(10)-240	Escherichia coli	b3774	[pn:ketol-acid reductoisomerase] [gn:ilvc]
CONTIG471	35986463_f3_48	2841	8503	432	144	113	6.2(10)-7	Escherichia coli	M87049	or:escherichia coli gn:o137 le:1223 re:1636 di:direct
CONTIG471	15819651_f3_55	2842	8504	288	96	381	2.5(10)-35	Escherichia coli	b3769	[pn:acetohydroxy acid synthase ii, small subunit] [gn:ilvm]
CONTIG471	24426711_f3_56	2843	8505	942	314	1571	2.0(10)-161	Escherichia coli	b3770	[pn:branched-chain amino-acid aminotransferase] [gn:ilve]
CONTIG471	23540917_f3_57	2844	8506	1854	618	2677	1.3(10)-278	Escherichia coli	b3771	[pn:dihydroxyacid dehydratase] [gn:ilvd]
CONTIG471	30352281_c1_66	2845	8507	426	142	437	2.8(10)-41	Escherichia coli	b3605	[pn:lctd] [gn:ildd]
CONTIG471	14845313_c1_67	2846	8508	1428	476	893	1.3(10)-89	Pseudomonas putida	U10895	or:pseudomonas putida pn:peak gn:peak le:261 re:1607 di:direct
CONTIG471	4567968_c1_68	2847	8509	483	161	787	2.3(10)-78	Escherichia coli	b3606	[pn:hypothetical 17.7 kd protein in lctd-cyse intergenic region] [gn:yibk]
CONTIG471	14959652_c1_81	2848	8510	855	285	776	3.5(10)-77	Escherichia coli	b3762	[pn:hypothetical 22.4 kd protein in trpt-pssr intergenic region] [gn:yifa]
CONTIG471	6932937_c2_95	2849	8511	909	303	1490	7.5(10)-153	Escherichia coli	b3773	[pn:transcriptional activator protein ilvy] [gn:ilvy]

CONTIG471	12773450_c3_117	2850	8512	228	76	99	0.00014	Escherichia coli	b3605	[pn:lctd] [gn:ildd]
CONTIG471	33386290_c3_138	2851	8513	1551	517	1973	5.0(10)-204	Escherichia coli	b3765	[pn:hypothetical 56.2 kd protein in pssr-ivl intergenic region] [gn:yifb]
CONTIG471	12781963_c3_148	2852	8514	189	63	101	1.2(10)-5	Homo sapiens	A44803	pgl protein - human (fragment)
CONTIG472	24350086_f1_14	2853	8515	1488	496	1897	5.7(10)-196	Escherichia coli	b1439	[pn:hypothetical protein]
CONTIG472	35428135_f1_21	2854	8516	267	89	272	9.0(10)-24	Escherichia coli	b1445	[pn:hypothetical protein]
CONTIG472	22113325_f2_45	2855	8517	834	278	252	1.2(10)-21	Escherichia coli	P52646	hypothetical 5.0 kd protein in hslj 3'region.
CONTIG472	22461461_f2_53	2856	8518	1461	487	2002	4.2(10)-207	Escherichia coli	b1444	[pn:hypothetical protein]
CONTIG472	4806693_f2_62	2857	8519	243	81	331	5.0(10)-30	Escherichia coli	b1446	[pn:hypothetical protein]
CONTIG472	4348510_f2_64	2858	8520	585	195	133	4.7(10)-9	Escherichia coli	b1434	[pn:hypothetical protein]
CONTIG472	26070290_f2_65	2859	8521	1101	367	1462	7.0(10)-150	Escherichia coli	b1449	[pn:hypothetical protein]
CONTIG472	24251918_f3_85	2860	8522	798	266	123	2.1(10)-5	Bacillus subtilis	ybfK	[pn:hypothetical protein]
CONTIG472	5098387_f3_96	2861	8523	1689	563	1524	1.8(10)-156	Escherichia coli	b3544	[pn:periplasmic dipeptide transport protein precursor] [gn:dppa]
CONTIG472	25519182_f3_101	2862	8524	714	238	469	1.2(10)-44	Escherichia coli	b1450	[pn:hypothetical protein]
CONTIG472	10944025_c1_106	2863	8525	693	231	760	1.7(10)-75	Escherichia coli	b1448	[pn:hypothetical protein]
CONTIG472	135836_c1_119	2864	8526	351	117	461	8.4(10)-44	Escherichia coli	b1797	[pn:hypothetical protein]
CONTIG472	23957058_c1_120	2865	8527	381	127	384	1.2(10)-35	Escherichia coli	b1797	[pn:hypothetical protein]
CONTIG472	23728427_c1_121	2866	8528	186	62	129	1.3(10)-8	Escherichia coli	b1796	[pn:hypothetical protein]
CONTIG472	6366068_c1_130	2867	8529	1023	341	1031	3.2(10)-104	Pseudomonas aeruginosa	Y10528	[PN:cyano insensitive terminal oxidase] [GN:cioB] [DE:P.aeruginosa cioA and cioB genes] [LE:1746] [RE:2753] [DI:direct]

CONTIG472	6131633_c1_138	2868	8530	243	81	249	5,4(10)-21	Escherichia coli	b1345	[pn:hypothetical protein]
CONTIG472	511665_c2_139	2869	8531	387	129	482	6,9(10)-46	Escherichia coli	b1451	[pn:hypothetical protein]
CONTIG472	11753260_c2_159	2870	8532	1452	484	1827	1,5(10)-188	Pseudomonas aeruginosa	Y10528	[PN:cyanide insensitive terminal oxidase] [GN:cioA] [DE:P.aeruginosa cioA and cioB genes.] [LE:276] [RE:1742] [DI:direct]
CONTIG472	24415937_c2_161	2871	8533	441	147	363	2,0(10)-33	Escherichia coli	b1379	[pn:beta-lactamase precursor] [gn:hsfj]
CONTIG472	10807708_c3_171	2872	8534	474	158	647	1,6(10)-63	Escherichia coli	b1447	[pn:hypothetical protein]
CONTIG472	11955093_c3_192	2873	8535	3537	1179	5614	0	Escherichia coli	b1378	[pn:hypothetical protein] [gn:ydbk]
CONTIG472	29876562_c3_193	2874	8536	1155	385	1487	1,6(10)-152	Escherichia coli	b1377	[pn:hypothetical protein]
CONTIG473	20586437_f1_1	2875	8537	567	189	712	2,1(10)-70	Escherichia coli	b3033	[pn:hypothetical 16.5 kd protein in ice-tole intergenic region] [gn:yqib]
CONTIG473	176443_f1_2	2876	8538	837	279	1158	1,2(10)-117	Escherichia coli	b3032	[pn:icc protein] [gn:icc]
CONTIG473	22775277_f1_3	2877	8539	1896	632	2898	4,7(10)-302	Escherichia coli	b3030	[pn:topoisomerase iv subunit] [gn:pare]
CONTIG473	10761003_f1_13	2878	8540	2277	759	3581	0	Escherichia coli	b3019	[pn:topoisomerase iv subunit] [gn:parc]
CONTIG473	5991325_f1_14	2879	8541	768	256	988	1,2(10)-99	Escherichia coli	b3018	[pn:1-acyl-glycerol-3-phosphate acyltransferase] [gn:plsc]
CONTIG473	4142253_f1_26	2880	8542	235	79	163	3,2(10)-12	Escherichia coli	b3005	[pn:biopolymer transport exbd protein] [gn:exbd]
CONTIG473	32223181_f2_27	2881	8543	702	234	965	3,2(10)-97	Escherichia coli	b3034	[pn:hypothetical protein] [gn:yqie]
CONTIG473	35678406_f2_33	2882	8544	1359	453	720	3,0(10)-71	Enterobacter cloacae	AB000622	or:enterobacter cloacae pn:mely gn:mely le:481 re:1758 di:direct sr:enterobacter cloacae (strain:iid977) dna
CONTIG473	4703276_f2_37	2883	8545	303	101	264	6,2(10)-23	Escherichia coli	I80320	hypothetical protein 1 - escherichia coli
CONTIG473	16924207_f2_38	2884	8546	417	139	347	1,0(10)-31	Escherichia coli	I80320	hypothetical protein 1 - escherichia coli

CONTIG473	4565840_f2_47	2885	8547	1539	513	2084	8.6(10)-216	Escherichia coli	b3017	[pn:sufi protein precursor] [gn:sufi]
CONTIG473	31924155_f2_54	2886	8548	618	206	121	1.6(10)-5	Escherichia coli	b3010	[pn:hypothetical protein]
CONTIG473	24648451_f2_55	2887	8549	906	302	1230	2.7(10)-125	Escherichia coli	b3010	[pn:hypothetical protein]
CONTIG473	32444783_f3_61	2888	8550	726	242	927	3.5(10)-93	Escherichia coli	b3031	[pn:hypothetical 15.2 kd protein in ice 3'''region] [gn:yqia]
CONTIG473	29787518_f3_78	2889	8551	453	151	387	5.7(10)-36	Escherichia coli	b3024	[pn:hypothetical protein] [gn:ygiw]
CONTIG473	13070218_f3_83	2890	8552	2265	755	1968	1.7(10)-203	Escherichia coli	b3015	[pn:hypothetical protein]
CONTIG473	29776000_f3_89	2891	8553	753	251	960	1.1(10)-96	Escherichia coli	b3006	[pn:biopolymer transport exbb protein] [gn:exbb]
CONTIG473	189540_c1_91	2892	8554	1347	449	1771	1.3(10)-182	Escherichia coli	b3008	[pn:cystathionine beta-lyase] [gn:metc]
CONTIG473	11047306_c1_119	2893	8555	840	280	184	4.5(10)-12	Haloflex sp.	P21562	hypothetical 80.2 kd protein in the 5'region of gyra and gyrb (orf 4).
CONTIG473	23489836_c1_122	2894	8556	378	126	191	5.0(10)-14	Haloflex sp.	P21562	hypothetical 80.2 kd protein in the 5'region of gyra and gyrb (orf 4).
CONTIG473	9771052_c2_125	2895	8557	669	223	140	8.6(10)-10	Escherichia coli	M16489	or:escherichia coli le:627 re:1199 di:complement sr:escherichia coli dna nt:orf 4; putative
CONTIG473	29720016_c2_128	2896	8558	690	230	857	9.0(10)-86	Escherichia coli	b3009	[pn:hypothetical 24.1 kd protein in metc-sufi intergenic region] [gn:yghb]
CONTIG473	2931541_c2_145	2897	8559	1353	451	1330	6.9(10)-136	Escherichia coli	b3026	[pn:hypothetical protein] [gn:ygiy]
CONTIG473	35370336_c2_148	2898	8560	453	151	498	1.0(10)-47	Escherichia coli	b2665	[pn:hypothetical protein] [gn:ygaug]
CONTIG473	24220313_c2_154	2899	8561	900	300	175	1.7(10)-11	Bacillus subtilis	ydeC	[pn:hypothetical protein]
CONTIG473	16118916_c3_166	2900	8562	1242	414	1761	1.5(10)-181	Escherichia coli	b3011	[pn:hypothetical protein]
CONTIG473	36141433_c3_167	2901	8563	846	282	1175	1.8(10)-119	Escherichia coli	b3012	[pn:hypothetical protein]
CONTIG473	36110841_c3_178	2902	8564	678	226	918	3.1(10)-92	Escherichia coli	b3025	[pn:hypothetical protein] [gn:ygiX]

CONTIG473	35288206_c3_180	2903	8565	699	233	959	1.3(10)-96	Escherichia coli	b3028	[pn:modulator of drug activity b] [gn:mdab]
CONTIG473	4698587_c3_181	2904	8566	327	109	459	1.3(10)-43	Escherichia coli	b3029	[pn:hypothetical 11.5 kd protein in mdab 3 ^{'''} region] [gn:ygin]
CONTIG474	14957706_f1_7	2905	8567	1239	413	314	3.2(10)-28	Bacillus subtilis	ydeR	[pn:hypothetical protein]
CONTIG474	14179715_f1_22	2906	8568	714	238	644	3.3(10)-63	Escherichia coli	b1072	[pn:flagellar basal body p-ring protein flga precursor] [gn:flga]
CONTIG474	22792015_f1_23	2907	8569	336	112	358	6.9(10)-33	Escherichia coli	b1071	[pn:anti-sigma factor] [gn:flgm]
CONTIG474	25488888_f1_31	2908	8570	621	207	784	5.0(10)-78	Escherichia coli	b1063	[pn:hypothetical 20.5 kd protein in pyrc 3 ^{'''} region] [gn:yceb]
CONTIG474	16495826_f2_33	2909	8571	360	120	189	5.5(10)-15	Haemophilus influenzae	U20229	or:haemophilus influenzae pn:unknown le:4561 re>4926 di:complement nt:orf121
CONTIG474	24650878_f2_38	2910	8572	3123	1041	2554	0	Escherichia coli	b1084	[pn:ribonuclease e] [gn:rne]
CONTIG474	22777150_f2_56	2911	8573	465	155	485	2.3(10)-46	Escherichia coli	b1070	[pn:flagella synthesis protein flgn] [gn:flgn]
CONTIG474	15729168_f2_65	2912	8574	1632	544	1518	8.1(10)-156	Escherichia coli	b1065	[pn:hypothetical protein]
CONTIG474	2923912_f2_66	2913	8575	357	119	320	7.2(10)-29	Escherichia coli	b1061	[pn:dna-damage-inducible protein i] [gn:dini]
CONTIG474	22896012_f3_68	2914	8576	624	208	788	1.8(10)-78	Escherichia coli	b1087	[pn:hypothetical 23.2 kd protein in rne-rpmf intergenic region] [gn:ycef]
CONTIG474	35634750_f3_99	2915	8577	1104	368	1539	4.9(10)-158	Escherichia coli	b1062	[pn:dihydroorotase] [gn:pyrc]
CONTIG474	2477266_c1_106	2916	8578	1068	356	1299	1.3(10)-132	Escherichia coli	b1068	[pn:virulence factor mvim homolog] [gn:mvim]
CONTIG474	31901507_c1_107	2917	8579	1620	540	2017	1.1(10)-208	Escherichia coli	b1069	[pn:virulence factor mvim homolog] [gn:mvim]
CONTIG474	26377035_c1_110	2918	8580	768	256	772	9.3(10)-77	Escherichia coli	b1075	[pn:flagellar hook formation protein flgd] [gn:flgd]
CONTIG474	35233306_c1_112	2919	8581	816	272	1108	2.2(10)-112	Escherichia coli	b1078	[pn:flagellar basal-body rod protein flgg] [gn:flgg]
CONTIG474	31772268_c1_113	2920	8582	756	252	1075	7.2(10)-109	Escherichia coli	b1079	[pn:flagellar l-ring protein precursor] [gn:flgh]
CONTIG474	23603381_c1_114	2921	8583	1101	367	1484	3.2(10)-152	Escherichia coli	b1080	[pn:flagellar p-ring protein precursor] [gn:flgi]

CONTIG474	25900202_c1_115	2922	8584	954	318	1165	2.1(10)-118	Escherichia coli	b1081	[pn:flagellar protein flgI] [gn:flgI]
CONTIG474	36022506_c1_116	2923	8585	1683	561	2059	3.8(10)-213	Escherichia coli	b1082	[pn:flagellar hook-associated protein 1] [gn:flgK]
CONTIG474	13862837_c1_127	2924	8586	195	65	135	2.8(10)-9	Escherichia coli	b1085	[pn:hypothetical protein]
CONTIG474	12369760_c1_131	2925	8587	534	178	757	3.6(10)-75	Escherichia coli	b1088	[pn:hypothetical 19.3 kd protein in rne-rpmf intergenic region]
CONTIG474	22866711_c2_135	2926	8588	621	207	996	1.7(10)-100	Escherichia coli	b1066	[pn:ribosomal-protein-alanine acetyltransferase] [gn:rnmJ]
CONTIG474	5273568_c2_136	2927	8589	660	220	786	3.1(10)-78	Escherichia coli	b1067	[pn:hypothetical protein in rimJ 3"] region] [gn:yceH]
CONTIG474	4312512_c2_142	2928	8590	441	147	526	1.1(10)-50	Escherichia coli	b1073	[pn:putative flagellar basal-body rod protein flgB] [gn:flgB]
CONTIG474	3129202_c2_143	2929	8591	405	135	643	4.2(10)-63	Escherichia coli	b1074	[pn:putative flagellar basal-body rod protein flgC] [gn:flgC]
CONTIG474	16289216_c2_147	2930	8592	768	256	1134	4.0(10)-115	Escherichia coli	b1077	[pn:putative flagellar basal-body rod protein flgF] [gn:flgF]
CONTIG474	4165937_c2_153	2931	8593	957	319	1123	5.9(10)-114	Escherichia coli	b1083	[pn:flagellar hook-associated protein 3] [gn:flgI]
CONTIG474	33369016_c2_156	2932	8594	957	319	329	8.1(10)-30	Escherichia coli	b3060	[pn:hypothetical protein] [gn:ygiP]
CONTIG474	11209818_c2_162	2933	8595	186	62	284	4.7(10)-25	Escherichia coli	b1089	[pn:50s ribosomal protein l32] [gn:rpmF]
CONTIG474	33645805_c2_163	2934	8596	321	107	218	7.0(10)-18	Escherichia coli	b1090	[pn:plsx protein] [gn:plsx]
CONTIG474	525278_c3_173	2935	8597	1212	404	1547	7.0(10)-159	Escherichia coli	b1076	[pn:flagellar hook protein flgE] [gn:flgE]
CONTIG474	34557338_c3_191	2936	8598	270	90	197	7.9(10)-16	Escherichia coli	b1085	[pn:hypothetical protein]
CONTIG474	26173166_c3_192	2937	8599	969	323	1383	1.7(10)-141	Escherichia coli	b1086	[pn:hypothetical 36.0 kd protein in rne-rpmf intergenic region] [gn:yceC]
CONTIG475	21501261_fl_10	2938	8600	1218	406	114	0.00051	Escherichia coli	b1053	[pn:hypothetical 43.9 kd protein in msyB-htrb intergenic region] [gn:yceC]
CONTIG475	12538181_fl_32	2939	8601	1206	402	328	1.0(10)-29	Escherichia coli	b2214	[pn:hypothetical 38.5 kd protein in ada-ompC intergenic region]
CONTIG475	5206911_fl_38	2940	8602	1014	338	450	1.2(10)-42	Escherichia coli	b2428	[pn:hypothetical protein] [gn:yfeU]

CONTIG475	6328406_f1_43	2941	8603	1506	502	1915	7.0(10)-198	Escherichia coli	b1961	[pn:dna-cytosine methyltransferase] [gn:dcm]
CONTIG475	21884378_f1_47	2942	8604	963	321	1088	3.0(10)-110	Escherichia coli	b1958	[pn:hypothetical protein in vsr 5' region] [gn:yedj]
CONTIG475	163125_f2_70	2943	8605	1008	336	164	5.5(10)-10	Escherichia coli	b0338	[pn:cyn operon transcriptional activator] [gn:cynr]
CONTIG475	29926551_f2_90	2944	8606	552	184	681	4.0(10)-67	Escherichia coli	b1960	[pn:patch repair protein] [gn:vsr]
CONTIG475	19540756_f2_93	2945	8607	1182	394	959	1.3(10)-96	Escherichia coli	b1956	[pn:hypothetical protein]
CONTIG475	19610027_f3_110	2946	8608	942	314	492	4.4(10)-47	Escherichia coli	b0768	[pn:hypothetical transcriptional regulator in mode-bioa intergenic region] [gn:ybhd]
CONTIG475	1365625_f3_123	2947	8609	2805	935	706	9.1(10)-70	Bacillus subtilis	yqiG	[pn:hypothetical protein]
CONTIG475	782525_f3_128	2948	8610	771	257	712	2.1(10)-70	Escherichia coli	b1962	[pn:hypothetical protein in seru-dem intergenic region] [gn:yedj]
CONTIG475	14064562_f3_135	2949	8611	213	71	205	1.1(10)-16	Escherichia coli	b1957	[pn:hypothetical protein]
CONTIG475	16207680_f3_136	2950	8612	258	86	193	1.8(10)-14	Escherichia coli	b1956	[pn:hypothetical protein]
CONTIG475	11197708_c1_146	2951	8613	519	173	267	3.0(10)-23	Escherichia coli	P09183	very hypothetical 20.3 kd protein in dcm 3' region (orf 3).
CONTIG475	6453252_c1_147	2952	8614	648	216	132	6.0(10)-9	Escherichia coli	P09183	very hypothetical 20.3 kd protein in dcm 3' region (orf 3).
CONTIG475	4070467_c1_148	2953	8615	1179	393	1096	4.2(10)-111	Escherichia coli	b1377	[pn:hypothetical protein]
CONTIG475	15656_c1_151	2954	8616	1644	548	1602	1.0(10)-164	Escherichia coli	b4125	[pn:hypothetical 60 kd protein in dcub-lys intergenic region]
CONTIG475	25437753_c1_166	2955	8617	1455	485	1821	6.4(10)-188	Klebsiella pneumoniae	P16482	citrate-proton symport (citrate transporter) (citrate carrier protein).
CONTIG475	3159530_c1_167	2956	8618	795	265	107	0.0011	Bacillus subtilis	yvgL	[pn:hypothetical protein] [gn:yvsd]
CONTIG475	175006_c1_169	2957	8619	837	279	1212	2.2(10)-123	Escherichia coli	b1976	[pn:hypothetical protein]
CONTIG475	4022768_c1_173	2958	8620	1752	584	1683	2.7(10)-173	Escherichia coli	S44018	iuca protein - escherichia coli

CONTIG475	9766281_c1_176	2959	8621	705	235	730	2.6(10)-72	Escherichia coli	AF016586	[de:escherichia coli plasmid pcolv-k311 lysine n6-hydroxylase (aera)gene, complete cds.] [pn:lysine n6-hydroxylase] [gn:aera] [nt:monooxygenase]
CONTIG475	36525756_c1_177	2960	8622	555	185	462	6.5(10)-44	Escherichia coli	AF016587	[de:escherichia coli plasmid pcolv-k311 lysine n6-hydroxylase mutant(aera) gene, complete cds.] [pn:lysine n6-hydroxylase mutant] [gn:aera] [nt:monooxygenase; p14g site-directed mutant]
CONTIG475	32454093_c2_184	2961	8623	921	307	1095	5.5(10)-111	Escherichia coli	b1959	[pn:hypothetical 32.2 kd protein in vsr 5'''region] [gn:yeda]
CONTIG475	4939042_c2_197	2962	8624	1569	523	928	2.7(10)-93	Escherichia coli	b3063	[pn:hypothetical 52.9 kd protein in tldb-rpsu intergenic region] [gn:ygje]
CONTIG475	2398507_c2_201	2963	8625	1329	443	363	2.0(10)-33	Plasmid pNAD2	D10678	or:plasmid pna2 pn:6-aminohexanoate-dimer hydrolase gn:nylb ec:3.5.1.46 le:611 re:1801 di:direct sr:plasmid pna2 dna
CONTIG475	35729157_c2_208	2964	8626	1908	636	1971	8.1(10)-204	Escherichia coli	S50883	iucc protein - escherichia coli
CONTIG475	16828512_c3_216	2965	8627	282	94	94	7.7(10)-5	Drosophila melanogaster	P13238	vitelline membrane protein vm26ab precursor (protien tu-4) (protein sv23).
CONTIG475	20526691_c3_219	2966	8628	735	245	882	2.0(10)-88	Escherichia coli	b4124	[pn:hypothetical 27.4 kd protein in deub-lysu intergenic region]
CONTIG475	4510206_c3_223	2967	8629	1695	565	2482	5.7(10)-258	Escherichia coli	b4122	[pn:fumarate hydratase class i, anaerobic] [gn:fumb]
CONTIG475	6539193_c3_237	2968	8630	960	320	1100	1.6(10)-111	Escherichia coli	S44019	iucb protein - escherichia coli
CONTIG475	12314388_c3_240	2969	8631	459	153	91	0.023	Escherichia coli	AF016587	[de:escherichia coli plasmid pcolv-k311 lysine n6-hydroxylase mutant(aera) gene, complete cds.] [pn:lysine n6-hydroxylase mutant] [gn:aera] [nt:monooxygenase; p14g site-directed mutant]
CONTIG475	23625277_c3_241	2970	8632	1221	407	1254	7.7(10)-128	Escherichia coli	S01042	cloacin receptor precursor - escherichia coli plasmidpcolv-k30

CONTIG476	3400177_f1_1	2971	8633	714	238	168	9.4(10)-13	Escherichia coli	b0375	[pn:hypothetical protein] [gn:yaiv]
CONTIG476	3912575_f1_18	2972	8634	207	69	140	8.6(10)-10	Escherichia coli	b1705	[pn:hypothetical 7.1 kd protein in aroh-nlpc intergenic region]
CONTIG476	16538217_f1_20	2973	8635	1197	399	1487	1.6(10)-152	Shigella dysenteriae	U64516	[dc:shigella dysenteriae shuv, shuu, shuy, shux, shuw pseudogene, shut, outer membrane heme receptor shua (shua), and shus genes, completecds.] [pn:unknown] [gn:shus]
CONTIG476	11110830_f2_37	2974	8636	684	228	182	3.1(10)-14	Escherichia coli	b0375	[pn:hypothetical protein] [gn:yaiv]
CONTIG476	12689051_f2_60	2975	8637	2067	689	2705	1.3(10)-281	Shigella dysenteriae	U64516	or:shigella dysenteriae pn:outer membrane heme receptor shua gn:shua le:491 re:2473 di:direct
CONTIG476	15724136_f2_64	2976	8638	1071	357	722	1.8(10)-71	Yersinia enterocolitica	S54438	hemin permease - yersinia enterocolitica
CONTIG476	7157942_f3_91	2977	8639	1176	392	1187	9.8(10)-121	Escherichia coli	b1688	[pn:hypothetical protein]
CONTIG476	581252_f3_99	2978	8640	1059	353	1279	1.7(10)-130	Escherichia coli	b1703	[pn:hypothetical 19.8 kd protein in ppsa-aroh intergenic region] [gn:ydia]
CONTIG476	976542_f3_100	2979	8641	1071	357	1553	1.6(10)-159	Escherichia coli	b1704	[pn:3-deoxy-d-arabinoheptulosonate 7-phosphate synthase]
CONTIG476	16219541_f3_108	2980	8642	846	282	741	1.8(10)-73	Yersinia enterocolitica	X77867	or:yersinia enterocolitica pn:hemin binding protein gn:hemt le:1175 re:2014 di:direct
CONTIG476	35397915_f3_110	2981	8643	972	324	370	3.7(10)-34	Escherichia coli	b0151	[pn:ferrichrome transport atp-binding protein fhuc] [gn:fhuc]
CONTIG476	30331908_c1_121	2982	8644	1071	357	1601	1.3(10)-164	Escherichia coli	b1714	[pn:phenylalanyl-trna synthetase alpha chain] [gn:phe5]
CONTIG476	13164051_c1_123	2983	8645	1074	358	1188	7.7(10)-121	Escherichia coli	b1711	[pn:vitamin b12 transport system permease protein btuc] [gn:btuc]
CONTIG476	4032843_c1_124	2984	8646	561	187	738	3.7(10)-73	Escherichia coli	b1710	[pn:vitamin b12 transport periplasmic protein btue] [gn:btue]
CONTIG476	21752052_c1_138	2985	8647	2433	811	3905	0	Escherichia coli	b1702	[pn:phosphoenolpyruvate synthase] [gn:ppsa]
CONTIG476	2618785_c1_139	2986	8648	1485	495	1219	4.0(10)-124	Escherichia coli	b0270	[pn:hypothetical 50.6 kd protein in perr-argf intergenic region]

CONTIG476	15744032_c1_140	2987	8649	2379	793	992	4.5(10)-100	Escherichia coli	b2132	[pn:periplasmic beta-glucosidase precursor] [gn:bglx]
CONTIG476	35234831_c2_151	2988	8650	2280	760	3516	0	Escherichia coli	b1713	[pn:phenylalanyl-trna synthetase beta chain] [gn:phet]
CONTIG476	34105290_c2_155	2989	8651	729	243	608	2.2(10)-59	Escherichia coli	b1707	[pn:hypothetical protein]
CONTIG476	12986466_c2_182	2990	8652	453	151	532	2.5(10)-51	Escherichia coli	b1686	[pn:hypothetical protein]
CONTIG476	12703468_c3_188	2991	8653	312	104	491	5.5(10)-47	Escherichia coli	b1712	[pn:integration host factor alpha-subunit] [gn:hima]
CONTIG476	35676636_c3_190	2992	8654	813	271	812	5.4(10)-81	Escherichia coli	b1709	[pn:vitamin b12 transport atp-binding protein btud] [gn:btud]
CONTIG476	34191502_c3_191	2993	8655	504	168	653	3.7(10)-64	Escherichia coli	b1708	[pn:probable lipoprotein nlpc precursor] [gn:nlpc]
CONTIG476	38136_c3_193	2994	8656	1584	528	1970	1.0(10)-203	Escherichia coli	b1706	[pn:hypothetical protein]
CONTIG476	6054688_c3_213	2995	8657	3129	1043	4774	0	Escherichia coli	b1687	[pn:hypothetical protein] [gn:ydi]
CONTIG476	21766510_c3_215	2996	8658	231	77	238	3.6(10)-20	Escherichia coli	b1685	[pn:hypothetical protein]
CONTIG476	36439017_c3_216	2997	8659	546	182	243	1.1(10)-20	Escherichia coli	b4314	[pn:type I fimbrial subunit] [gn:fima]
CONTIG477	35187530_fl_3	2998	8660	1884	628	2268	2.7(10)-235	Escherichia coli	b1222	[pn:nitrate/nitrite sensor protein narx] [gn:narx]
CONTIG477	15817592_fl_23	2999	8661	678	226	537	7.4(10)-52	Escherichia coli	b1219	[pn:hypothetical 12.7 kd protein in chac-nar1 intergenic region] [gn:ychn]
CONTIG477	12632675_fl_27	3000	8662	1131	377	1379	4.4(10)-141	Escherichia coli	b1216	[pn:putative calcium/proton antiporter] [gn:chaa]
CONTIG477	21994077_fl_33	3001	8663	870	290	1241	1.8(10)-126	Escherichia coli	b1208	[pn:hypothetical 30.9 kd protein in hemm-prs intergenic region] [gn:ychn]
CONTIG477	24656552_fl_34	3002	8664	1686	562	2131	9.0(10)-221	Escherichia coli	b1206	[pn:hypothetical protein in pth-prs intergenic region] [gn:ychn]
CONTIG477	26753326_f2_41	3003	8665	669	223	865	1.3(10)-86	Escherichia coli	b1221	[pn:nitrate/nitrite response regulator protein nar1] [gn:nar1]
CONTIG477	11988405_f2_47	3004	8666	246	82	102	0.00012	Murine herpesvirus 68	U97553	[de: murine herpesvirus 68 strain wums, complete genome.] [pn:unknown] [gn:gammahv.m6]

CONTIG477	23625001_f2_62	3005	8667	1899	633	565	8.0(10)-55	Escherichia coli	b4355	[pn:methyl-accepting chemotaxis protein i] [gn:tsr]
CONTIG477	12634832_f2_78	3006	8668	522	174	638	1.5(10)-62	Escherichia coli	b1209	[pn:hemm protein] [gn:hemm]
CONTIG477	5197277_f2_81	3007	8669	588	196	818	1.2(10)-81	Escherichia coli	b1204	[pn:peptidyl-tRNA hydrolase] [gn:pth]
CONTIG477	26173518_f2_82	3008	8670	1107	369	1584	8.4(10)-163	Escherichia coli	b1203	[pn:hypothetical gtp-binding protein in pth 3''' region] [gn:yehf]
CONTIG477	33228141_f3_131	3009	8671	1017	339	1563	1.3(10)-160	Escherichia coli	b1207	[pn:ribose-phosphate pyrophosphokinase] [gn:prsa]
CONTIG477	32228386_c1_148	3010	8672	279	93	433	7.7(10)-41	Escherichia coli	b1205	[pn:hypothetical 10.5 kd protein in pth-prs intergenic region] [gn:yehh]
CONTIG477	23694406_c1_149	3011	8673	1116	372	507	1.1(10)-48	Klebsiella oxytoca	P10488	albicidin resistance protein.
CONTIG477	15876283_c1_159	3012	8674	888	296	972	5.9(10)-98	Escherichia coli	b1212	[pn:possibly protoporphyrinogen oxidase] [gn:hemk]
CONTIG477	32690636_c1_163	3013	8675	843	281	1020	4.9(10)-103	Escherichia coli	b1218	[pn:cation transport protein chac] [gn:chac]
CONTIG477	22062836_c1_170	3014	8676	1365	455	1689	6.2(10)-174	Klebsiella pneumoniae	L27431	[de:klebsiella pneumoniae nitrate transporter component (nasf), nitratetransporter component (nase), nitrate transporter atpase component(nasd), and"] [pn:nitrate transporter component] [gn:nasf]
CONTIG477	6047667_c1_186	3015	8677	1440	480	1753	1.0(10)-180	Escherichia coli	b1223	[pn:nitrite extrusion protein] [gn:nark]
CONTIG477	24032082_c2_203	3016	8678	1164	388	1698	6.9(10)-175	Escherichia coli	b1211	[pn:peptide chain release factor 1] [gn:prfa]
CONTIG477	34585931_c2_209	3017	8679	249	83	251	1.5(10)-21	Escherichia coli	b1217	[pn:cation transport regulator chab] [gn:chab]
CONTIG477	24724187_c2_212	3018	8680	1227	409	900	2.5(10)-90	Klebsiella pneumoniae	A55859	regulatory protein nasr - klebsiella pneumoniae
CONTIG477	25672942_c2_226	3019	8681	2505	835	732	1.6(10)-72	Methanobacterium thermoautotrophicum	MTH1552	[pn:formate dehydrogenase, alpha subunit homolog]
CONTIG477	1291575_c2_227	3020	8682	1419	473	1532	2.7(10)-157	Escherichia coli	b1220	[pn:hypothetical protein in narl 5'''region] [gn:yehp]

CONTIG477	3144165_c3_243	3021	8683	1302	434	1913	1.1(10)-197	Escherichia coli	b1210	[pn:glutamyl-trna reductase] [gn:hema]
CONTIG477	16219457_c3_248	3022	8684	417	139	395	8.3(10)-37	Escherichia coli	b1213	[pn:hypothetical protein]
CONTIG477	11212778_c3_249	3023	8685	813	271	1139	1.2(10)-115	Escherichia coli	b1214	[pn:hypothetical protein in hemk-kdsa] [gn:ycha]
CONTIG477	4001668_c3_250	3024	8686	864	288	1362	2.7(10)-139	Escherichia coli	b1215	[pn:2-dehydro-3-deoxyphosphoactonate aldolase] [gn:kdsa]
CONTIG477	34396092_c3_265	3025	8687	891	297	895	8.5(10)-90	Klebsiella pneumoniae	L27431	[de:klebsiella pneumoniae nitrate transporter component (nasf), nitrate transporter component (nase), nitrate transporter apase component(nasd), and nitrate reductase smal"] [pn:nitrate transporter component] [gn:nase]
CONTIG477	5275443_c3_266	3026	8688	798	266	1270	1.6(10)-129	Klebsiella pneumoniae	L27431	[de:klebsiella pneumoniae nitrate transporter component (nasf), nitrate transporter component (nase), nitrate transporter apase component(nasd)] [pn:nitrate transporter apase component] [gn:nasd]
CONTIG477	5192968_c3_267	3027	8689	3996	1332	2499	9.1(10)-260	Escherichia coli	b3365	[pn:nadh-nitrate oxidoreductase apoprotein] [gn:nitb]
CONTIG478	32453438_fl_1	3028	8690	582	194	111	7.2(10)-5	Bacillus subtilis	pksA	[pn:transcriptional regulator]
CONTIG478	12548567_fl_15	3029	8691	918	306	878	5.4(10)-88	Escherichia coli	b1466	[pn:respiratory nitrate reductase 2 delta chain] [gn:narw]
CONTIG478	12213952_fl_18	3030	8692	765	255	854	1.8(10)-85	Escherichia coli	b1462	[pn:hypothetical protein]
CONTIG478	6735393_fl_19	3031	8693	285	95	446	3.2(10)-42	Escherichia coli	b4294	[pn:insertion element isf protein insa] [gn:insa_7]
CONTIG478	2242625_f2_52	3032	8694	219	73	251	1.5(10)-21	Escherichia coli	b2215	[pn:outer membrane protein c precursor] [gn:ompc]
CONTIG478	4725761_f2_57	3033	8695	1473	491	1795	3.7(10)-185	Escherichia coli	b1469	[pn:nitrite extrusion protein] [gn:naru]
CONTIG478	32313576_f2_62	3034	8696	1590	530	2635	3.5(10)-274	Escherichia coli	b1467	[pn:respiratory nitrate reductase 2 beta chain] [gn:nary]

CONTIG478	2911290_f2_67	3035	8697	234	78	296	2.6(10)-26	Escherichia coli	S40546	hypothetical protein - escherichia coli
CONTIG478	25437756_f2_71	3036	8698	345	115	237	4.5(10)-20	Bacillus subtilis	yczG	[pn:hypothetical protein]
CONTIG478	1207283_f2_89	3037	8699	897	299	693	2.2(10)-68	Escherichia coli	b1328	[pn:hypothetical protein] [gn:ycjz]
CONTIG478	22929826_f2_90	3038	8700	1599	533	2129	1.5(10)-220	Escherichia coli	b1453	[pn:hypothetical protein] [gn:ansp]
CONTIG478	10312956_f2_93	3039	8701	996	332	1314	3.3(10)-134	Escherichia coli	b1451	[pn:hypothetical protein]
CONTIG478	2456415_f3_100	3040	8702	3783	1261	6042	0	Escherichia coli	b1468	[pn:respiratory nitrate reductase 2 alpha chain] [gn:narz]
CONTIG478	31508556_f3_105	3041	8703	729	243	885	9.9(10)-89	Escherichia coli	b1465	[pn:respiratory nitrate reductase 2 gamma chain] [gn:narv]
CONTIG478	25567885_f3_108	3042	8704	525	175	898	4.0(10)-90	Escherichia coli	b0264	[pn:insertion element is1 protein insb] [gn:insb_2]
CONTIG478	21500925_f3_110	3043	8705	537	179	237	3.5(10)-19	Eikenella corrodens	P35649	hypothetical 66.3 kd protein in hag2 5'region
CONTIG478	16987716_f3_111	3044	8706	270	90	185	1.5(10)-13	Eikenella corrodens	P35649	hypothetical 66.3 kd protein in hag2 5'region.
CONTIG478	21970417_f3_112	3045	8707	954	318	479	1.0(10)-45	Eikenella corrodens	P35649	hypothetical 66.3 kd protein in hag2 5'region.
CONTIG478	4884652_c1_148	3046	8708	402	134	102	9.3(10)-6	Enterobacter aerogenes	U67194	or:enterobacter aerogenes pn pep1 gn:tnpa le:11649 re:12071 di:complement nt:orf1
CONTIG478	26429653_c1_151	3047	8709	1020	340	539	4.5(10)-52	Bacillus subtilis	ymtO	[pn:hypothetical protein]
CONTIG478	24667250_c1_154	3048	8710	1329	443	1352	3.2(10)-138	Bacillus subtilis	ymJ	[pn:hypothetical protein]
CONTIG478	35664657_c1_158	3049	8711	837	279	559	3.5(10)-54	Escherichia coli	b1917	[pn:hypothetical protein] [gn:yecc]
CONTIG478	5260443_c1_159	3050	8712	897	299	165	1.2(10)-10	Escherichia coli	b1920	[pn:fly protein precursor] [gn:fly]
CONTIG478	6439130_c1_160	3051	8713	273	91	244	8.3(10)-21	Escherichia coli	b1461	[pn:hypothetical 8.7 kd protein in rhse-narv intergenic region] [gn:ydee]
CONTIG478	189212_c1_161	3052	8714	1017	339	1053	1.6(10)-106	Escherichia coli	b1054	[pn:membrane protein affecting cell division, growth and high temperature survival] [gn:htrb]

CONTIG478	33787750_c1_169	3053	8715	882	294	1153	3.8(10)-117	Escherichia coli	b1463	[pn:hypothetical protein]
CONTIG478	4329693_c2_205	3054	8716	2112	704	2500	7.2(10)-260	Escherichia coli	b3340	[pn:fusa] [gn:fusa]
CONTIG478	5899187_c3_232	3055	8717	1074	358	1425	5.9(10)-146	Escherichia coli	b1452	[pn:hypothetical protein]
CONTIG478	1267275_c3_237	3056	8718	576	192	97	0.00259	Bacillus subtilis	yqaC	[pn:hypothetical protein]
CONTIG478	19821086_c3_239	3057	8719	1137	379	879	4.2(10)-88	Bacillus subtilis	yxeP	[pn:hypothetical protein] [gn:lp9h]
CONTIG478	15908556_c3_241	3058	8720	1062	354	206	1.7(10)-16	Escherichia coli	b1920	[pn:fly protein precursor] [gn:fly]
CONTIG478	4036693_c3_242	3059	8721	519	173	134	3.7(10)-9	Methanobacterium thermoautotrophicum	MT1676	[pn:unknown]
CONTIG478	5197943_c3_243	3060	8722	936	312	215	9.8(10)-18	Escherichia coli	b1918	[pn:yecc]
CONTIG478	4489843_c3_244	3061	8723	627	209	851	3.8(10)-85	Escherichia coli	b1454	[pn:hypothetical protein]
CONTIG478	14885165_c3_249	3062	8724	297	99	390	2.7(10)-36	Escherichia coli	D93826	hypothetical 11k protein (insertion sequence is1) -escherichia coli this protein is coded by the insertion sequence is1.
CONTIG478	1290917_c3_265	3063	8725	1395	465	1230	2.7(10)-125	Salmonella typhimurium	P37594	methyl viologen resistance protein smva.
CONTIG478	26175336_c3_266	3064	8726	216	72	137	1.8(10)-9	Bacteriophage PA2	E25647	hypothetical lc protein - phage pa2
CONTIG479	34552086_f1_3	3065	8727	786	262	1064	1.1(10)-107	Escherichia coli	b1868	[pn:hypothetical protein in asps 5'''region] [gn:yecc]
CONTIG479	4423942_f1_4	3066	8728	429	143	581	1.6(10)-56	Escherichia coli	b1869	[pn:hypothetical protein]
CONTIG479	10167501_f1_5	3067	8729	1011	337	1481	6.9(10)-152	Escherichia coli	b1871	[pn:hypothetical protein]
CONTIG479	7206518_f1_8	3068	8730	1743	581	2582	1.5(10)-268	Escherichia coli	b1876	[pn:arginyl-trna synthetase] [gn:args]
CONTIG479	16048255_f2_45	3069	8731	1347	449	1223	1.5(10)-124	Escherichia coli	b1579	[pn:hypothetical protein]

CONTIG479	3364465_f2_47	3070	8732	840	280	1190	4.7(10)-121	Escherichia coli	b1870	[pn:hypothetical protein]
CONTIG479	39052_f2_76	3071	8733	1317	439	646	2.1(10)-63	Escherichia coli	b4077	[pn:glutamate- aspartate carrier] [gn:glp]
CONTIG479	6104837_f3_140	3072	8734	441	147	516	1.2(10)-49	Escherichia coli	b1895	[pn:hypothetical 17.1 kd protein in flhd-otsa intergenic region]
CONTIG479	24645818_c1_144	3073	8735	936	312	1293	5.7(10)-132	Escherichia coli	b1889	[pn:chemotaxis motb protein] [gn:motb]
CONTIG479	35330006_c1_149	3074	8736	792	264	103	0.0023	Escherichia coli	b0944	[pn:hypothetical fimbrial chaperone in pepn-pyrd intergenic region] [gn:ycbf]
CONTIG479	13080431_c1_161	3075	8737	465	155	371	2.8(10)-34	Escherichia coli	b1882	[pn:chemotaxis protein chey] [gn:chey]
CONTIG479	35188562_c2_181	3076	8738	1431	477	1957	2.5(10)-202	Escherichia coli	b1896	[pn:alpha trehalose phosphate synthase] [gn:otsa]
CONTIG479	26661516_c2_183	3077	8739	606	202	934	6.2(10)-94	Escherichia coli	b1891	[pn:flagellar transcriptional activator] [gn:flhc]
CONTIG479	25604716_c2_184	3078	8740	903	301	1159	9.0(10)-118	Escherichia coli	b1890	[pn:chemotaxis mota protein] [gn:mota]
CONTIG479	36349037_c2_186	3079	8741	2076	692	2572	1.7(10)-267	Escherichia coli	b1888	[pn:chemotaxis protein chea] [gn:chea]
CONTIG479	24492202_c2_187	3080	8742	573	191	102	0.0004	Myxococcus xanthus	p27755	protein u precursor.
CONTIG479	15760407_c2_197	3081	8743	1635	545	1629	1.3(10)-167	Escherichia coli	b1885	[pn:methyl-accepting chemotaxis protein iv] [gn:tap]
CONTIG479	4570318_c2_199	3082	8744	1059	353	1653	4.0(10)-170	Escherichia coli	b1883	[pn:protein-glutamate methyltransferase] [gn:cheb]
CONTIG479	12579542_c2_200	3083	8745	720	240	795	3.3(10)-79	Escherichia coli	b1881	[pn:chemotaxis protein chez] [gn:chez]
CONTIG479	3407752_c2_201	3084	8746	1173	391	1419	2.6(10)-145	Escherichia coli	b1880	[pn:hypothetical protein] [gn:flhb]
CONTIG479	9929581_c2_205	3085	8747	432	144	472	5.7(10)-45	Escherichia coli	b1878	[pn:hypothetical protein] [gn:flhe]
CONTIG479	14855425_c2_206	3086	8748	1599	533	197	1.2(10)-12	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-selc intergenic region] [gn:yicj]
CONTIG479	24744006_c2_212	3087	8749	564	188	860	4.4(10)-86	Escherichia coli	b1875	[pn:hypothetical protein] [gn:yecm]
CONTIG479	23445328_c2_213	3088	8750	765	255	478	1.3(10)-45	Escherichia coli	b1874	[pn:copper homeostasis protein] [gn:cutc]

CONTIG479	30101377_c3_221	3089	8751	462	154	503	3.0(10)-48	Escherichia coli	b1892	[pn:flagellar transcriptional activator flhA] [gn:flhA]
CONTIG479	23726553_c3_224	3090	8752	519	173	693	2.2(10)-68	Escherichia coli	b1887	[pn:purine binding chemotaxis protein] [gn:chew]
CONTIG479	31806341_c3_227	3091	8753	609	203	119	3.1(10)-6	Myxococcus xanthus	P27755	protein u precursor.
CONTIG479	20604540_c3_229	3092	8754	2400	800	169	7.2(10)-9	Escherichia coli	b3144	[pn:hypothetical outer membrane usher protein in agal-mtr intergenic region] [gn:yra]
CONTIG479	11056950_c3_230	3093	8755	1773	591	1501	5.2(10)-154	Escherichia coli	b1886	[pn:methyl-accepting chemotaxis protein ii] [gn:tar]
CONTIG479	4036688_c3_232	3094	8756	876	292	1309	1.2(10)-133	Escherichia coli	b1884	[pn:chemotaxis protein methyltransferase] [gn:cher]
CONTIG479	15117832_c3_237	3095	8757	2094	698	2605	5.4(10)-271	Escherichia coli	b1879	[pn:flagellar biosynthesis protein flhA] [gn:flhA]
CONTIG479	13852002_c3_239	3096	8758	1167	389	422	1.1(10)-39	Bacillus subtilis	yesR	[pn:hypothetical protein]
CONTIG48	6023461_c1_7	3097	8759	333	111	110	1.3(10)-6	Bacteriophage P1	L01408	or:bacteriophage p1 pn:partition protein gn:parb le<1 re:456 di:direct sr:bacteriophage p1 (individual_isolate p1kc) dna
CONTIG480	26740760_f1_13	3098	8760	621	207	631	8.0(10)-62	Helicobacter pylori	HPI563	[pn:alkyl hydroperoxide reductase] [gn:tsaa]
CONTIG480	24477316_f1_35	3099	8761	3147	1049	2369	5.5(10)-246	Escherichia coli	b0397	[pn:exonuclease sbcc] [gn:sbcc]
CONTIG480	24035875_f1_39	3100	8762	942	314	1343	2.8(10)-137	Escherichia coli	b0393	[pn:hypothetical 34.0 kd protein in arom-araj intergenic region]
CONTIG480	6461591_f1_45	3101	8763	822	274	1206	9.5(10)-123	Escherichia coli	b0386	[pn:pyrroline-5-carboxylate reductase] [gn:proc]
CONTIG480	4580282_f2_49	3102	8764	900	300	1472	6.2(10)-151	Escherichia coli	b0411	[pn:nucleoside-specific channel-forming protein tsx precursor] [gn:tsx]
CONTIG480	25547211_f2_80	3103	8765	1323	441	1708	6.0(10)-176	Escherichia coli	b0398	[pn:exonuclease sbcc] [gn:sbcd]
CONTIG480	21611505_f3_104	3104	8766	639	213	798	1.6(10)-79	Escherichia coli	b0404	[pn:hypothetical 23.0 kd protein in malz-quea intergenic region] [gn:yajb]
CONTIG480	14329693_c1_138	3105	8767	273	91	306	2.2(10)-27	Escherichia coli	b0382	[pn:hypothetical protein fragment in ddla-phoa intergenic region]

CONTIG480	14556508_c1_141	3106	8768	195	65	284	4.7(10)-25	Escherichia coli	b0389	[pn:hypothetical 7.3 kd protein in aro-arom intergenic region]
CONTIG480	21875076_c1_145	3107	8769	1107	369	1330	6.9(10)-136	Escherichia coli	b0394	[pn:hypothetical protein in aro-arom intergenic region] [gn:yajf]
CONTIG480	25945251_c1_157	3108	8770	717	239	1153	3.8(10)-117	Escherichia coli	b0399	[pn:phosphate regulon transcriptional regulatory protein]
CONTIG480	26587916_c1_158	3109	8771	1299	433	1920	2.1(10)-198	Escherichia coli	b0400	[pn:phosphate regulon sensor protein phor] [gn:phor]
CONTIG480	14875018_c1_159	3110	8772	1326	442	1898	4.4(10)-196	Escherichia coli	b0401	[pn:branched chain amino acid transport system ii carrier protein] [gn:brnq]
CONTIG480	14588430_c1_160	3111	8773	1455	485	1858	7.7(10)-192	Escherichia coli	b0402	[pn:hypothetical protein] [gn:proy]
CONTIG480	21492016_c1_161	3112	8774	1845	615	2711	3.1(10)-282	Escherichia coli	b0403	[pn:maltodextrin glucosidase] [gn:malz]
CONTIG480	6536091_c1_165	3113	8775	474	158	97	0.0008	Nephila clavipes	AF027735	[de:nephila clavipes minor ampullate silk protein misp1 mrna, partialcds] [pn:minor ampullate silk protein misp1]
CONTIG480	12994007_c1_172	3114	8776	1107	369	1748	3.5(10)-180	Escherichia coli	b0405	[pn:trna ribosyltransferase-isomerase] [gn:quca]
CONTIG480	5327_c1_175	3115	8777	333	111	531	3.2(10)-51	Escherichia coli	b0407	[pn:hypothetical 11.9 kd protein in tgt-secd intergenic region] [gn:yajc]
CONTIG480	23280_c1_176	3116	8778	1875	625	2610	1.6(10)-271	Escherichia coli	b0408	[pn:protein-export membrane protein secd] [gn:secd]
CONTIG480	36073311_c1_178	3117	8779	384	128	130	2.3(10)-8	Mycobacterium tuberculosis	Z95210	unknown, mtey21c12.05, mtey21c12.05, len
CONTIG480	15055465_c2_187	3118	8780	471	157	613	6.5(10)-60	Escherichia coli	b0387	[pn:yaii]
CONTIG480	35629031_c2_188	3119	8781	669	223	569	3.0(10)-55	Escherichia coli	b0388	[pn:shikimate kinase ii] [gn:arol]
CONTIG480	1953465_c2_189	3120	8782	321	107	435	4.7(10)-41	Escherichia coli	b0391	[pn:hypothetical 10.2 kd protein in aro-araj intergenic region]
CONTIG480	13911282_c2_215	3121	8783	1026	342	1414	8.5(10)-145	Escherichia coli	b0409	[pn:protein-export membrane protein secf] [gn:secf]
CONTIG480	12501906_c2_217	3122	8784	744	248	218	4.7(10)-18	Bacillus subtilis	yobV	[pn:hypothetical protein]

CONTIG480	35251317_c3_219	3123	8785	591	197	549	4.0(10)-53	Escherichia coli	b1053	[pn:hypothetical 43.9 kd protein in msyb-hrb intergenic region] [gn:ycee]
CONTIG480	3004066_c3_220	3124	8786	363	121	447	2.6(10)-42	Escherichia coli	b0384	[pn:phosphate starvation-inducible protein psif] [gn:psif]
CONTIG480	21759841_c3_221	3125	8787	1200	400	996	1.7(10)-100	Escherichia coli	b0385	[pn:hypothetical 41.5 kd protein in psif-proc intergenic region] [gn:yaic]
CONTIG480	5214091_c3_225	3126	8788	693	231	799	1.3(10)-79	Escherichia coli	b0390	[pn:arom protein] [gn:arom]
CONTIG480	36580083_c3_251	3127	8789	1197	399	1968	1.7(10)-203	Escherichia coli	b0406	[pn:queuine trna-ribosyltransferase] [gn:tgt]
CONTIG481	34042063_fl_6	3128	8790	1419	473	2247	4.5(10)-233	Escherichia coli	b3962	[pn:unknown dehydrogenase a] [gn:udha]
CONTIG481	14541018_fl_13	3129	8791	1164	388	1789	1.6(10)-184	Escherichia coli	b3957	[pn:acetylornithine deacetylase] [gn:arge]
CONTIG481	9806318_fl_26	3130	8792	2523	841	2841	5.2(10)-296	Escherichia coli	b3947	[pn:phosphoenolpyruvate-protein phosphotransferase pisa] [gn:ptsa]
CONTIG481	29892965_f2_59	3131	8793	2670	890	4102	0	Escherichia coli	b3956	[pn:phosphoenolpyruvate carboxylase] [gn:ppc]
CONTIG481	27137_f2_60	3132	8794	912	304	1168	1.0(10)-118	Escherichia coli	b3954	[pn:hypothetical transcriptional regulator in glda-ppc intergenic] [gn:yijo]
CONTIG481	4428176_f3_85	3133	8795	1179	393	1788	2.0(10)-184	Escherichia coli	b3965	[pn:uracil-5-methyltransferase] [gn:trma]
CONTIG481	33620166_f3_116	3134	8796	732	244	900	2.5(10)-90	Escherichia coli	b3946	[pn:transaldolase-like protein] [gn:talc]
CONTIG481	5977218_f3_117	3135	8797	1116	372	1734	1.1(10)-178	Escherichia coli	b3945	[pn:glycerol dehydrogenase] [gn:glda]
CONTIG481	4103427_c1_149	3136	8798	921	307	1508	9.5(10)-155	Escherichia coli	b3961	[pn:hydrogen peroxide-inducible genes activator] [gn:oxyr]
CONTIG481	10004056_c1_158	3137	8799	885	295	1324	3.0(10)-135	Escherichia coli	b3967	[pn:glutamate racemase] [gn:mun]
CONTIG481	29484442_c2_159	3138	8800	2487	829	3802	0	Escherichia coli	b3940	[pn:aspartokinase ii/homoserine dehydrogenase ii] [gn:metl]
CONTIG481	26765951_c2_174	3139	8801	339	113	436	3.7(10)-41	Escherichia coli	b3950	[pn:phosphotransferase] [gn:frwb]
CONTIG481	16110041_c2_175	3140	8802	2349	783	3547	0	Escherichia coli	b3951	[pn:formate acetyltransferase 2] [gn:pflD]

CONTIG481	26050393_c2_177	3141	8803	420	140	437	2.8(10)-41	Escherichia coli	b3953	[pn:phosphotransferase] [gn:frwd]
CONTIG481	5176592_c2_187	3142	8804	1014	338	1561	2.2(10)-160	Escherichia coli	b3958	[pn:n-acetyl-gamma-glutamyl-phosphate reductase] [gn:argc]
CONTIG481	5119143_c2_188	3143	8805	783	261	1143	4.5(10)-116	Escherichia coli	b3959	[pn:acetylglutamate kinase] [gn:argb]
CONTIG481	22135833_c2_189	3144	8806	1419	473	2100	1.7(10)-217	Escherichia coli	b3960	[pn:argininosuccinate lyase] [gn:argh]
CONTIG481	24788962_c2_192	3145	8807	807	269	942	9.0(10)-95	Escherichia coli	b3963	[pn:hypothetical 26.6 kd protein in udha-trna intergenic region]
CONTIG481	22462803_c2_193	3146	8808	378	126	463	5.2(10)-44	Escherichia coli	b3964	[pn:hypothetical 13.0 kd protein in udha-trna intergenic region]
CONTIG481	477291_c3_199	3147	8809	624	208	888	4.7(10)-89	Escherichia coli	b3939	[pn:cystathionine gamma-synthase] [gn:metb]
CONTIG481	665893_c3_206	3148	8810	894	298	1444	5.7(10)-148	Escherichia coli	b3941	[pn:5,10 methylenetetrahydrofolate reductase] [gn:mctf]
CONTIG481	36126911_c3_207	3149	8811	2202	734	3234	0	Escherichia coli	b3942	[pn:catalase hydroperoxidase i] [gn:katg]
CONTIG481	5891450_c3_214	3150	8812	1131	377	1281	1.1(10)-130	Escherichia coli	b3949	[pn:phosphotransferase] [gn:frwc]
CONTIG481	22464582_c3_219	3151	8813	987	329	1123	5.9(10)-114	Escherichia coli	b3952	[pn:probable pyruvate formate-lyase 2 activating enzyme] [gn:pflc]
CONTIG481	22915793_c3_239	3152	8814	1890	630	2190	5.0(10)-227	Escherichia coli	b3966	[pn:vitamin b12 receptor precursor] [gn:btub]
CONTIG482	820216_fl_1	3153	8815	984	328	300	9.6(10)-27	Haemophilus influenzae	HI1248	[pn:hypothetical protein]
CONTIG482	5115718_fl_6	3154	8816	1002	334	961	8.6(10)-97	Escherichia coli	b3909	[pn:2-keto-3-deoxygluconate permease] [gn:kdgt]
CONTIG482	24423878_fl_12	3155	8817	531	177	608	2.2(10)-59	Escherichia coli	b4107	[pn:protein] [gn:phnb]
CONTIG482	26602316_fl_13	3156	8818	1029	343	1594	7.2(10)-164	Escherichia coli	b4105	[pn:carbon phosphorus lyase] [gn:phnd]
CONTIG482	14317706_fl_18	3157	8819	669	223	837	1.2(10)-83	Escherichia coli	b4100	[pn:phnh protein] [gn:phnh]
CONTIG482	24066662_fl_21	3158	8820	870	290	1440	1.5(10)-147	Escherichia coli	b4098	[pn:phnj protein] [gn:phnj]
CONTIG482	34239388_fl_25	3159	8821	648	216	641	7.0(10)-63	Escherichia coli	b4094	[pn:phosphonates transport atp-binding protein phnn] [gn:phnn]

CONTIG482	17054132_f1_37	3160	8822	1080	360	499	7.9(10)-48	Bacillus subtilis	rbsC	[pn:ribose abc transporter]
CONTIG482	884702_f1_39	3161	8823	864	288	566	6.2(10)-55	Bacillus subtilis	fbaA	[pn:fructose-1,6-bisphosphate aldolase] [gn:tsr]
CONTIG482	24644438_f1_45	3162	8824	492	164	412	1.3(10)-38	Escherichia coli	b4078	[pn:hypothetical 25.1 kd protein in gltp-fdhf intergenic region] [gn:yjco]
CONTIG482	32612590_f1_46	3163	8825	189	63	263	8.0(10)-23	Escherichia coli	b4078	[pn:hypothetical 25.1 kd protein in gltp-fdhf intergenic region] [gn:yjco]
CONTIG482	10987586_f2_54	3164	8826	492	164	568	3.7(10)-55	Escherichia coli	b4108	[pn:phna protein] [gn:phna]
CONTIG482	2125183_f2_61	3165	8827	759	253	1098	2.6(10)-111	Escherichia coli	b4102	[pn:phnf protein] [gn:phnf]
CONTIG482	25785827_f2_62	3166	8828	453	151	522	2.8(10)-50	Escherichia coli	b4101	[pn:phng protein] [gn:phng]
CONTIG482	33854562_f2_69	3167	8829	1266	422	1630	1.1(10)-167	Escherichia coli	b4095	[pn:phnm protein] [gn:phnm]
CONTIG482	12927258_f2_70	3168	8830	774	258	598	2.5(10)-58	Escherichia coli	b4093	[pn:phno protein] [gn:phno]
CONTIG482	3958592_f2_71	3169	8831	768	256	1084	8.0(10)-110	Escherichia coli	b4092	[pn:phnp protein] [gn:phnp]
CONTIG482	4116642_f2_75	3170	8832	1548	516	1154	3.1(10)-117	Bacillus subtilis	rbsA	[pn:ribose abc transporter]
CONTIG482	13866580_f2_77	3171	8833	1008	336	332	3.8(10)-30	Bacillus subtilis	rbsB	[pn:ribose abc transporter]
CONTIG482	19567043_f3_99	3172	8834	816	272	1144	3.5(10)-116	Escherichia coli	b4106	[pn:phosphonates transport atp-binding protein] [gn:phnc]
CONTIG482	6767917_f3_102	3173	8835	846	282	607	2.7(10)-59	Escherichia coli	b4104	[pn:phnc]
CONTIG482	16661008_f3_106	3174	8836	1170	390	1563	1.3(10)-160	Escherichia coli	b4099	[pn:phni protein] [gn:phni]
CONTIG482	35283517_f3_108	3175	8837	840	280	1119	1.6(10)-113	Escherichia coli	b4097	[pn:phosphonates transport atp-binding protein phnk] [gn:phnk]
CONTIG482	4488588_f3_109	3176	8838	690	230	1003	3.1(10)-101	Escherichia coli	b4096	[pn:phosphonates transport atp-binding protein phnl] [gn:phnl]
CONTIG482	19708567_f3_123	3177	8839	1083	361	152	2.0(10)-8	Bacillus subtilis	ydjE	[pn:hypothetical protein]

CONTIG482	23447063_f3_127	3178	8840	444	148	701	3.1(10)-69	Escherichia coli	b4079	[pn:formate dehydrogenase, formate-hydrogen-lyase-linked, selenocysteine-containing polypeptide] [gn:fdhf]
CONTIG482	10646036_f3_128	3179	8841	1728	576	2902	1.8(10)-302	Escherichia coli	b4079	[pn:formate dehydrogenase, formate-hydrogen-lyase-linked, selenocysteine-containing polypeptide] [gn:fdhf]
CONTIG482	2756663_c2_176	3180	8842	189	63	175	1.0(10)-12	Escherichia coli	b4077	[pn:glutamate- aspartate carrier] [gn:gltp]
CONTIG482	14629593_c2_194	3181	8843	2310	770	593	8.5(10)-58	Rhizobium leguminosarum	Z70305	or:rhizobium leguminosarum pn:fixl gn:fixl le:1546 re:3471 di:direct nt:putative heme-binding, oxygen sensing protein
CONTIG482	10337827_c2_205	3182	8844	237	79	276	3.3(10)-24	Escherichia coli	B35720	hypothetical 28.6k protein - escherichia coli
CONTIG482	4375276_c2_215	3183	8845	417	139	94	6.5(10)-5	Escherichia coli	C35720	hypothetical 12.4k protein - escherichia coli
CONTIG482	2538135_c2_221	3184	8846	909	303	788	1.8(10)-78	Escherichia coli	b4110	[pn:hypothetical 31.8 kd protein in phna-prop intergenic region] [gn:yjez]
CONTIG482	22736068_c2_225	3185	8847	1587	529	2169	8.5(10)-225	Escherichia coli	b4111	[pn:proline/betaine transporter] [gn:prop]
CONTIG482	15807841_c3_231	3186	8848	744	248	369	4.7(10)-34	Escherichia coli	b3405	[pn:ompr] [gn:ompr]
CONTIG482	14112961_c3_242	3187	8849	240	80	173	2.7(10)-13	Escherichia coli	D35720	hypothetical 13.7k protein - escherichia coli
CONTIG482	25833337_c3_256	3188	8850	1023	341	172	3.5(10)-13	Escherichia coli	A35720	hypothetical 16.1k protein (phnq 3 region) - escherichiacoli
CONTIG482	135968_c3_261	3189	8851	2370	790	1679	9.0(10)-228	Escherichia coli	b4109	[pn:hypothetical 84.2 kd protein in phna-prop intergenic region] [gn:yjda]
CONTIG483	22834691_f1_6	3190	8852	891	297	1234	1.0(10)-125	Escherichia coli	b3455	[pn:high-affinity branched-chain amino acid transport atp-binding protein livg] [gn:livg]
CONTIG483	10677010_f1_8	3191	8853	1350	450	2061	2.3(10)-213	Escherichia coli	b3453	[pn:glycerol-3-phosphate-binding periplasmic protein precursor] [gn:ugpb]

CONTIG483	10634631_f1_9	3192	8854	891	297	1261	1.3(10)-128	Escherichia coli	b3452	[pn:sn-glycerol-3-phosphate transport system permease protein]
CONTIG483	16286306_f1_10	3193	8855	1119	373	1701	3.2(10)-175	Escherichia coli	b3450	[pn:sn-glycerol-3-phosphate transport atp-binding protein]
CONTIG483	2534500_f1_18	3194	8856	1083	361	1456	3.1(10)-149	Escherichia coli	b3438	[pn:gtnkr operon regulator]
CONTIG483	25509436_f1_19	3195	8857	549	183	687	9.4(10)-68	Escherichia coli	b3437	[gn:gntk]
CONTIG483	13946878_f1_20	3196	8858	1344	448	1223	1.5(10)-124	Escherichia coli	b3436	[pn:gntk]
CONTIG483	13132087_f1_25	3197	8859	2049	683	2777	3.2(10)-289	Escherichia coli	b3431	[pn:glycogen operon protein glgx]
CONTIG483	34010260_f2_35	3198	8860	927	309	1431	1.3(10)-146	Escherichia coli	b3458	[pn:leucine-specific binding protein precursor] [gn:livk]
CONTIG483	6142567_f2_39	3199	8861	1362	454	1638	1.6(10)-168	Escherichia coli	b3456	[pn:high-affinity branched-chain amino acid transport permease protein livm] [gn:livm]
CONTIG483	13854155_f2_40	3200	8862	741	247	1145	2.7(10)-116	Escherichia coli	b3454	[pn:high-affinity branched-chain amino acid transport atp-binding] [gn:livf]
CONTIG483	5348437_f2_60	3201	8863	2205	735	3757	0	Escherichia coli	b3432	[pn:1,4-alpha-glucan branching enzyme] [gn:ggb]
CONTIG483	35555135_f2_66	3202	8864	1647	549	2222	2.1(10)-230	Escherichia coli	b3429	[pn:glycogen synthase] [gn:gga]
CONTIG483	6849191_f2_67	3203	8865	2466	822	3732	0	Escherichia coli	b3428	[pn:alpha-glucan phosphorylase] [gn:glp]
CONTIG483	22658562_f3_72	3204	8866	939	313	1163	3.3(10)-118	Escherichia coli	b3457	[pn:high-affinity branched-chain amino acid transport permease protein livh] [gn:livh]
CONTIG483	12526018_f3_79	3205	8867	858	286	1098	2.6(10)-111	Escherichia coli	b3451	[pn:sn-glycerol-3-phosphate transport system permease protein]
CONTIG483	14574037_f3_84	3206	8868	756	252	1016	1.3(10)-102	Escherichia coli	b3449	[pn:glycerophosphoryl diester phosphodiesterase] [gn:ugpq]
CONTIG483	4105458_f3_85	3207	8869	1782	594	2482	5.7(10)-258	Escherichia coli	b3447	[pn:gamma-glutamyltranspeptidase] [gn:ggt]
CONTIG483	2853408_f3_88	3208	8870	1041	347	1700	4.2(10)-175	Escherichia coli	b3440	[pn:hypothetical 38.8 kd protein in gnt-egg intergenic region] [gn:yhhx]
CONTIG483	16914058_f3_89	3209	8871	819	273	1145	2.7(10)-116	Escherichia coli	b3439	[pn:hypothetical 26.3 kd protein in gnt-egg intergenic region]

CONTIG483	20445390_f3_95	3210	8872	1173	391	1793	6 0(10)-185	Escherichia coli	b3433	[pn:aspartate semialdehyde dehydrogenase] [gn:asd]
CONTIG483	19767905_f3_104	3211	8873	1374	458	1994	3.0(10)-206	Escherichia coli	b3430	[pn:glucose-1-phosphate adenylyltransferase] [gn:glgc]
CONTIG483	12605291_f3_113	3212	8874	258	86	94	0.00077	Saccharomyces cerevisiae	YNL138W	[pn:adenylate cyclase-associated protein, 70kda] [gn:srcv2]
CONTIG483	20411717_c1_144	3213	8875	477	159	159	4.9(10)-17	Escherichia coli	b3448	[pn:hypothetical 16.6 kd protein in ggt-ugpq intergenic region precursor] [gn:yhha]
CONTIG483	13019705_c2_186	3214	8876	318	106	104	5 7(10)-6	Escherichia coli	D90866	or: escherichia coli pn d-serine dehydratase transcriptional activator gn dsdc lc:10864 re:11133 di. complement sr. escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [pir accession number a28674];
CONTIG483	17000951_c2_191	3215	8877	507	169	724	1 1(10)-71	Escherichia coli	b3441	[pn:hypothetical protein] [gn:yhyh]
CONTIG483	24725008_c3_207	3216	8878	1536	512	2144	3.7(10)-222	Escherichia coli	b3426	[pn:aerobic glycerol-3-phosphate dehydrogenase] [gn:glpd]
CONTIG483	34417125_c3_229	3217	8879	600	200	763	8.3(10)-76	Escherichia coli	b3434	[pn:hypothetical protein] [gn:yhgn]
CONTIG484	22737668_f1_1	3218	8880	639	213	782	8.0(10)-78	Escherichia coli	b0687	[pn:seqa protein] [gn:scqa]
CONTIG484	21665656_f1_2	3219	8881	1665	555	2446	3.7(10)-254	Escherichia coli	b0688	[pn:phosphoglucomutase] [gn:pgm]
CONTIG484	975428_f1_21	3220	8882	303	101	315	2.5(10)-28	Escherichia coli	b0699	[pn:hypothetical 8.3 kd protein in rhsc 5'''region] [gn:ybfa]
CONTIG484	25494783_f1_25	3221	8883	1125	375	1214	1.3(10)-123	Escherichia coli	b0712	[pn:hypothetical protein] [gn:ybgk]
CONTIG484	16618761_f1_31	3222	8884	501	167	604	5.9(10)-59	Escherichia coli	b0721	[pn:succinate dehydrogenase cytochrome b-556 subunit] [gn:sdhc]
CONTIG484	15663465_f2_67	3223	8885	1434	478	1878	5.9(10)-194	Escherichia coli	b0708	[pn:deoxyribodipyrimidine photolyase] [gn:phrb]
CONTIG484	16667078_f2_68	3224	8886	657	219	989	9.4(10)-100	Escherichia coli	b0711	[pn:hypothetical protein] [gn:ybgj]
CONTIG484	33878962_f2_69	3225	8887	792	264	887	6 0(10)-89	Escherichia coli	b0713	[pn:hypothetical protein] [gn:ybgj]

CONTIG484	23629837_f2_70	3226	8888	804	268	1138	1.5(10)-115	Escherichia coli	b0714	[pn:endonuclease viii, dna n-glycosylase with an ap lyase activity] [gn:nei]
CONTIG484	26063532_f2_72	3227	8889	1860	620	2955	0	Escherichia coli	b0723	[pn:succinate dehydrogenase flavoprotein subunit] [gn:sdha]
CONTIG484	33805415_f2_73	3228	8890	732	244	1234	1.0(10)-125	Escherichia coli	b0724	[pn:succinate dehydrogenase iron-sulfur protein] [gn:sdhb]
CONTIG484	32235416_f2_75	3229	8891	1260	420	1765	5.5(10)-182	Escherichia coli	b0727	[pn:e2] [gn:sucb]
CONTIG484	25495836_f2_76	3230	8892	948	316	1117	2.6(10)-113	Escherichia coli	b0729	[pn:succinyl-coa synthetase alpha chain] [gn:sucd]
CONTIG484	24726711_f2_80	3231	8893	1686	562	2440	1.6(10)-253	Escherichia coli	b0732	[pn:ybgbl] [gn:ybgg]
CONTIG484	6347132_f3_100	3232	8894	834	278	1208	5.7(10)-123	Escherichia coli	b0710	[pn:hypothetical protein] [gn:ybgj]
CONTIG484	29331261_f3_109	3233	8895	399	133	470	9.3(10)-45	Escherichia coli	b0722	[pn:succinate dehydrogenase 13 kd hydrophobic protein] [gn:sdhd]
CONTIG484	5190968_f3_114	3234	8896	2817	939	4678	0	Escherichia coli	b0726	[pn:2-oxoglutarate dehydrogenase e1 component] [gn:suca]
CONTIG484	25490691_f3_116	3235	8897	1194	398	1622	7.9(10)-167	Escherichia coli	b0728	[pn:succinyl-coa synthetase beta chain] [gn:succ]
CONTIG484	433468_f3_119	3236	8898	1929	643	2228	4.7(10)-231	Escherichia coli	b0731	[pn:heat-responsive regulatory protein] [gn:hrrsa]
CONTIG484	4586665_c1_147	3237	8899	1695	565	2180	5.7(10)-226	Escherichia coli	b0698	[pn:potassium-transporting atpase, a chain] [gn:kdpa]
CONTIG484	26458125_c1_148	3238	8900	2067	689	2744	1.0(10)-285	Escherichia coli	b0697	[pn:potassium-transporting atpase, b chain] [gn:kdpb]
CONTIG484	11931712_c1_149	3239	8901	588	196	632	6.4(10)-62	Escherichia coli	b0696	[pn:potassium-transporting atpase, c chain] [gn:kdpc]
CONTIG484	25988452_c1_150	3240	8902	2688	896	3570	0	Escherichia coli	b0695	[pn:sensor protein kdpd] [gn:kdpd]
CONTIG484	1423512_c1_151	3241	8903	195	65	90	0.00017	Haemophilus influenzae	H10592	[pn:hypothetical protein]
CONTIG484	5289012_c1_152	3242	8904	2214	738	3359	0	Escherichia coli	b0693	[pn:ornithine decarboxylase, inducible] [gn:spef]
CONTIG484	24422650_c2_163	3243	8905	750	250	904	9.5(10)-91	Escherichia coli	b0730	[pn:fatty acyl responsive regulator] [gn:farr]
CONTIG484	10413587_c2_177	3244	8906	1221	407	1940	1.6(10)-200	Escherichia coli	b0720	[pn:gla] [gn:gla]

CONTIG484	36207127_c3_243	3245	8907	693	231	871	3.0(10)-87	Escherichia coli	b0694	[pn:kdp operon transcriptional regulatory protein kdpE] [gn:kdpe]
CONTIG484	14635091_c3_246	3246	8908	1389	463	1945	4.7(10)-201	Escherichia coli	b0692	[pn:putrescine-ornithine antiporter] [gn:pote]
CONTIG485	1992963_f1_1	3247	8909	531	177	215	9.8(10)-18	Saccharomyces cerevisiae	S62019	hypothetical protein ydr540c - yeast (saccharomycescerevisiae)
CONTIG485	26595012_f1_2	3248	8910	600	200	293	5.2(10)-26	Thiobacillus ferrooxidans	U66426	or:thiobacillus ferrooxidans
CONTIG485	25681417_f1_3	3249	8911	315	105	117	1.8(10)-6	Ralstonia eutropha	A47041	pn:transposase le:73 re:1284
CONTIG485	5985443_f2_60	3250	8912	807	269	1184	2.0(10)-120	Escherichia coli	P15026	transposase homolog (insertion element isac1) - alcaligenesutrophus
CONTIG485	14238143_f3_100	3251	8913	1200	400	1910	2.3(10)-197	Escherichia coli	P15025	istb protein (insertion sequence is21).
CONTIG485	14657086_f3_101	3252	8914	333	111	132	4.2(10)-8	Bordetella parapertussis	Q06126	ista protein (insertion sequence is21)
CONTIG485	25491665_c1_154	3253	8915	597	199	587	3.7(10)-57	Escherichia coli	b4059	transposase for insertion sequence element is1001
CONTIG485	15027217_c1_162	3254	8916	2112	704	107	0.01099	Oenococcus oeni	S42039	[pn:single-strand dna-binding protein] [gn:ssb]
CONTIG485	22933541_c2_190	3255	8917	2025	675	1098	2.6(10)-111	Haemophilus influenzae	H10444	hypothetical protein 2 - leuconostoc oenos
CONTIG485	34412908_c2_198	3256	8918	579	193	345	1.6(10)-31	Salmonella typhimurium	AF000360	[pn:topoisomerase iii] [gn:topb]
CONTIG485	34415760_c2_216	3257	8919	1482	494	99	0.17999	Escherichia coli	b1372	[PN:hypothetical protein] [DE:Salmonella typhimurium IncN plasmid pKM101 IS26 (IS46) element TnpA(tpa) gene, complete cds.] [LE:1033] [RE:1674] [DI:complement]
CONTIG485	1258591_c3_230	3258	8920	294	98	100	1.5(10)-5	Synechocystis sp.	S77531	[pn:hypothetical protein]
CONTIG485	13167787_c3_248	3259	8921	1518	506	97	0.42999	Saccharomyces cerevisiae	YHR023 W	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR-PCC 6803, PCC 6803] [SR:PCC 6803, J]
CONTIG485	32714125_c3_266	3260	8922	327	109	208	5.4(10)-17	Escherichia coli	b1183	[pn:myo ii myosin heavy chain] [gn:myoII]
CONTIG485										[pn:umud protein] [gn:umud]

CONTIG486	5112518_f1_1	3261	8923	1428	476	1982	5.5(10)-205	Escherichia coli	b4240	[pn:phosphotransferase system trehalose permease] [gn:treb]
CONTIG486	9781900_f1_2	3262	8924	1695	565	2480	9.4(10)-258	Escherichia coli	b4239	[pn:trehalose-6-phosphate hydrolase] [gn:treb]
CONTIG486	7204593_f1_4	3263	8925	483	161	778	2.1(10)-77	Escherichia coli	b4237	[pn:anaerobic ribonucleoside-triphosphate reductase activating pr] [gn:nrdg]
CONTIG486	8973326_f1_24	3264	8926	588	196	785	3.8(10)-78	Escherichia coli	b4234	[pn:x] [gn:yga]
CONTIG486	4947281_f1_36	3265	8927	468	156	318	1.2(10)-28	Escherichia coli	b4223	[pn:ile repressor protein] [gn:yjfa]
CONTIG486	4410943_f1_51	3266	8928	567	189	681	4.0(10)-67	Escherichia coli	b4216	[pn:f18] [gn:ytfj]
CONTIG486	3219057_f1_54	3267	8929	2073	691	2954	0	Escherichia coli	b4213	[pn:2'''',3'''',cyclic-nucleotide 2'''',phosphodiesterase] [gn:cpdb]
CONTIG486	5133512_f2_59	3268	8930	2151	717	3486	0	Escherichia coli	b4238	[pn:anaerobic ribonucleoside-triphosphate reductase] [gn:nrdl]
CONTIG486	15080013_f2_78	3269	8931	1050	350	1627	2.2(10)-167	Escherichia coli	b4232	[pn:fructose-1,6-bisphosphatase] [gn:fbp]
CONTIG486	36536467_f2_87	3270	8932	630	210	899	3.2(10)-90	Escherichia coli	b4226	[pn:pyrophosphate phospho] [gn:ppa]
CONTIG486	32210956_f2_102	3271	8933	672	224	910	2.2(10)-91	Escherichia coli	b4219	[pn:peptide methionine sulfoxide reductase] [gn:msra]
CONTIG486	24228382_f3_156	3272	8934	1341	447	1948	2.2(10)-201	Escherichia coli	b4218	[pn:hypothetical 49.8 kd protein in cysq-msra intergenic region]
CONTIG486	26460400_c1_163	3273	8935	225	75	335	1.8(10)-30	Escherichia coli	b4217	[pn:hypothetical 9.6 kd protein in cysq-msra intergenic region] [gn:ytfk]
CONTIG486	275252_c1_167	3274	8936	2940	980	4140	0	Escherichia coli	b4221	[pn:hypothetical 136.8 kd protein in msra-chpb intergenic region] [gn:ytfh]
CONTIG486	25439541_c1_168	3275	8937	834	278	1142	5.7(10)-116	Escherichia coli	b4221	[pn:hypothetical 136.8 kd protein in msra-chpb intergenic region] [gn:ytfh]
CONTIG486	32507077_c1_174	3276	8938	1053	351	1069	3.1(10)-108	Escherichia coli	b4230	[pn:hypothetical 35.7 kd protein in ppa-fbp intergenic region] [gn:ytfi]
CONTIG486	2050705_c1_192	3277	8939	1209	403	332	3.8(10)-30	Bacillus subtilis	ykgB	[pn:hypothetical protein]

CONTIG486	14165878_c2_209	3278	8940	774	258	1110	1.3(10)-112	Escherichia coli	b4214	[pn:cysq protein] [gn:cysq]
CONTIG486	35162813_c2_216	3279	8941	1860	620	2678	9.8(10)-279	Escherichia coli	b4220	[pn:hypothetical 64.8 kd protein in msra-chpbi intergenic region] [gn:yffm]
CONTIG486	11027152_c2_222	3280	8942	1089	363	1366	1.1(10)-139	Escherichia coli	b4231	[pn:hypothetical 34.0 kd protein in ppa-fbp intergenic region] [gn:yfff]
CONTIG486	2775841_c2_223	3281	8943	1623	541	863	2.1(10)-86	Escherichia coli	b1886	[pn:methyl-accepting chemotaxis protein ii] [gn:tar]
CONTIG486	4556516_c2_226	3282	8944	1377	459	2270	1.7(10)-235	Escherichia coli	b4233	[pn:hypothetical 48.5 kd protein in fbp-pmba intergenic region]
CONTIG486	17057035_c2_235	3283	8945	1176	392	102	0.019	Escherichia coli	b0512	[pn:hypothetical protein] [gn:ybbx]
CONTIG486	25973588_c2_239	3284	8946	1923	641	567	4.9(10)-55	Bacillus subtilis	licR	[pn:transcriptional regulator] [gn:celr]
CONTIG486	4818753_c3_259	3285	8947	354	118	554	1.2(10)-53	Escherichia coli	b4222	[pn:hypothetical 12.9 kd protein in msra-chpbi intergenic region] [gn:ytfp]
CONTIG486	26054762_c3_261	3286	8948	1104	368	1511	4.5(10)-155	Escherichia coli	b4227	[pn:c318] [gn:ytfq]
CONTIG486	31719406_c3_262	3287	8949	1614	538	1694	1.8(10)-174	Escherichia coli	b4228	[pn:hypothetical abc transporter in ppa-fbp intergenic region] [gn:ytftr]
CONTIG486	3401562_c3_268	3288	8950	1434	478	2089	2.6(10)-216	Escherichia coli	b4235	[pn:pmba protein] [gn:pmba]
CONTIG486	23697183_c3_269	3289	8951	390	130	376	8.5(10)-35	Escherichia coli	b4236	[pn:cytochrome b562] [gn:cybc]
CONTIG486	36520331_c3_274	3290	8952	1140	380	140	1.3(10)-6	Haemophilus influenzae	HI0708	[pn:l-seryl-tna] [gn:sela]
CONTIG487	4689187_fl_1	3291	8953	789	263	1065	8.3(10)-108	Escherichia coli	b3364	[pn:hypothetical 43.2 kd protein in ppia-nirb intergenic region]
CONTIG487	35626332_fl_4	3292	8954	360	120	481	6.4(10)-46	Escherichia coli	b3366	[pn:nadph small subunit] [gn:nird]
CONTIG487	6439205_fl_31	3293	8955	756	252	1041	2.8(10)-105	Escherichia coli	b3399	[pn:hypothetical 27.1 kd protein in mrca-pcka intergenic region] [gn:yrfg]
CONTIG487	26612631_fl_44	3294	8956	249	83	335	1.8(10)-30	Escherichia coli	b3408	[pn:ferrous iron transport protein a] [gn:feoal]
CONTIG487	35816686_fl_45	3295	8957	2349	783	3358	0	Escherichia coli	b3409	[pn:ferrous iron transport protein b] [gn:feob]

CONTIG487	4039033_f1_47	3296	8958	585	195	962	6.7(10)-97	Escherichia coli	b3414	[pn:hypothetical 21.0 kd protein in bioh-gntt intergenic region]
CONTIG487	30331875_f2_49	3297	8959	747	249	647	1.6(10)-63	Escherichia coli	b3364	[pn:hypothetical 43.2 kd protein in ppia-nirb intergenic region]
CONTIG487	25517283_f2_50	3298	8960	2469	823	3923	0	Escherichia coli	b3365	[pn:nadh-nitrate oxidoreductase apoprotein] [gn:nirb]
CONTIG487	22696061_f2_53	3299	8961	183	61	155	2.2(10)-11	Escherichia coli	b3369	[pn:hypothetical 5.8 kd protein in cysg-trps intergenic region] [gn:yhfl]
CONTIG487	15652152_f2_70	3300	8962	2625	875	3985	0	Escherichia coli	b3396	[pn:mrea]
CONTIG487	29926075_f2_88	3301	8963	351	117	359	5.4(10)-33	Escherichia coli	b3410	[pn:hypothetical 8.7 kd protein in feob-bioh intergenic region]
CONTIG487	6301518_f3_102	3302	8964	1383	461	2088	3.2(10)-216	Escherichia coli	b3368	[gn:yhgg]
CONTIG487	34199138_f3_122	3303	8965	2151	717	2807	2.1(10)-292	Escherichia coli	b3398	[pn:hypothetical 79.5 kd protein in mrea-pcka intergenic region]
CONTIG487	10573437_f3_123	3304	8966	477	159	545	1.1(10)-52	Escherichia coli	b3400	[gn:yrff]
CONTIG487	15725656_f3_124	3305	8967	903	301	1313	4.4(10)-134	Escherichia coli	b3401	[pn:hypothetical 32.8 kd protein in mrea-pcka intergenic region]
CONTIG487	24785136_f3_129	3306	8968	1677	559	2513	3.0(10)-261	Escherichia coli	b3403	[pn:phosphoenolpyruvate carboxykinase] [gn:pcka]
CONTIG487	14491316_f3_132	3307	8969	801	267	154	3.1(10)-11	Rhizobium sp.	S28675	[pn:hypothetical protein 5 - rhizobium sp. (strain ic3342)]
CONTIG487	32158437_f3_133	3308	8970	654	218	776	3.5(10)-77	Escherichia coli	b3406	[pn:transcription elongation factor greb] [gn:greb]
CONTIG487	16292280_f3_134	3309	8971	2418	806	3440	0	Escherichia coli	b3407	[pn:hypothetical 81.4 kd protein in greb-feoa intergenic region]
CONTIG487	7207652_f3_140	3310	8972	855	285	770	1.5(10)-76	Escherichia coli	b3413	[gn:yhgf]
CONTIG487	6454662_f3_143	3311	8973	1200	400	1635	3.2(10)-168	Escherichia coli	b3415	[pn:hypothetical 27.7 kd protein in bioh-gntt intergenic region]
CONTIG487	32697167_c1_153	3312	8974	1350	450	1961	9.4(10)-203	Escherichia coli	b3404	[pn:high-affinity gluconate transporter] [gn:gnt]
CONTIG487								Escherichia coli		[pn:osmolarity sensor protein envz] [gn:envz]

CONTIG487	10978206_c1_170	3313	8975	486	162	189	2.6(10)-14	Escherichia coli	b3391	[pn:protein transport protein hofq precursor] [gn:hofq]
CONTIG487	9767138_c1_172	3314	8976	642	214	940	1.5(10)-94	Escherichia coli	b3390	[pn:shikimic acid kinase i] [gn:arok]
CONTIG487	31492893_c1_173	3315	8977	1104	368	1535	1.3(10)-157	Escherichia coli	b3389	[pn:3-dehydroquinate synthase] [gn:arob]
CONTIG487	30366667_c1_176	3316	8978	873	291	1187	9.8(10)-121	Escherichia coli	b3387	[pn:dna adenine methylase] [gn:dami]
CONTIG487	23829557_c1_177	3317	8979	699	233	1124	4.5(10)-114	Escherichia coli	b3386	[pn:dod protein] [gn:rpe]
CONTIG487	31886465_c1_180	3318	8980	252	84	90	0.00119	Plasmid R751	L13688	or:plasmid r751 gn:kfra le:2408 re:3466 di:direct sr:plasmid r751 dna
CONTIG487	15040951_c2_196	3319	8981	786	262	1084	8.0(10)-110	Escherichia coli	b3412	[pn:bioh] [gn:bioh]
CONTIG487	5864427_c2_205	3320	8982	834	278	1212	2.2(10)-123	Escherichia coli	b3405	[pn:ompr] [gn:ompr]
CONTIG487	14073292_c2_219	3321	8983	591	197	885	9.9(10)-89	Escherichia coli	b3397	[pn:hypothetical 21.2 kd protein in mrca-pcka intergenic region] [gn:yrfc]
CONTIG487	2207675_c2_223	3322	8984	534	178	172	3.5(10)-13	Escherichia coli	b3394	[pn:hypothetical 20.8 kd protein in hofq-mrca intergenic region] [gn:yrfc]
CONTIG487	4197331_c2_224	3323	8985	456	152	197	7.9(10)-16	Escherichia coli	b3393	[pn:hypothetical 16.8 kd protein in hofq-mrca intergenic region] [gn:yrfb]
CONTIG487	32557191_c2_226	3324	8986	315	105	94	0.00022	Escherichia coli	b3390	[pn:shikimic acid kinase i] [gn:arok]
CONTIG487	23650278_c2_230	3325	8987	765	255	1045	1.1(10)-105	Escherichia coli	b3385	[pn:hypothetical 27.4 kd protein in trps-dod intergenic region] [gn:gph]
CONTIG487	24736537_c3_243	3326	8988	501	167	118	1.8(10)-7	Escherichia coli	D90866	or:escherichia coli pn:d-serine dehydratase transcriptional activator gn:dsdc le:10864 re:11133 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [pir accession number a28674];
CONTIG487	24431563_c3_258	3327	8989	1761	587	950	1.3(10)-95	Escherichia coli	b3402	[pn:hypothetical 64.6 kd protein in mrca-pcka intergenic region] [gn:yhge]

CONTIG487	134667_c3_269	3328	8990	777	259	535	1.2(10)-51	Escherichia coli	b3395	[pn:hypothetical 30.0 kd protein in hofq-mrca intergenic region] [gn:yrfd]
CONTIG487	11720828_c3_270	3329	8991	468	156	295	3.2(10)-26	Escherichia coli	b3392	[pn:hypothetical 16.9 kd protein in hofq-mrca intergenic region] [gn:yrfd]
CONTIG487	35441390_c3_271	3330	8992	1149	383	1180	5.4(10)-120	Escherichia coli	b3391	[pn:protein transport protein hofq precursor] [gn:hofq]
CONTIG487	986077_c3_272	3331	8993	1290	430	902	1.1(10)-105	Escherichia coli	b3388	[pn:damx protein] [gn:damx]
CONTIG487	23556552_c3_273	3332	8994	1008	336	1646	2.2(10)-169	Escherichia coli	b3384	[pn:tryptophanyl-trna synthetase] [gn:trps]
CONTIG488	26458418_f1_32	3333	8995	1638	546	171	7.2(10)-10	Escherichia coli	b0591	[pn:hypothetical membrane protein p43] [gn:ybda]
CONTIG488	5960056_f1_33	3334	8996	846	282	963	5.2(10)-97	Pseudomonas fluorescens	U12537	or:pseudomonas fluorescens pn:esterase lc:248 re:1066 di:direct
CONTIG488	25448950_f1_48	3335	8997	1017	339	119	0.00014	Neisseria gonorrhoeae	AF001598	[de:neisseria gonorrhoeae strain wr302 tex gene, partial cds, 5-methylcytosine methyltransferase (dmh), n6-methyladeninemethyltransferase (damh) and restriction endonuclease (dc") [pn:restriction endonuclease] [gn:dcrh]
CONTIG488	31343942_f2_70	3336	8998	858	286	92	0.094	Pseudomonas alcaligenes	U84154	or:pseudomonas alcaligenes pn:putative transposase subunit gn:orf2 lc:1104 re:2426 di:direct
CONTIG488	26457290_f2_74	3337	8999	1179	393	168	5.0(10)-10	Escherichia coli	b4345	[pn:mrcr protein] [gn:mrcr]
CONTIG488	16023540_f2_78	3338	9000	1035	345	334	2.3(10)-30	Bacillus subtilis	degA	[pn:transcriptional regulator]
CONTIG488	4476702_f3_93	3339	9001	618	206	456	2.7(10)-43	Pseudomonas sp.	AJ000330	[de:pseudomonas sp. dna for styrene catabolism genes.] [pn:styrene response regulator] [gn:styr]
CONTIG488	2086630_f3_108	3340	9002	1884	628	393	3.2(10)-36	Bacillus subtilis	ycj	[pn:hypothetical protein]
CONTIG488	21596925_f3_115	3341	9003	2028	676	549	4.0(10)-53	Escherichia coli	b4346	[pn:5-methylcytosine-specific restriction enzyme b] [gn:mcrb]

CONTIG488	3909818_f3_122	3342	9004	1014	338	825	2.2(10)-82	Clostridium longisporum	Q46127	tryptophanyl-trna synthetase (ec 6.1.1.2) (tryptophan--trna ligase) (trps).
CONTIG488	35214849_c1_125	3343	9005	370	123	498	1.0(10)-47	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG488	23930317_c1_134	3344	9006	414	138	101	0.00019	Pseudomonas aeruginosa	Z54213	or:pseudomonas aeruginosa pn:alginate lyase gn:algy le:1820 re:3874 di:direct
CONTIG488	1192705_c1_160	3345	9007	1155	385	1353	2.5(10)-138	Escherichia coli	b1128	[pn:hypothetical protein in pept-phoq intergenic region] [gn:yvfd]
CONTIG488	34647887_c2_169	3346	9008	516	172	186	1.2(10)-14	Vibrio cholerae	S81006	or:vibrio cholerae pn:hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nt 28 kda secreted hydrophilic protein; this sequence unknown,,mtcy164 07,mtcy164 07.
CONTIG488	6725052_c2_174	3347	9009	1113	371	602	9.5(10)-59	Mycobacterium tuberculosis	Z95150	unknown, len
CONTIG488	16300816_c2_175	3348	9010	1434	478	425	5.5(10)-40	Bacillus subtilis	yjmB	[pn:hypothetical protein]
CONTIG488	25892702_c2_189	3349	9011	468	156	151	5.9(10)-11	Haemophilus influenzae	H10884	[pn:aerobic respiration control protein arca] [gn:arca]
CONTIG488	5338193_c2_190	3350	9012	5595	1865	235	1.0(10)-15	Bacillus subtilis	yloP	[pn:hypothetical protein]
CONTIG488	16586458_c2_192	3351	9013	630	210	406	5.7(10)-38	Bacillus subtilis	clpP	[pn:class iii heat-shock protein] [gn:yvvdn]
CONTIG488	884575_c2_194	3352	9014	1017	339	307	1.7(10)-27	Bordetella pertussis	AF018255	[de:bordetella pertussis alcaligin siderophore system regulator (aler)gene, complete cds.] [pn:aler] [gn:aler] [nt:member of arae family; regulator of alcaligin]
CONTIG488	5908451_c3_195	3353	9015	279	93	327	1.3(10)-29	Escherichia coli	b4308	[pn:hypothetical 38.0 kd protein in feci-fimb intergenic region] [gn:yjhr]
CONTIG488	4071963_c3_197	3354	9016	477	159	95	0.00013	Escherichia coli	b4347	[pn:hypothetical 14.6 kd protein in mcrb-hsds intergenic region] [gn:yjiw]

CONTIG488	15814391_c3_203	3355	9017	612	204	734	9.9(10)-73	Escherichia coli	A60635	glutathione transferase (ec 2.5.1.18), fosfomycin-modifying -escherichia coli plasmid psu961 transposon tn2921 this enzyme inactivates the antibiotic phosphomycin by opening the epoxide ring and creating an adduct with glutathione.
CONTIG488	10271881_c3_220	3356	9018	711	237	259	2.1(10)-22	Escherichia coli	b0897	[pn:hypothetical 23.1 kd protein in dm5c 3'''region] [gn:yeac]
CONTIG488	2037813_c3_233	3357	9019	2112	704	1451	1.0(10)-148	Erwinia amylovora	AJ223062	[de:erwinia amylovora foxr gene.] [pn:ferrioxamine receptor] [gn:foxr]
CONTIG489	7120253_f1_1	3358	9020	1143	381	1780	1.3(10)-183	Escherichia coli	b2097	[pn:hypothetical protein]
CONTIG489	17065668_f1_38	3359	9021	618	206	936	3.8(10)-94	Escherichia coli	b2065	[pn:deoxycytidine triphosphate deaminase] [gn:dcd]
CONTIG489	22299168_f1_45	3360	9022	2235	745	2883	1.8(10)-300	Escherichia coli	b2060	[pn:hypothetical protein]
CONTIG489	36407341_f1_47	3361	9023	510	170	780	1.3(10)-77	Escherichia coli	b2058	[pn:putative acetyl transferase] [gn:wca]
CONTIG489	14163325_f1_49	3362	9024	1116	372	1176	1.3(10)-119	Escherichia coli	b2056	[pn:hypothetical protein] [gn:wca]
CONTIG489	24650305_f2_74	3363	9025	1140	380	1771	1.3(10)-182	Escherichia coli	b2062	[pn:hypothetical protein] [gn:wza]
CONTIG489	1213533_f2_75	3364	9026	450	150	606	3.6(10)-59	Escherichia coli	b2061	[pn:hypothetical protein] [gn:wzb]
CONTIG489	4101718_f2_79	3365	9027	852	284	1378	5.5(10)-141	Escherichia coli	b2059	[pn:hypothetical protein] [gn:wca]
CONTIG489	4782830_f3_108	3366	9028	1020	340	1061	2.2(10)-107	Escherichia coli	b2068	[pn:dna-3-methyladenine glycosidase ii] [gn:alka]
CONTIG489	21900836_f3_113	3367	9029	534	178	95	0.01799	Methanobacterium thermoautotrophicum	MTH954	[pn:atp synthase, subunit b]
CONTIG489	6535041_f3_116	3368	9030	693	231	1071	1.8(10)-108	Escherichia coli	b2066	[pn:uridine kinase] [gn:udk]
CONTIG489	29728317_f3_117	3369	9031	1881	627	2079	2.8(10)-215	Escherichia coli	b2064	[pn:yega] [gn:asma]
CONTIG489	29504766_f3_127	3370	9032	1308	436	1789	1.6(10)-184	Escherichia coli	b2057	[pn:hypothetical protein] [gn:wca]

CONTIG489	24395411_c1_168	3371	9033	1449	483	1938	2.6(10)-200	Escherichia coli	b2078	[pn:sensor protein baes] [gn:baes]
CONTIG489	13906637_c2_191	3372	9034	3417	1139	4069	0	Escherichia coli	b2067	[pn:hypothetical 123.9 kd protein in udk-alka intergenic region] [gn:yegel]
CONTIG489	31844831_c2_194	3373	9035	3186	1062	3946	0	Escherichia coli	b2075	[pn:hypothetical protein]
CONTIG489	10953_c2_195	3374	9036	3078	1026	4028	0	Escherichia coli	b2076	[pn:hypothetical protein]
CONTIG489	2550952_c2_196	3375	9037	1416	472	1529	5.5(10)-157	Escherichia coli	b2077	[pn:hypothetical protein] [gn:yegb]
CONTIG489	650700_c2_197	3376	9038	357	119	91	0.00013	Daucus carota	U47097	or:daucus carota pn:glycine-rich protein le:<1 re:336 di:direct sr:carrot strain=danver half-long
CONTIG489	33628506_c2_202	3377	9039	1386	462	2084	8.6(10)-216	Escherichia coli	b2081	[pn:hypothetical protein] [gn:yegq]
CONTIG489	25635955_c3_216	3378	9040	1629	543	2101	1.3(10)-217	Escherichia coli	b2063	[pn:hypothetical protein]
CONTIG489	10820407_c3_228	3379	9041	1452	484	1977	1.8(10)-204	Escherichia coli	b2069	[pn:yegd]
CONTIG489	14486438_c3_230	3380	9042	1215	405	1533	2.1(10)-157	Escherichia coli	b2074	[pn:hypothetical protein]
CONTIG489	33473136_c3_236	3381	9043	768	256	1094	7.0(10)-111	Escherichia coli	b2079	[pn:transcriptional regulatory protein baer] [gn:baer]
CONTIG489	36523426_c3_241	3382	9044	921	307	1081	1.7(10)-109	Escherichia coli	b2086	[pn:hypothetical protein] [gn:yegs]
CONTIG49	31437686_c1_1	3383	9045	285	95	91	0.00083	Escherichia coli	D90807	or:escherichia coli pn:fusaric acid resistance protein fuse. le:18869 re:19858 di:direct sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:orf_id:o316#23, similar to [swissprot accession]
CONTIG490	32464583_fl_1	3384	9046	1392	464	1788	2.0(10)-184	Escherichia coli	b3035	[pn:tolc] [gn:tolc]
CONTIG490	35644442_fl_2	3385	9047	204	68	160	6.5(10)-12	Escherichia coli	b3036	[pn:hypothetical 9.9 kd protein in tole-ribb/htrp intergenic region]
CONTIG490	3379790_fl_3	3386	9048	1200	400	1939	2.0(10)-200	Escherichia coli	b3038	[pn:hypothetical 45.0 kd protein in tole-ribb/htrp intergenic region] [gn:yegic]

CONTIG490	23632140_f1_6	3387	9049	2532	844	2377	7.7(10)-247	Escherichia coli	b0718	[pn:hypothetical protein]
CONTIG490	4331563_f1_7	3388	9050	771	257	698	6.4(10)-69	Escherichia coli	b0717	[pn:hypothetical protein]
CONTIG490	10672833_f1_31	3389	9051	600	200	350	4.9(10)-32	Bacillus subtilis	ureA	[pn:urease]
CONTIG490	22917040_f1_40	3390	9052	255	85	357	8.8(10)-33	Escherichia coli	b3065	[pn:30s ribosomal subunit protein s21] [gn:rpsu]
CONTIG490	4103953_f1_42	3391	9053	1980	660	2670	6.9(10)-278	Escherichia coli	b3067	[pn:rna polymerase sigma-70 factor] [gn:rpoD]
CONTIG490	554651_f1_44	3392	9054	1203	401	93	0.34999	Escherichia coli	b2592	[pn:clpb protein] [gn:clpb]
CONTIG490	24707030_f2_54	3393	9055	783	261	1044	1.3(10)-105	Escherichia coli	b3037	[pn:hypothetical 24.9 kd protein in tolc-ribb/htrp intergenic region] [gn:ygiB]
CONTIG490	14932812_f2_64	3394	9056	375	125	290	1.1(10)-25	Escherichia coli	b0716	[pn:hypothetical protein]
CONTIG490	32304812_f2_79	3395	9057	1578	526	207	7.4(10)-14	Bacillus subtilis	yfiG	[pn:hypothetical protein]
CONTIG490	35430415_f2_80	3396	9058	846	282	931	1.3(10)-93	Klebsiella aerogenes	Q09063	urease operon ured protein.
CONTIG490	823905_f2_81	3397	9059	399	133	317	1.5(10)-28	Haemophilus influenzae	H10540	[pn:urease beta subunit] [gn:ureb]
CONTIG490	30718912_f2_87	3398	9060	726	242	817	1.6(10)-81	Klebsiella aerogenes	P18318	urease accessory protein uref.
CONTIG490	4097318_f2_88	3399	9061	627	209	691	3.6(10)-68	Helicobacter pylori	HP0068	[pn:urease accessory protein] [gn:ureg]
CONTIG490	9892668_f2_91	3400	9062	1812	604	2662	4.9(10)-277	Escherichia coli	b3066	[pn:dna primase] [gn:dnag]
CONTIG490	4492818_f2_94	3401	9063	504	168	526	1.1(10)-50	Escherichia coli	b3071	[pn:hypothetical protein]
CONTIG490	4539193_f3_102	3402	9064	783	261	1124	4.5(10)-114	Escherichia coli	b3040	[pn:hypothetical 26.5 kd protein in tolc-ribb/htrp intergenic region] [gn:ygie]
CONTIG490	24235787_f3_103	3403	9065	681	227	376	8.5(10)-35	Escherichia coli	b0719	[pn:hypothetical fimbrial-like protein in glta 3'''region] [gn:ybgd]
CONTIG490	36051013_f3_104	3404	9066	741	247	739	2.8(10)-73	Escherichia coli	b0716	[pn:hypothetical protein]

CONTIG490	4797911_f3_107	3405	9067	342	114	424	7.0(10)-40	Escherichia coli	b3042	[pn:hypothetical protein]
CONTIG490	5086400_f3_121	3406	9068	702	234	852	3.1(10)-85	Escherichia coli	b3055	[pn:hypothetical protein in glne-cca intergenic region] [gn:ygim]
CONTIG490	10159776_f3_122	3407	9069	1302	434	1840	6.2(10)-190	Escherichia coli	b3056	[pn:trna nucleotidyltransferase] [gn:cca]
CONTIG490	11882677_f3_124	3408	9070	735	245	921	1.5(10)-92	Escherichia coli	b3059	[pn:hypothetical 22.2 kd protein in bac-a-ttda intergenic region]
CONTIG490	25525287_f3_129	3409	9071	1707	569	1859	6.0(10)-192	Bacillus subtilis	ureC	[pn:urease]
CONTIG490	5119193_f3_130	3410	9072	474	158	405	7.2(10)-38	Klebsiella aerogenes	P18317	urase accessory protein uree.
CONTIG490	23471885_f3_144	3411	9073	888	296	103	0.012	Rhodobacter sphaeroides	AJ000977	[dc:rhodobacter sphaeroides dna for second chemotaxis operon and flanking genes] [pn:transducer-like protein, tpc] [gn:tpc] [nt:tpc shows weak homology to ttpa (formerly orf1) of]
CONTIG490	21692187_c1_148	3412	9074	1644	548	525	1.3(10)-50	Escherichia coli	b4355	[pn:methyl-accepting chemotaxis protein i] [gn:tsr]
CONTIG490	10553811_c1_150	3413	9075	825	275	991	5.7(10)-100	Escherichia coli	b3070	[pn:hypothetical protein]
CONTIG490	33867181_c1_172	3414	9076	390	130	555	9.1(10)-54	Escherichia coli	b3058	[pn:hypothetical 13.6 kd protein in bac-a-ttda intergenic region]
CONTIG490	4114702_c1_173	3415	9077	822	274	1144	3.5(10)-116	Escherichia coli	b3057	[pn:bacitracin resistance protein] [gn:baca]
CONTIG490	10969692_c2_196	3416	9078	1512	504	1862	2.8(10)-192	Escherichia coli	b3072	[pn:aerolaxis receptor protein] [gn:aer]
CONTIG490	26227307_c2_199	3417	9079	519	173	678	8.5(10)-67	Escherichia coli	b3068	[pn:hypothetical protein] [gn:ygif]
CONTIG490	24400916_c2_223	3418	9080	1323	441	1573	1.2(10)-161	Escherichia coli	b3054	[pn:hypothetical 48.4 kd protein in glne-cca intergenic region] [gn:ygif]
CONTIG490	36120650_c2_224	3419	9081	2877	959	3854	0	Escherichia coli	b3053	[pn:adenyl-transferase] [gn:glne]
CONTIG490	24276662_c3_255	3420	9082	1032	344	1552	2.1(10)-159	Escherichia coli	b3064	[pn:hypothetical 36.0 kd protein in ttdb-rpsu intergenic region]
CONTIG490	26578152_c3_282	3421	9083	1449	483	2299	1.3(10)-238	Escherichia coli	b3052	[pn:hypothetical protein]

CONTIG490	13671893_c3_284	3422	9084	666	222	995	2.2(10)-100	Escherichia coli	b3041	[pn:3,4-dihydroxy-2-butanone 4-phosphate synthase] [gn:ribb]
CONTIG490	4470033_c3_291	3423	9085	825	275	1230	2.7(10)-125	Escherichia coli	b3039	[pn:hypothetical 29.9 kd protein in tole-ribb intergenic region] [gn:ygid]
CONTIG491	2223307_f1_1	3424	9086	906	302	170	5.7(10)-11	Bacillus subtilis	ydeE	[pn:hypothetical protein]
CONTIG491	2056402_f1_9	3425	9087	1386	462	951	1.0(10)-95	Synechocystis sp.	S76228	[PN hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG491	25682967_f1_13	3426	9088	1092	364	322	1.8(10)-58	Synechocystis sp	S77535	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG491	30728318_f1_22	3427	9089	681	227	729	3.2(10)-72	Escherichia coli	b1529	[pn:hypothetical protein in marr 5'''region] [gn:ydeb]
CONTIG491	1432191_f1_23	3428	9090	849	283	292	6.7(10)-26	Synechococcus PCC7942	U59236	or:synechococcus pcc7942 pn:unknown le:4337 re:>4953 di:direct nt-orf205
CONTIG491	13158461_f1_25	3429	9091	1428	476	1645	2.8(10)-169	Escherichia coli	b1525	[pn:hypothetical protein]
CONTIG491	24120381_f1_26	3430	9092	948	316	1338	9.8(10)-137	Escherichia coli	b1524	[pn:hypothetical protein] [gn:yneb]
CONTIG491	11069415_f1_27	3431	9093	987	329	225	1.7(10)-18	Escherichia coli	b0385	[pn:hypothetical 41.5 kd protein in psif-proc intergenic region] [gn:yaic]
CONTIG491	4379092_f1_28	3432	9094	1464	488	2225	9.9(10)-231	Escherichia coli	b1521	[pn:altronate oxidoreductase] [gn:uxab]
CONTIG491	32117968_f1_29	3433	9095	963	321	1268	2.6(10)-129	Escherichia coli	b1520	[pn:hypothetical protein]
CONTIG491	30494702_f1_32	3434	9096	1296	432	236	1.0(10)-17	Escherichia coli	b3911	[pn:cpxa] [gn:cpxa]
CONTIG491	29816950_f1_33	3435	9097	1326	442	210	1.1(10)-16	Bacillus subtilis	ykuV	[pn:hypothetical protein]
CONTIG491	4180191_f2_41	3436	9098	1974	658	3043	0	Escherichia coli	b1435	[pn:hypothetical protein]
CONTIG491	4305318_f2_44	3437	9099	420	140	106	7.7(10)-6	Mycobacterium tuberculosis	AL022002	[de:mycobacterium tuberculosis sequence v047] [pn:hypothetical protein mtv047.09c] [gn:mtv047.09c] [nt:mtv047.09c, [pn:hypothetical protein] [gn:n15nr]
CONTIG491	15023916_f2_45	3438	9100	1128	376	926	4.5(10)-93	Bacillus subtilis	yxiG	

CONTIG491	16510187_f2_48	3439	9101	1614	538	412	1.3(10)-38	Methylophilus methylophilus	Y14964	[dc:methylophilus methylophilus fmd, fmd genes and partial fmd gene.] [pn:putative transport protein] [gn:fmd]
CONTIG491	12145260_f2_52	3440	9102	681	227	723	1.3(10)-71	Escherichia coli	b1973	[pn:hypothetical protein]
CONTIG491	14554838_f2_60	3441	9103	825	275	155	3.7(10)-9	Escherichia coli	b1464	[pn:hypothetical 32.3 kd protein in rhse-narv intergenic region] [gn:ydde]
CONTIG491	21721965_f2_64	3442	9104	1653	551	485	2.3(10)-46	Escherichia coli	b1886	[pn:methyl-accepting chemotaxis protein ii] [gn:tar]
CONTIG491	4817693_f2_68	3443	9105	537	179	195	1.3(10)-15	Pseudomonas syringae	P16966	acetyltransferase (ec 2.3.1.-) (tabtoxin resistance protein)
CONTIG491	22479765_f2_72	3444	9106	453	151	262	1.0(10)-22	Acinetobacter calcoaceticus	AF009672	[PN:unknown] [DE:Acinetobacter calcoaceticus ADP1 vanillate demethylase region, vanillate demethylase (vanB) and vanillate demethylase (vanA) genes, complete cds] [NT:putative acetyl transferase; ORF2] [L:E-535] [RE:1002] [DI: complement]
CONTIG491	30118883_f2_75	3445	9107	792	264	503	3.0(10)-48	Escherichia coli	b3405	[pn:ompr] [gn:ompr]
CONTIG491	4429568_f2_80	3446	9108	1302	434	232	4.5(10)-17	Erwinia carotovora	JC1219	polygalacturonase (ec 3.2.1.15) precursor - erwinia carotovora this enzyme plays an important role in plant tissue maceration.
CONTIG491	5972143_f3_84	3447	9109	585	195	600	1.6(10)-58	Escherichia coli	b1434	[pn:hypothetical protein]
CONTIG491	34198965_f3_90	3448	9110	459	153	94	0.035	Caenorhabditis elegans	Z81518	[de:caenorhabditis elegans cosmid f28d9, complete sequence.] [pn:f28d9.a] [nt:protein predicted using genefinder; preliminary]
CONTIG491	992843_f3_96	3449	9111	810	270	319	9.4(10)-29	Escherichia coli	b3455	[pn:high-affinity branched-chain amino acid transport atp-binding protein livg] [gn:livg]
CONTIG491	5370443_f3_97	3450	9112	594	198	299	1.2(10)-26	Escherichia coli	b3454	[pn:high-affinity branched-chain amino acid transport atp-binding] [gn:livf]

CONTIG491	23984767_f3_102	3451	9113	936	312	1014	2.1(10)-102	Escherichia coli	b1533	[pn:hypothetical 28.7 kd protein in marb-dcp intergenic region] [gn:yded]
CONTIG491	29558277_f3_111	3452	9114	513	171	506	1.3(10)-48	Escherichia coli	b1523	[pn:hypothetical protein]
CONTIG491	31677037_f3_115	3453	9115	1074	358	153	1.1(10)-8	Bacillus subtilis	yfmM	[pn:hypothetical protein]
CONTIG491	13697152_f3_121	3454	9116	762	254	291	8.6(10)-26	Bacillus subtilis	fruR	[pn:transcriptional regulator]
CONTIG491	25484625_c1_125	3455	9117	669	223	496	1.6(10)-47	Escherichia coli	b2467	[pn:hypothetical 21.7 kd protein in tktb-narq intergenic region] [gn:yfth]
CONTIG491	22438307_c1_126	3456	9118	783	261	953	6.0(10)-96	Escherichia coli	b1519	[pn:hypothetical protein]
CONTIG491	24737775_c1_148	3457	9119	615	205	96	0.035	Microbacterium ammoniaphilum	X79027	or: microbacterium ammoniaphilum pn: unknown lc-3382 re->4972 di: complement
CONTIG491	12600660_c1_150	3458	9120	912	304	1155	2.3(10)-117	Escherichia coli	b1526	[pn:hypothetical protein] [gn:ynej]
CONTIG491	21593758_c1_156	3459	9121	429	143	633	5.0(10)-62	Escherichia coli	b1531	[pn: multiple antibiotic resistance protein] [gn:mara]
CONTIG491	12986452_c1_173	3460	9122	1011	337	290	1.1(10)-25	Azorhizobium caulinodans	S52856	arac-like protein - azorhizobium caulinodans
CONTIG491	33603452_c1_176	3461	9123	237	79	292	6.7(10)-26	Escherichia coli	b1436	[pn:hypothetical protein]
CONTIG491	12140785_c1_180	3462	9124	1206	402	1035	1.3(10)-104	Escherichia coli	b1433	[pn:hypothetical protein]
CONTIG491	31442539_c2_184	3463	9125	476	158	264	6.2(10)-23	Escherichia coli	b3558	[pn: insertion element is150 hypothetical 33.3 kd protein] [gn:yi5b]
CONTIG491	24785687_c2_197	3464	9126	600	200	113	2.5(10)-5	Bacillus subtilis	ydaF	[pn:hypothetical protein]
CONTIG491	10584683_c2_216	3465	9127	480	160	592	1.1(10)-57	Escherichia coli	b1530	[pn: multiple antibiotic resistance protein] [gn:marr]
CONTIG491	23626905_c2_219	3466	9128	1266	422	917	4.0(10)-92	Escherichia coli	b1534	[pn:hypothetical protein in marb-dcp intergenic region] [gn:ydef]
CONTIG491	35679180_c3_250	3467	9129	801	267	154	2.8(10)-11	Rhizobium sp.	S28675	hypothetical protein 5 - rhizobium sp. (strain ic3342)

CONTIG491	5265668_c3_274	3468	9130	1248	416	1474	3.7(10)-151	Escherichia coli	b1528	[pn:hypothetical protein in marr 5 ^{'''} region] [gn:ydea]
CONTIG491	25897288_c3_276	3469	9131	234	78	142	5.2(10)-10	Escherichia coli	b1532	[pn:multiple antibiotic resistance protein marb] [gn:marb]
CONTIG491	6364437_c3_301	3470	9132	489	163	148	1.0(10)-9	Escherichia coli	b1433	[pn:hypothetical protein]
CONTIG492	16601011_f1_9	3471	9133	369	123	357	8.8(10)-33	Escherichia coli	b1273	[pn:hypothetical 9.4 kd protein in sobh-topa intergenic region]
CONTIG492	25554807_f1_16	3472	9134	1584	528	2099	2.2(10)-217	Escherichia coli	b1264	[pn:anthranilate synthase component ii] [gn:trpc]
CONTIG492	31832017_f1_17	3473	9135	1272	424	1623	6.2(10)-167	Haemophilus influenzae	HI1431	[pn:tryptophan synthase, beta chain] [gn:trpb]
CONTIG492	29687656_f1_23	3474	9136	1050	350	926	4.5(10)-93	Escherichia coli	b1255	[pn:hypothetical protein in tonb-tpa intergenic region] [gn:ycic]
CONTIG492	2032531_f1_25	3475	9137	465	155	485	2.3(10)-46	Haemophilus influenzae	HI0827	[pn:p14 protein]
CONTIG492	46905_f1_43	3476	9138	2745	915	3902	0	Escherichia coli	b1241	[pn:alcohol/acetaldehyde dehydrogenase] [gn:adhe]
CONTIG492	25589537_f2_62	3477	9139	642	214	696	1.1(10)-68	Escherichia coli	b1270	[pn:1 alamin adenosyltransferase] [gn:btur]
CONTIG492	26460037_f2_72	3478	9140	252	84	396	6.5(10)-37	Escherichia coli	b1930	[pn:hypothetical 8.6 kd protein in amya-flie intergenic region]
CONTIG492	23706650_f2_74	3479	9141	564	188	386	7.4(10)-36	Haemophilus influenzae	HI0826	[pn:sp]
CONTIG492	22853333_f2_76	3480	9142	2052	684	1755	6.2(10)-181	Escherichia coli	b0584	[pn:ferrienterobactin receptor precursor] [gn:fepa]
CONTIG492	21720266_f2_80	3481	9143	333	111	449	1.6(10)-42	Escherichia coli	b1251	[pn:hypothetical protein in kch-tonb intergenic region] [gn:ycii]
CONTIG492	32462652_f2_84	3482	9144	1512	504	2392	2.0(10)-248	Escherichia coli	U24201	or:escherichia coli pn:cardiolipin synthase gn:cls le:5896 re:7356 di:direct
CONTIG492	4350461_f2_85	3483	9145	342	114	555	9.1(10)-54	Escherichia coli	b1248	[pn:hypothetical protein]
CONTIG492	26282780_f3_101	3484	9146	654	218	960	1.1(10)-96	Escherichia coli	b1277	[pn:gtp cyclohydrolase ii] [gn:riba]
CONTIG492	6363568_f3_113	3485	9147	771	257	1039	4.7(10)-105	Escherichia coli	b1271	[pn:hypothetical oxidoreductase in blur-sobh intergenic region]
CONTIG492	35807292_f3_119	3486	9148	1653	551	2248	3.6(10)-233	Escherichia coli	b1263	[pn:anthranilate synthase component ii] [gn:trpd]

CONTIG492	15025302_f3_120	3487	9149	1362	454	1894	1.2(10)-195	Escherichia coli	b1262	[pn:indole-3-glycerol phosphate synthase] [gn:trpc]
CONTIG492	2117811_f3_121	3488	9150	861	287	693	2.2(10)-68	Haemophilus influenzae	H11432	[pn:tryptophan synthase alpha subunit] [gn:trpa]
CONTIG492	1448253_f3_122	3489	9151	1227	409	1588	3.1(10)-163	Escherichia coli	b1929	[pn:hypothetical 44.4 kd protein in amya-flie intergenic region] [gn:yede]
CONTIG492	1298500_f3_124	3490	9152	435	145	435	4.7(10)-41	Escherichia coli	b0288	[pn:hypothetical protein]
CONTIG492	9819786_c1_153	3491	9153	351	117	330	6.4(10)-30	Escherichia coli	b1242	[pn:hypothetical protein in adhe-oppa intergenic region] [gn:yche]
CONTIG492	36022511_c1_156	3492	9154	954	318	1349	6.7(10)-138	Escherichia coli	b1244	[pn:oligopeptide transport system permease protein oppb] [gn:oppb]
CONTIG492	16198576_c1_157	3493	9155	921	307	1170	6.2(10)-119	Escherichia coli	b1245	[pn:oligopeptide transport system permease protein] [gn:oppc]
CONTIG492	6720317_c1_200	3494	9156	813	271	924	7.2(10)-93	Escherichia coli	b1278	[pn:phosphatidylglycerophosphatase b] [gn:pgpb]
CONTIG492	3909503_c2_206	3495	9157	471	157	562	1.7(10)-54	Escherichia coli	b1242	[pn:hypothetical protein in adhe-oppa intergenic region] [gn:yche]
CONTIG492	36219783_c2_208	3496	9158	1023	341	1588	3.1(10)-163	Escherichia coli	b1247	[pn:oligopeptide transport atp-binding protein oppf] [gn:oppf]
CONTIG492	495140_c2_209	3497	9159	864	288	175	5.5(10)-12	Bacillus subtilis	yugO	[pn:hypothetical protein]
CONTIG492	880092_c2_212	3498	9160	648	216	104	1.1(10)-5	Plasmid ColE1	J01566	or:plasmid col1 le:3943 re:4362 di:complement sr:plasmid col1 (clone: pew2762 and pmm1.) dna nt:entry exclusion protein 2 (exc2)
CONTIG492	23679576_c2_215	3499	9161	876	292	391	4.4(10)-63	Escherichia coli	b1252	[pn:tonb protein] [gn:tonb]
CONTIG492	25973287_c2_221	3500	9162	654	218	860	4.4(10)-86	Escherichia coli	b1256	[pn:hypothetical 22.9 kd protein in tonb-trpa intergenic region]
CONTIG492	34276692_c2_240	3501	9163	633	211	1025	1.3(10)-103	Escherichia coli	b1267	[pn:hypothetical 24.5 kd protein in trp1-btr intergenic region] [gn:yicio]
CONTIG492	26620277_c2_244	3502	9164	1062	354	1170	6.2(10)-119	Escherichia coli	b1272	[pn:possible protease] [gn:sohb]
CONTIG492	12694152_c2_247	3503	9165	2841	947	4175	0	Escherichia coli	b1276	[pn:aconitate hydratase 1] [gn:acna]
CONTIG492	3911432_c2_250	3504	9166	348	116	342	3.3(10)-31	Escherichia coli	b1279	[pn:hypothetical protein]

CONTIG492	3157830_c2_251	3505	9167	1089	363	1473	4.7(10)-151	Escherichia coli	b1280	[pn:hypothetical protein in pyrF 5' region] [gn:ycim]
CONTIG492	24273561_c3_254	3506	9168	1749	583	2422	1.3(10)-251	Escherichia coli	b1243	[pn:periplasmic oligopeptide-binding protein precursor] [gn:oppa]
CONTIG492	12750790_c3_257	3507	9169	1050	350	1607	3.1(10)-165	Escherichia coli	b1246	[pn:oligopeptide transport atp-binding protein oppd] [gn:oppd]
CONTIG492	15634788_c3_263	3508	9170	639	213	750	2.0(10)-74	Escherichia coli	b1798	[pn:hypothetical protein]
CONTIG492	167000_c3_286	3509	9171	951	317	1262	1.1(10)-128	Escherichia coli	b1266	[pn:hypothetical protein]
CONTIG492	4770943_c3_287	3510	9172	885	295	1355	1.5(10)-138	Escherichia coli	b1269	[pn:hypothetical 32.7 kd protein in trpL-btr intergenic region] [gn:ycil]
CONTIG492	24667178_c3_291	3511	9173	2610	870	4117	0	Escherichia coli	b1274	[pn:dna topoisomerase I, omega protein I] [gn:topa]
CONTIG492	11180402_c3_292	3512	9174	990	330	1557	6.0(10)-160	Escherichia coli	b1275	[pn:cys regulon transcriptional activator] [gn:cysb]
CONTIG493	26306510_fl_4	3513	9175	192	64	213	1.6(10)-17	Escherichia coli	b1259	[pn:hypothetical protein in tonB-trpA intergenic region] [gn:yeig]
CONTIG493	26426302_fl_5	3514	9176	567	189	444	5.2(10)-42	Escherichia coli	U25418	or:escherichia coli gn:ycif le:4030 re:4530 di:direct
CONTIG493	1445785_fl_11	3515	9177	1653	551	870	3.7(10)-87	Streptomyces coelicolor	AJ001206	[de:streptomyces coelicolor a3(2), glycogen metabolism clusterii.]
CONTIG493	554561_fl_16	3516	9178	435	145	415	6.2(10)-39	Escherichia coli	b1536	[pn:putative trehalose synthase]
CONTIG493	22844032_fl_22	3517	9179	573	191	629	1.3(10)-61	Escherichia coli	b2889	[pn:hypothetical 14.1 kd protein in marB-dep intergenic region]
CONTIG493	16174013_fl_32	3518	9180	534	178	848	8.1(10)-85	Escherichia coli	b2895	[pn:hypothetical protein]
CONTIG493	11957058_fl_42	3519	9181	633	211	551	2.3(10)-53	Salmonella typhimurium	U75949	[de:salmonella typhimurium curved dna-binding protein (cbpa) gene andagp (agp) gene, partial cds; operon 1 containing suppressor for copper-sensitivity a (scsa) gene,"]
CONTIG493	4882917_fl_53	3520	9182	903	301	345	1.6(10)-31	Bacillus subtilis	yjqC	[pn:suppressor for copper-sensitivity c] [gn:scsc]
CONTIG493										[pn:hypothetical protein]

CONTIG493	22940910_f2_55	3521	9183	1077	359	910	2.2(10)-91	Pseudomonas aeruginosa	Y10528	[PN:cyanide insensitive terminal oxidase] [GN:cloB] [DE:P.aeruginosa cioA and cioB genes.] [LE:1746] [RE:2753] [DI:direct]
CONTIG493	20111291_f2_62	3522	9184	930	310	784	5.0(10)-78	Bacillus subtilis	yhxD	[pn:hypothetical protein]
CONTIG493	4797186_f2_93	3523	9185	1527	509	2399	3.6(10)-249	Escherichia coli	b2901	[pn:6-phospho-beta-glucosidase bgla] [gn:bgla]
CONTIG493	7300052_f2_97	3524	9186	606	202	322	4.5(10)-29	Haemophilus influenzae	II11115	[pn:thioredoxin]
CONTIG493	16854160_f3_101	3525	9187	921	307	1189	6.0(10)-121	Escherichia coli	b2845	[pn hypothetical protein]
CONTIG493	23626681_f3_103	3526	9188	534	178	769	1.8(10)-76	Escherichia coli	U25423	or:escherichia coli gn:yciC le:4576 re:5082 di:direct
CONTIG493	16814418_f3_105	3527	9189	1452	484	1752	1.3(10)-180	Pseudomonas aeruginosa	Y10528	[PN:cyanide insensitive terminal oxidase] [GN:cloA] [DE:P.aeruginosa cioA and cioB genes.] [LE:276] [RE:1742] [DI:direct]
CONTIG493	26734683_f3_126	3528	9190	999	333	1451	1.0(10)-148	Escherichia coli	b2898	[pn:hypothetical protein] [gn:ygfZ]
CONTIG493	16525765_f3_129	3529	9191	762	254	181	7.5(10)-14	Bacillus subtilis	yfiA	[pn:hypothetical protein]
CONTIG493	17000052_f3_131	3530	9192	375	125	243	1.1(10)-20	Salmonella typhimurium	U75949	[de:salmonella typhimurium curved dna-binding protein (cbpa) gene andagp (agp) gene, partial cds; operon 1 containing suppressor forcopper-sensitivity a (scsa) gene,"] [pn:suppressor for copper-sensitivity a] [gn:scsa]
CONTIG493	13681500_f3_132	3531	9193	2013	671	1246	6.9(10)-173	Salmonella typhimurium	U75949	[de:salmonella typhimurium curved dna-binding protein (cbpa) gene andagp (agp) gene, partial cds; operon 1 containing suppressor forcopper-sensitivity a (scsa) gene,"] [pn:suppressor for copper-sensitivity b] [gn:scsb]

CONTIG493	16148542_c1_140	3532	9194	783	261	1016	1.3(10)-102	Escherichia coli	b2902	[pn:hypothetical oxidoreductase] [gn:ygff]
CONTIG493	5860055_c1_148	3533	9195	687	229	885	9.9(10)-89	Escherichia coli	b2899	[pn:hypothetical protein]
CONTIG493	3260282_c1_154	3534	9196	873	291	1007	1.2(10)-101	Escherichia coli	b2893	[pn:disulfide interchange protein, precursor] [gn:dsbc]
CONTIG493	910312_c1_156	3535	9197	1077	359	1581	1.7(10)-162	Escherichia coli	b2891	[pn:peptide chain release factor 2] [gn:prfb]
CONTIG493	448443_c1_157	3536	9198	1527	509	2300	1.1(10)-238	Escherichia coli	b2890	[pn:lysyl tna synthetase] [gn:lyss]
CONTIG493	6813751_c1_164	3537	9199	636	212	392	1.7(10)-36	Escherichia coli	b0957	[pn:outer membrane protein a] [gn:ompa]
CONTIG493	10320330_c1_169	3538	9200	1035	345	280	1.3(10)-24	Bacillus subtilis	yxnA	[pn:hypothetical protein]
CONTIG493	16971016_c1_180	3539	9201	297	99	343	2.7(10)-31	Escherichia coli	b4126	[pn:hypothetical 8.6 kd protein in dcub-lysu intergenic region]
CONTIG493	2246465_c2_198	3540	9202	282	94	431	1.3(10)-40	Escherichia coli	b2897	[pn:hypothetical protein] [gn:ygy]
CONTIG493	21519790_c2_203	3541	9203	771	257	914	8.3(10)-92	Escherichia coli	b2865	[pn:hypothetical protein]
CONTIG493	23679591_c2_206	3542	9204	702	234	354	1.8(10)-32	Escherichia coli	b0897	[pn:hypothetical 23.1 kd protein in dmec 3'''region] [gn:ycac]
CONTIG493	4103838_c2_217	3543	9205	456	152	142	5.2(10)-10	Bacillus subtilis	ydfR	[pn:hypothetical protein]
CONTIG493	26597818_c2_226	3544	9206	279	93	408	3.5(10)-38	Escherichia coli	b4127	[pn:hypothetical 10.5 kd protein in dcub-lysu intergenic region]
CONTIG493	30365655_c3_228	3545	9207	2958	986	4326	0	Escherichia coli	b2903	[pn:glycine dehydrogenase] [gn:gcvp]
CONTIG493	35726525_c3_244	3546	9208	432	144	478	1.3(10)-45	Escherichia coli	b2896	[pn:hypothetical protein]
CONTIG493	29507090_c3_245	3547	9209	927	309	1341	4.7(10)-137	Escherichia coli	b2894	[pn:site-specific integrase/recombinase, with xerc] [gn:xerd]
CONTIG493	6500302_c3_247	3548	9210	1743	581	2600	1.8(10)-270	Escherichia coli	b2892	[pn:single-stranded dna-specific exonuclease] [gn:recj]
CONTIG493	23476500_c3_252	3549	9211	1260	420	197	7.5(10)-15	Escherichia coli	b2344	[pn:long-chain fatty acid transport protein precursor] [gn:fadl]
CONTIG493	36141327_c3_253	3550	9212	648	216	209	4.2(10)-17	Escherichia coli	b0375	[pn:hypothetical protein] [gn:yaiv]

CONTIG493	12110131_c3_254	3551	9213	2034	678	1566	6.7(10)-161	Escherichia coli	b4083	[pn:hypothetical 73.7 kd protein in fdhF-phn intergenic region]
CONTIG493	807137_c3_257	3552	9214	585	195	426	4.2(10)-40	Escherichia coli	b1537	[pn:hypothetical 18.3 kd protein in marB-dcp intergenic region]
CONTIG494	14860206_f1_2	3553	9215	1092	364	1449	1.7(10)-148	Escherichia coli	b0888	[pn:thioredoxin reductase] [gn:trxb]
CONTIG494	14484500_f1_3	3554	9216	1797	599	2423	1.0(10)-251	Escherichia coli	b0887	[pn:transport atp-binding protein cydd] [gn:cydd]
CONTIG494	34376252_f1_26	3555	9217	819	273	679	6.7(10)-67	Escherichia coli	b0875	[pn:aquaporin 2] [gn:aqp2]
CONTIG494	32659515_f1_27	3556	9218	942	314	1044	1.3(10)-105	Escherichia coli	b0874	[pn:hypothetical protein]
CONTIG494	115887_f1_28	3557	9219	1677	559	2665	2.2(10)-277	Escherichia coli	b0873	[pn:hypothetical protein]
CONTIG494	15745303_f1_65	3558	9220	744	248	1094	7.0(10)-111	Escherichia coli	b0864	[pn:arginine transport atp-binding protein artp] [gn:artp]
CONTIG494	26828515_f1_66	3559	9221	750	250	1117	2.6(10)-113	Escherichia coli	b0863	[pn:arginine-binding periplasmic protein 1 precursor] [gn:artil]
CONTIG494	33714207_f1_68	3560	9222	684	228	975	2.8(10)-98	Escherichia coli	b0861	[pn:arginine transport system permease protein artm] [gn:artm]
CONTIG494	26363577_f2_79	3561	9223	219	73	362	2.6(10)-33	Escherichia coli	b0884	[pn:initiation factor if-1] [gn:infa]
CONTIG494	14160432_f2_84	3562	9224	288	96	364	1.6(10)-33	Escherichia coli	b0880	[pn:cold shock-like protein cspd] [gn:cspd]
CONTIG494	4114637_f2_89	3563	9225	990	330	743	1.1(10)-73	Escherichia coli	b0877	[pn:hypothetical protein]
CONTIG494	4415901_f2_95	3564	9226	972	324	1441	1.2(10)-147	Escherichia coli	b0872	[pn:hypothetical protein]
CONTIG494	4423318_f2_99	3565	9227	1011	337	1468	1.6(10)-150	Escherichia coli	b0870	[pn:hypothetical protein] [gn:ybjv]
CONTIG494	14642176_f2_102	3566	9228	1110	370	1597	3.5(10)-164	Escherichia coli	b0868	[pn:hypothetical protein]
CONTIG494	12994811_f2_135	3567	9229	696	232	1090	1.8(10)-110	Escherichia coli	b0862	[pn:arginine transport system permease protein artq] [gn:artq]
CONTIG494	2995933_f3_140	3568	9230	1776	592	2045	1.2(10)-211	Escherichia coli	b0886	[pn:transport atp-binding protein cydc] [gn:cydc]
CONTIG494	5865882_f3_141	3569	9231	750	250	1032	2.6(10)-104	Escherichia coli	b0885	[pn:leucyl/phenylalanyl-trna--protein transferase] [gn:aat]

CONTIG494	15117842_f3_159	3570	9232	1734	578	2699	5.9(10)-281	Escherichia coli	b0871	[pn:cytochrome] [gn:poxb]
CONTIG494	33875912_f3_161	3571	9233	1476	492	2080	2.2(10)-215	Escherichia coli	b0869	[pn:hypothetical protein]
CONTIG494	36597081_f3_183	3572	9234	1818	606	393	2.8(10)-36	Escherichia coli	b3323	[pn:putative general secretion pathway protein b] [gn:yhed]
CONTIG494	23631550_f3_186	3573	9235	540	180	729	3.2(10)-72	Escherichia coli	b0865	[pn:hypothetical protein]
CONTIG494	13150827_c1_199	3574	9236	675	225	177	1.0(10)-13	Escherichia coli	b0375	[pn:hypothetical protein] [gn:yaiv]
CONTIG494	15761437_c1_206	3575	9237	1293	431	847	1.0(10)-84	Escherichia coli	b3327	[pn:putative general secretion pathway protein f] [gn:hoff]
CONTIG494	134652_c1_207	3576	9238	453	151	474	3.5(10)-45	Escherichia coli	b3328	[pn:putative general secretion pathway protein g precursor] [gn:hofg]
CONTIG494	16838437_c1_208	3577	9239	387	129	144	3.2(10)-10	Escherichia coli	b3330	[pn:putative general secretion pathway protein i precursor] [gn:yheh]
CONTIG494	32632827_c1_212	3578	9240	486	162	102	0.00013	Escherichia coli	b3334	[pn:putative general secretion pathway protein m] [gn:pshml]
CONTIG494	26735627_c1_213	3579	9241	2721	907	2118	7.2(10)-248	Aeromonas caviae	U09139	or:aeromonas caviae pn:chitinase protein precursor le:154 re:2751 di:direct
CONTIG494	30664092_c1_230	3580	9242	1689	563	2468	1.8(10)-256	Escherichia coli	b0876	[pn:hypothetical protein]
CONTIG494	16975466_c1_248	3581	9243	210	70	172	3.5(10)-13	Escherichia coli	b0889	[pn:leucine-responsive regulatory protein] [gn:lrp]
CONTIG494	32055135_c2_255	3582	9244	909	303	1016	1.3(10)-102	Escherichia coli	b0867	[pn:hypothetical protein]
CONTIG494	1447187_c2_263	3583	9245	777	259	155	1.5(10)-9	Escherichia coli	b3324	[pn:putative general secretion pathway protein c] [gn:yhec]
CONTIG494	32694192_c2_265	3584	9246	1500	500	1407	4.7(10)-144	Escherichia coli	b3326	[pn:type ii traffic] [gn:yheg]
CONTIG494	36222885_c2_268	3585	9247	1116	372	285	3.7(10)-25	Escherichia coli	b3332	[pn:putative general secretion pathway protein k] [gn:yhej]
CONTIG494	24641037_c2_269	3586	9248	1140	380	307	1.7(10)-27	Escherichia coli	b3333	[pn:putative general secretion pathway protein l] [gn:yhek]

CONTIG494	24726625_c2_276	3587	9249	1845	615	299	6.2(10)-26	Oryza sativa	L37289	or:oryza sativa pn:chitinase ec:3.2.1.14 le:43 re:1044 di:direct sr:oryza sativa (strain ir36) seedling etiolated leaf cdna to mrna
CONTIG494	21767817_c2_299	3588	9250	1980	660	2714	1.5(10)-282	Escherichia coli	b0879	[pn:hypothetical protein]
CONTIG494	26449052_c3_323	3589	9251	339	113	493	3.3(10)-47	Escherichia coli	b0866	[pn:hypothetical protein]
CONTIG494	24015932_c3_328	3590	9252	1944	648	1216	8.3(10)-124	Escherichia coli	b3325	[pn:putative general secretion pathway protein d precursor] [gn:yhef]
CONTIG494	4899063_c3_332	3591	9253	498	166	158	1.1(10)-11	Escherichia coli	b3329	[pn:putative general secretion pathway protein h precursor] [gn:hofh]
CONTIG494	35678963_c3_334	3592	9254	708	236	142	5.2(10)-10	Escherichia coli	b3331	[pn:putative general secretion pathway protein j precursor] [gn:yhef]
CONTIG494	32594556_c3_336	3593	9255	849	283	366	9.8(10)-34	Escherichia coli	b2972	[pn:hypothetical protein]
CONTIG494	21672156_c3_337	3594	9256	537	179	208	5.4(10)-17	Escherichia coli	b2854	[pn:hypothetical protein]
CONTIG494	2914181_c3_353	3595	9257	1140	380	1393	1.5(10)-142	Escherichia coli	b0878	[pn:hypothetical protein]
CONTIG494	32507211_c3_355	3596	9258	393	131	528	6.7(10)-51	Escherichia coli	b0881	[pn:hypothetical protein] [gn:yjja]
CONTIG494	975293_c3_356	3597	9259	2304	768	3480	0	Escherichia coli	b0882	[pn:atp-dependent clp protease atp- binding subunit clpa] [gn:clpa]
CONTIG495	11724086_fl_17	3598	9260	618	206	772	9.3(10)-77	Escherichia coli	b3465	[pn:hypothetical 21.7 kd protein in fts-y-nika intergenic region]
CONTIG495	20976555_fl_25	3599	9261	681	227	999	8.1(10)-101	Escherichia coli	b3471	[pn:hypothetical 25.3 kd protein in fts-y-nika intergenic region]
CONTIG495	13095332_fl_26	3600	9262	600	200	874	1.3(10)-87	Escherichia coli	b3472	[pn:hypothetical protein]
CONTIG495	32300666_fl_27	3601	9263	1113	371	1421	1.6(10)-145	Escherichia coli	b3474	[pn:hypothetical 38.5 kd protein in fts-y-nika intergenic region] [gn:yhht]
CONTIG495	5195317_fl_32	3602	9264	1356	452	120	0.0032	Bacillus subtilis	srfAB	[pn:surfactin synthetase] [gn:com]

CONTIG495	22369816_f1_34	3603	9265	1728	576	173	2.6(10)-12	Methanobacterium thermoautotrophicum	MTH136	[pn:dolichyl-phosphate mannose synthase]
CONTIG495	14869217_f1_35	3604	9266	426	142	119	1.5(10)-7	Bacillus subtilis	yneP	[pn:hypothetical protein]
CONTIG495	16912907_f1_38	3605	9267	1251	417	354	1.8(10)-32	Escherichia coli	b1095	[pn:3-oxoacyl-acyl-carrier-protein synthase ii] [gn:fabf]
CONTIG495	10626391_f1_39	3606	9268	330	110	96	0.00289	Homo sapiens	AF004884	[PN:neuronal calcium channel alpha 1A subunit] [SR:human] [DE:Homo sapiens neuronal calcium channel alpha 1A subunit isoform A-1mRNA, complete cds.] [LE:237] [RE:7769] [DI-direct]
CONTIG495	15808466_f1_40	3607	9269	1242	414	624	4.5(10)-61	Bacillus subtilis	yjaY	[pn:hypothetical protein]
CONTIG495	14229752_f2_48	3608	9270	432	144	498	1.0(10)-47	Escherichia coli	b3459	[pn:hypothetical 14.5 kd protein in livk-livj intergenic region] [gn:yhhk]
CONTIG495	24619625_f2_58	3609	9271	408	136	341	4.4(10)-31	Escherichia coli	b3466	[pn:hypothetical 10.3 kd protein in ftsy-nika intergenic region] [gn:yhlh]
CONTIG495	10644062_f2_60	3610	9272	753	251	833	3.2(10)-83	Escherichia coli	b3468	[pn:hypothetical protein] [gn:yhhn]
CONTIG495	16269817_f2_71	3611	9273	921	307	122	1.3(10)-5	Helicobacter pylori	HP1348	[pn:1-acyl-glycerol-3-phosphate acyltransferase] [gn:plsc]
CONTIG495	11064191_f2_72	3612	9274	330	110	94	6.5(10)-5	Helicobacter pylori	HP0559	[pn:acyl carrier protein] [gn:acpp]
CONTIG495	31347015_f2_82	3613	9275	813	271	400	2.3(10)-37	Bacillus subtilis	fabG	[pn:3-oxoacyl-acyl-carrier protein reductase] [gn:ylpf]
CONTIG495	4884707_f2_86	3614	9276	798	266	552	1.8(10)-53	Bacillus subtilis	yvaG	[pn:hypothetical protein]
CONTIG495	2071916_f3_103	3615	9277	2244	748	2482	5.7(10)-258	Escherichia coli	b3469	[pn:hypothetical protein] [gn:yhho]
CONTIG495	447686_f3_113	3616	9278	291	97	92	0.00011	Leuconthrix mucor	P80920	
CONTIG495	13016416_f3_120	3617	9279	384	128	95	0.00034	Streptomyces fradiae	P20186	hypothetical 35.5 kd protein in transposon tn4556.

CONTIG495	11924157_f3_129	3618	9280	543	181	107	2.6(10)-5	Brucella abortus	U51683	or:brucella abortus pn:fabz gn:fabz ec:4.2.1-1e:6377 re:6844 di:direct sr:brucella abortus strain=s2308 nt:similar to swiss-prot accession number p21774
CONTIG495	6540832_f3_133	3619	9281	609	203	705	1.2(10)-69	Escherichia coli	b3475	[pn:hypothetical 21.8 kd protein in ftsy-nika intergenic region]
CONTIG495	30104052_f3_135	3620	9282	927	309	225	8.5(10)-19	Escherichia coli	b0504	[pn:hypothetical protein] [gn:ybbs]
CONTIG495	1307918_c1_142	3621	9283	318	106	229	2.2(10)-18	Rhizobium sp.	p50360	hypothetical 29.3 kd protein in region 2 of sym plasmid (no1265).
CONTIG495	20984450_c1_143	3622	9284	468	156	432	9.9(10)-41	Escherichia coli	S70162	,
CONTIG495	29329043_c1_187	3623	9285	699	233	1086	4.9(10)-110	Escherichia coli	b3463	[pn:cell division atp-binding protein ftsf] [gn:ftsif]
CONTIG495	29713291_c1_190	3624	9286	1344	448	1578	3.6(10)-162	Escherichia coli	b1302	[pn:gaba-aminotransferase] [gn:goag]
CONTIG495	4957587_c1_192	3625	9287	336	112	387	5.7(10)-36	Escherichia coli	b3458	[pn:leucine-specific binding protein precursor] [gn:livk]
CONTIG495	10282891_c2_194	3626	9288	1098	366	1388	4.9(10)-142	Plasmid R478	L38824	or:plasmid r478 gn:terc le:2277 re:3317 di:direct sr:plasmid r478 dna nt:putative
CONTIG495	5189842_c2_202	3627	9289	546	182	478	1.3(10)-45	Bacillus subtilis	padC	[pn:ferulate decarboxylase] [gn:yveh]
CONTIG495	14504207_c2_216	3628	9290	246	82	90	0.00017	Haemophilus influenzae	HI1355	[pn:hypothetical protein]
CONTIG495	24271091_c2_227	3629	9291	285	95	391	2.2(10)-36	Escherichia coli	b3470	[pn:hypothetical 9.1 kd protein in ftsy-nika intergenic region]
CONTIG495	21568791_c2_228	3630	9292	1002	334	395	8.3(10)-37	Escherichia coli	b3579	[pn:hypothetical 36.0 kd protein in avia-selb intergenic region] [gn:yiao]
CONTIG495	32086658_c2_229	3631	9293	522	174	114	5.0(10)-7	Haemophilus influenzae	HI1030	[pn:sp]
CONTIG495	16838955_c2_240	3632	9294	1467	489	1423	1.3(10)-152	Escherichia coli	b3464	[pn:cell division protein ftsy] [gn:ftsif]
CONTIG495	4587833_c2_241	3633	9295	1083	361	1361	3.6(10)-139	Escherichia coli	b3462	[pn:cell division protein ftsx] [gn:ftsif]
CONTIG495	15837807_c3_277	3634	9296	1290	430	548	5.0(10)-53	Haemophilus influenzae	HI1029	[pn:sp]

CONTIG495	9767340_c3_283	3635	9297	369	123	211	2.6(10)-17	Escherichia coli	b3467	[pn:hypothetical 13.5 kd protein in flsy-nika intergenic region] [gn:yhhm]
CONTIG495	26363452_c3_287	3636	9298	858	286	1211	2.7(10)-123	Escherichia coli	b3461	[pn:rna polymerase sigma-32 subunit] [gn:rpoh]
CONTIG495	3257762_c3_291	3637	9299	1164	388	1772	1.0(10)-182	Escherichia coli	b3460	[pn:ileu/ile/val-binding protein precursor] [gn:livj]
CONTIG496	4304068_f1_8	3638	9300	2394	798	680	5.2(10)-67	Porphyromonas gingivalis	P49008	beta-hexosaminidase precursor (cc 3.1.52) (n-acetyl-beta-glucosaminidase) (beta-glcnaase) (beta-n-acetylhexosaminidase) (beta-nahase).
CONTIG496	29589130_f1_21	3639	9301	468	156	670	6.0(10)-66	Escherichia coli	b4252	[pn:hypothetical 17.3 kd protein in pyl-argi intergenic region] [gn:yjgk]
CONTIG496	24353408_f1_32	3640	9302	429	143	358	6.9(10)-33	Escherichia coli	b4255	[pn:hypothetical 15.6 kd protein in argi-vals intergenic region] [gn:yjgd]
CONTIG496	30369653_f1_49	3641	9303	3330	1110	1018	7.9(10)-103	Escherichia coli	b4308	[pn:hypothetical 38.0 kd protein in feci-fimb intergenic region] [gn:yjhr]
CONTIG496	23609515_f1_50	3642	9304	294	98	419	2.3(10)-39	Enterobacter agglomerans	A38965	hypothetical protein a (insertion sequence is1222) -enterobacter agglomerans
CONTIG496	3381711_f2_55	3643	9305	2775	925	3895	0	Escherichia coli	b4242	[pn:mg2+ transport apase, p-type 1] [gn:mgia]
CONTIG496	25522918_f2_76	3644	9306	2025	675	3216	0	Escherichia coli	b0269	[pn:hypothetical 69.4 kd protein in per-argf intergenic region] [gn:yagf]
CONTIG496	30332633_f2_81	3645	9307	1725	575	2884	1.5(10)-300	Escherichia coli	b0271	[pn:hypothetical protein] [gn:yagh]
CONTIG496	34480032_f2_86	3646	9308	936	312	1124	4.5(10)-114	Salmonella typhimurium	Q08015	trna-(ms2)io[6]a-hydroxylase (ec 1.-.-).
CONTIG496	3984643_f3_102	3647	9309	489	163	183	2.3(10)-14	Vibrio cholerae	S81006	or:vibrio cholerae pn.hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nt:28 kda secreted hydrophilic protein; this sequence

CONTIG496	954637_f3_104	3648	9310	222	74	100	1.5(10)-5	Escherichia coli	ID21157	[PN:unknown] [SR:Escherichia coli (sub_strain W3110, strain K-12) (library: librar] [DE:E.coli gene for unknown product, partial cds.] [NT:the coding frame was determined by the Lac fusion] [LE:57] [RE:192] [DI:direct]
CONTIG496	4470443_f3_123	3649	9311	918	306	1207	7.4(10)-123	Escherichia coli	b0268	[pn:hypothetical 33.3 kd protein in per-argf intergenic region]
CONTIG496	2849025_f3_126	3650	9312	1413	471	2155	2.6(10)-223	Escherichia coli	b0270	[pn:hypothetical 50.6 kd protein in per-argf intergenic region]
CONTIG496	9896067_f3_151	3651	9313	186	62	196	1.0(10)-15	Enterobacter agglomerans	B38965	hypothetical protein b (insertion sequence is1222) -enterobacter agglomerans
CONTIG496	26370678_c1_160	3652	9314	1488	496	2397	5.9(10)-249	Escherichia coli	I41293	ecoe type i restriction modification enzyme m subunit -escherichia coli
CONTIG496	29863508_c1_183	3653	9315	951	317	739	2.8(10)-73	Haemophilus influenzae	HI0595	[pn:carbamate kinase] [gn:arec]
CONTIG496	11214091_c1_185	3654	9316	1551	517	756	4.0(10)-83	Haemophilus influenzae	HI0594	[pn:hypothetical protein]
CONTIG496	33603340_c1_195	3655	9317	300	100	94	6.5(10)-5	Saccharomyces cerevisiae	X85757	or:saccharomyces cerevisiae pn:unknown gn:internal orf g1669 le:6964 re:7365 di:direct sr:baker's yeast
CONTIG496	6251280_c2_204	3656	9318	2466	822	3981	0	Escherichia coli	I41292	ecoe type i restriction-modification enzyme r subunit -escherichia coli
CONTIG496	2599015_c2_216	3657	9319	915	305	1072	1.5(10)-108	Escherichia coli	b0272	[pn:hypothetical transcriptional regulator in per-argf intergenic region] [gn:yagi]
CONTIG496	31328187_c2_226	3658	9320	1014	338	759	2.2(10)-75	Escherichia coli	U70214	or:escherichia coli le:112561 re:113301 di:complement nt.similar to e. coli yjhh
CONTIG496	21954407_c2_234	3659	9321	993	331	1409	2.8(10)-144	Escherichia coli	b4245	[pn:aspartate carbomoyltransferase catalytic subunit] [gn:pyrb]
CONTIG496	14964218_c2_235	3660	9322	474	158	679	6.7(10)-67	Escherichia coli	b4244	[pn:aspartate carbomoyltransferase regulatory subunit] [gn:pyri]
CONTIG496	32547931_c3_258	3661	9323	1794	598	1274	5.9(10)-130	Citrobacter freundii	X17591	or:citrobacter freundii pn:hds polypeptide, part of cfr family gn:hds le:234 re:1970 di:direct

CONTIG496	30657775_c3_266	3662	9324	1038	346	1701	3.2(10)-175	Escherichia coli	b0273	[pn:ornithine carbamoyltransferase chain f] [gn:argf]
CONTIG496	24347205_c3_275	3663	9325	213	71	117	6.2(10)-7	Escherichia coli	U70214	or:escherichia coli lc:112561 re:113301 di:complement nt:similar to e. coli yjhh
CONTIG496	4469557_c3_276	3664	9326	1275	425	912	1.3(10)-91	Pseudomonas aeruginosa	P13981	arginine deiminase (ec 3.5.3.6).
CONTIG496	24406311_c3_279	3665	9327	1026	342	1230	2.7(10)-125	Escherichia coli	b4254	[pn:ornithine carbamoyltransferase] [gn:argi]
CONTIG496	10329756_c3_283	3666	9328	708	236	206	8.8(10)-17	Escherichia coli	b3237	[pn:arginine repressor] [gn:argr]
CONTIG496	9955041_c3_285	3667	9329	408	136	642	5.5(10)-63	Escherichia coli	b4243	[pn 13 5 kd protein in mgta-pyri intergenic region] [gn:yjgf]
CONTIG496	10179702_c3_286	3668	9330	1449	483	377	6.7(10)-35	Streptomyces olivaceoviridis	S55000	alpha-chitin binding protein precursor - streptomycetolivaccoviridis (strain [pn.trehalose operon repressor] [gn.trer])
CONTIG496	31406300_c3_297	3669	9331	978	326	1381	2.7(10)-141	Escherichia coli	b4241	[pn:serine hydroxymethyltransferase] [gn:glya]
CONTIG497	26736576_f1_1	3670	9332	1272	424	1955	4.0(10)-202	Escherichia coli	b2551	[pn:hypothetical protein] [gn:yfhs]
CONTIG497	25969791_f1_2	3671	9333	1206	402	1637	2.0(10)-168	Escherichia coli	b2536	
CONTIG497	4181268_f1_15	3672	9334	333	111	452	7.5(10)-43	Escherichia coli	b2528	[pn:hypothetical protein in hscA 5'''region] [gn:yfhf]
CONTIG497	34235307_f1_17	3673	9335	1896	632	2657	1.7(10)-276	Escherichia coli	b2526	[pn:heat shock protein hscA] [gn:hscA]
CONTIG497	12397806_f1_27	3674	9336	4983	1661	6480	0	Escherichia coli	b2520	[pn:hypothetical protein]
CONTIG497	11953427_f1_43	3675	9337	535	179	637	1.8(10)-62	Escherichia coli	b2512	[pn:hypothetical protein]
CONTIG497	16266057_f2_47	3676	9338	1008	336	406	5.7(10)-38	Haemophilus influenzae	HI1248	[pn:hypothetical protein]
CONTIG497	12219836_f2_50	3677	9339	537	179	789	1.5(10)-78	Escherichia coli	b2527	[pn:hypothetical 20.1 kd protein in hscA 5'''region] [gn:yfhe]
CONTIG497	11988587_f2_52	3678	9340	363	121	539	4.5(10)-52	Escherichia coli	b2525	[pn:ferredoxin, 2fe-2s] [gn:fdx]
CONTIG497	31650080_f2_70	3679	9341	2343	781	3091	0	Escherichia coli	b2519	[pn:hypothetical protein] [gn:pbpc]

CONTIG497	21759667_f2_72	3680	9342	633	211	585	6.0(10)-57	Escherichia coli	b0895	[pn:anaerobic dimethyl sulfoxide reductase chain b] [gn:dmsb]
CONTIG497	15751633_f2_74	3681	9343	912	304	126	1.5(10)-7	Methanobacterium thermoautotrophicum	MTH1241	[pn:polyferredoxin]
CONTIG497	4805165_f2_76	3682	9344	1170	390	1691	3.7(10)-174	Escherichia coli	b2515	[pn:gcpe protein] [gn:gcpc]
CONTIG497	879700_f2_77	3683	9345	1323	441	2088	3.2(10)-216	Escherichia coli	b2514	[pn:histidyl-trna synthetase] [gn:hiss]
CONTIG497	22479766_f3_82	3684	9346	651	217	356	1.1(10)-32	Haemophilus influenzae	HI1249	[pn:hypothetical protein precursor]
CONTIG497	31464586_f3_85	3685	9347	807	269	1032	2.6(10)-104	Escherichia coli	b2532	[pn:hypothetical protein]
CONTIG497	3009663_f3_86	3686	9348	495	165	640	9.0(10)-63	Escherichia coli	b2531	[pn:hypothetical protein]
CONTIG497	4956303_f3_87	3687	9349	1320	440	2020	5.2(10)-209	Escherichia coli	b2530	[pn:hypothetical protein]
CONTIG497	23616080_f3_88	3688	9350	411	137	642	5.5(10)-63	Escherichia coli	b2529	[pn:hypothetical protein]
CONTIG497	5275331_f3_92	3689	9351	264	88	346	1.3(10)-31	Escherichia coli	b2524	[pn:hypothetical 7.7 kd protein in fdx 3'''region] [gn:yfhj]
CONTIG497	34022075_f3_93	3690	9352	1308	436	1833	3.3(10)-189	Escherichia coli	b2523	[pn:hypothetical protein in fdx 3'''region] [gn:yfhi]
CONTIG497	9961718_f3_94	3691	9353	804	268	1144	3.5(10)-116	Escherichia coli	b2522	[pn:sseb protein] [gn:sseb]
CONTIG497	34492187_f3_104	3692	9354	2418	806	1485	2.6(10)-152	Escherichia coli	b1588	[pn:hypothetical protein]
CONTIG497	4557805_f3_106	3693	9355	819	273	133	7.0(10)-7	Escherichia coli	b1590	[pn:hypothetical protein]
CONTIG497	3259683_f3_108	3694	9356	516	172	696	1.1(10)-68	Escherichia coli	b2518	[pn:nucleoside diphosphate kinase] [gn:ndk]
CONTIG497	30267625_f3_109	3695	9357	1311	437	1854	2.0(10)-191	Escherichia coli	b2517	[pn:hypothetical 43.1 kd protein in ndk-gcpe intergenic region]
CONTIG497	13869066_f3_110	3696	9358	1011	337	1100	1.6(10)-111	Escherichia coli	b2516	[pn:hypothetical 36.2 kd protein in ndk-gcpe intergenic region]
CONTIG497	16839666_f3_113	3697	9359	678	226	695	1.3(10)-68	Escherichia coli	b2513	[pn:hypothetical protein]

CONTIG497	24424167_c1_147	3698	9360	951	317	1162	4.4(10)-118	Escherichia coli	b2521	[pn:putative thiosulfate sulfoxidase] [gn:ssaa]
CONTIG497	31879212_c1_163	3699	9361	1353	451	1344	2.2(10)-137	Escherichia coli	b2535	[pn:stationary phase inducible protein csc] [gn:csc]
CONTIG497	10052078_c2_204	3700	9362	1572	524	691	3.6(10)-68	Escherichia coli	b1621	[pn:pts system, maltose and glucose-specific ii abc component] [gn:malx]
CONTIG497	24245462_c2_205	3701	9363	1380	460	1013	2.7(10)-102	Bacillus subtilis	glvA	[pn:6-phospho-alpha-glucosidase] [gn:glvg]
CONTIG497	5180338_c2_223	3702	9364	813	271	1258	2.8(10)-128	Escherichia coli	b2533	[pn:extragenic suppressor protein subb] [gn:subb]
CONTIG497	13705037_c2_229	3703	9365	468	156	583	9.9(10)-57	Escherichia coli	b2543	[pn:hypothetical protein]
CONTIG497	4896032_c3_266	3704	9366	783	261	137	3.0(10)-7	Bacillus subtilis	ybbH	[pn:hypothetical protein]
CONTIG498	5947212_f1_1	3705	9367	447	149	651	6.2(10)-64	Escherichia coli	b1778	[pn:hypothetical protein] [gn:yeaa]
CONTIG498	16228431_f1_6	3706	9368	555	185	729	3.2(10)-72	Escherichia coli	b1765	[pn:hypothetical 20 kD protein in seld-sppa intergenic region]
CONTIG498	6336575_f1_8	3707	9369	1926	642	2996	0	Escherichia coli	b1763	[pn:dna topoisomerase iii] [gn:topb]
CONTIG498	24740925_f1_14	3708	9370	636	212	479	1.0(10)-45	Escherichia coli	b1753	[pn:hypothetical protein]
CONTIG498	19535307_f1_22	3709	9371	1251	417	1800	1.1(10)-185	Escherichia coli	b1748	[pn:hypothetical protein] [gn:cstc]
CONTIG498	34039076_f1_34	3710	9372	516	172	491	5.5(10)-47	Escherichia coli	b1743	[pn:hypothetical protein] [gn:spy]
CONTIG498	34567181_f1_39	3711	9373	339	113	454	4.5(10)-43	Escherichia coli	b1738	[pn:pts system, cellobiose-specific iib component] [gn:cela]
CONTIG498	36516660_f1_43	3712	9374	1374	458	2120	1.3(10)-219	Escherichia coli	b1734	[pn:phospho-beta-glucosidase b] [gn:celf]
CONTIG498	14492058_f1_56	3713	9375	570	190	609	1.7(10)-59	Escherichia coli	b1726	[pn:hypothetical protein]
CONTIG498	32539012_f1_60	3714	9376	936	312	1221	2.3(10)-124	Escherichia coli	b1722	[pn:hypothetical protein]
CONTIG498	4876318_f1_62	3715	9377	1938	646	3261	0	Escherichia coli	b1719	[pn:threonyl-tRNA synthetase] [gn:thrs]
CONTIG498	36125268_f1_63	3716	9378	321	107	373	1.8(10)-34	Escherichia coli	b1718	[pn:initiation factor if-3] [gn:inf3]

CONTIG498	33594575_f2_80	3717	9379	705	235	788	1.8(10)-78	Escherichia coli	b1758	[pn:hypothetical protein]
CONTIG498	33789193_f2_88	3718	9380	1500	500	2058	4.9(10)-213	Escherichia coli	b1746	[pn:hypothetical protein]
CONTIG498	32320932_f2_96	3719	9381	360	120	548	5.0(10)-53	Escherichia coli	b1739	[pn:osmotically inducible protein e precursor] [gn:osme]
CONTIG498	5289837_f3_111	3720	9382	291	97	398	4.0(10)-37	Escherichia coli	b1777	[pn:hypothetical protein]
CONTIG498	11057961_f3_120	3721	9383	1056	352	1608	2.3(10)-165	Escherichia coli	b1764	[pn:scleophosphate synthase] [gn:seld]
CONTIG498	892316_f3_124	3722	9384	342	114	335	1.8(10)-30	Escherichia coli	b1760	[pn:hypothetical protein]
CONTIG498	3252266_f3_141	3723	9385	1140	380	1521	4.0(10)-156	Escherichia coli	b1747	[pn:hypothetical protein]
CONTIG498	29980152_f3_144	3724	9386	1359	453	1724	1.2(10)-177	Escherichia coli	b1745	[pn:hypothetical protein]
CONTIG498	4504818_f3_145	3725	9387	975	325	977	1.8(10)-98	Escherichia coli	b1744	[pn:hypothetical protein] [gn:yd[s]
CONTIG498	17052038_f3_146	3726	9388	708	236	644	3.3(10)-63	Escherichia coli	b1742	[pn:hypothetical protein]
CONTIG498	11720093_f3_151	3727	9389	1371	457	1873	2.0(10)-193	Escherichia coli	b1737	[pn:pts system, cellobiose-specific iic component] [gn:celb]
CONTIG498	26181562_f3_152	3728	9390	351	117	467	1.8(10)-44	Escherichia coli	M93573	or:escherichia coli pn:pts enzyme iii cel:gn:celc lc:1 re:351 di:direct sr:escherichia coli (individual isolate fn23/human/sweden, strain cco nt:putative
CONTIG498	33651711_f3_153	3729	9391	834	278	1136	2.5(10)-115	Escherichia coli	b1735	[pn:cel operon repressor] [gn:celd]
CONTIG498	14657188_f3_155	3730	9392	786	262	949	1.6(10)-95	Escherichia coli	b1733	[pn:ydjc]
CONTIG498	125063_f3_159	3731	9393	267	89	359	5.4(10)-33	Escherichia coli	b1731	[pn:hypothetical protein]
CONTIG498	33869002_c1_181	3732	9394	294	98	295	3.2(10)-26	Escherichia coli	b1724	[pn:hypothetical protein]
CONTIG498	22536630_c1_182	3733	9395	888	296	1320	7.9(10)-135	Escherichia coli	b1725	[pn:hypothetical protein]
CONTIG498	270402_c1_186	3734	9396	615	205	968	1.6(10)-97	Escherichia coli	b1728	[pn:hypothetical protein]

CONTIG498	26734393_c1_190	3735	9397	2283	761	3404	0	Escherichia coli	b1732	[pn:catalase hpii] [gn:kate]
CONTIG498	35647706_c1_197	3736	9398	951	317	1117	2.6(10)-113	Escherichia coli	b1741	[pn:hypothetical protein]
CONTIG498	32109831_c1_203	3737	9399	483	161	95	0.001	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr le:59 rc:580 di:direct nt:orf2
CONTIG498	16688291_c1_210	3738	9400	1545	515	635	2.0(10)-106	Escherichia coli	b1755	[pn:hypothetical protein]
CONTIG498	1961575_c1_212	3739	9401	1404	468	1916	5.5(10)-198	Escherichia coli	b1757	[pn:hypothetical protein]
CONTIG498	24728175_c1_216	3740	9402	429	143	435	4.7(10)-41	Escherichia coli	b1759	[pn:hypothetical protein]
CONTIG498	29890942_c2_244	3741	9403	924	308	1015	1.7(10)-102	Escherichia coli	b2842	[pn:2-deoxy-d-gluconate 3-dehydrogenase] [gn:kdud]
CONTIG498	14730277_c2_245	3742	9404	1407	469	1752	1.3(10)-180	Escherichia coli	b1729	[pn:hypothetical protein]
CONTIG498	16614825_c2_276	3743	9405	882	294	1322	4.7(10)-135	Escherichia coli	b1749	[pn:exodeoxyribonuclease iii] [gn:xtha]
CONTIG498	24663132_c2_277	3744	9406	690	230	173	2.7(10)-13	Escherichia coli	b1750	[pn:hypothetical protein]
CONTIG498	32453418_c2_278	3745	9407	1176	392	1434	6.5(10)-147	Escherichia coli	b1754	[pn:hypothetical protein]
CONTIG498	3922338_c2_288	3746	9408	1359	453	2125	3.8(10)-220	Escherichia coli	b1761	[pn:nadp-specific glutamate dehydrogenase] [gn:gdha]
CONTIG498	13100905_c2_297	3747	9409	1128	376	1636	2.6(10)-168	Escherichia coli	b1767	[pn:l-asparaginase i] [gn:ansa]
CONTIG498	4392318_c2_298	3748	9410	651	217	969	1.2(10)-97	Escherichia coli	b1768	[pn:hypothetical 23.4 kd protein in ansa 3 ^{'''} region] [gn:yqjb]
CONTIG498	22738257_c2_299	3749	9411	1365	455	403	5.4(10)-37	Bacillus circulans	P20533	chitinase a1 precursor (ec 3.2.1.14).
CONTIG498	4354837_c3_304	3750	9412	945	315	1266	4.2(10)-129	Escherichia coli	b1723	[pn:6-phosphofructokinase isozyme] [gn:pfkb]
CONTIG498	5907943_c3_307	3751	9413	684	228	980	8.4(10)-99	Escherichia coli	b1727	[pn:hypothetical protein]
CONTIG498	24266652_c3_320	3752	9414	936	312	1257	3.7(10)-128	Escherichia coli	b1740	[pn:nh3-dependent nad synthetase] [gn:nadc]
CONTIG498	12230453_c3_336	3753	9415	1143	381	568	3.7(10)-55	Escherichia coli	b1756	[pn:hypothetical protein]

CONTIG498	2860216_c3_340	3754	9416	261	87	91	0.0093	Pseudomonas aeruginosa	M32077	or:pseudomonas aeruginosa le:2079 re:3137 di:direct sr:p.aeruginosa (strain pao, isolate pa02003) dna, from patient nt:alginate regulatory protein p; (put.); putative
CONTIG498	4461068_c3_346	3755	9417	1866	622	2525	1.6(10)-262	Escherichia coli	b1766	[pn:protease iv] [gn:sppa]
CONTIG499	22150281_f1_23	3756	9418	1575	525	2423	1.0(10)-251	Escherichia coli	b0074	[pn:2-isopropylmalate synthase] [gn:leua]
CONTIG499	26750286_f1_37	3757	9419	1521	507	2481	7.4(10)-258	Escherichia coli	b0062	[pn:l-arabinose isomerase] [gn:araa]
CONTIG499	14570792_f1_42	3758	9420	2919	973	4561	0	Escherichia coli	b0059	[pn:probable atp-dependent helicase hepa] [gn:hepa]
CONTIG499	24089208_f1_43	3759	9421	499	167	724	1.1(10)-71	Escherichia coli	b0058	[pn:hypothetical 24.9 kd protein in sura-hepa intergenic region] [gn:yabo]
CONTIG499	4736717_f2_82	3760	9422	1413	471	2250	2.2(10)-233	Escherichia coli	b0072	[pn:3-isopropylmalate dehydratase] [gn:leuc]
CONTIG499	32538577_f2_90	3761	9423	1611	537	2192	3.1(10)-227	Escherichia coli	b0067	[pn:hypothetical 59.6 kd protein in arac-tbpa intergenic region] [gn:yabk]
CONTIG499	22445442_f3_131	3762	9424	1116	372	1535	1.3(10)-157	Escherichia coli	b0073	[pn:3-isopropylmalate dehydrogenase] [gn:leub]
CONTIG499	15057762_f3_132	3763	9425	621	207	946	3.3(10)-95	Escherichia coli	b0071	[pn:3-isopropylmalate dehydratase] [gn:leud]
CONTIG499	33640625_f3_134	3764	9426	1680	560	2374	1.6(10)-246	Escherichia coli	b0069	[pn:hypothetical 63.9 kd protein in tbpa-leud intergenic region] [gn:yabn]
CONTIG499	34245791_f3_135	3765	9427	1047	349	1413	1.1(10)-144	Escherichia coli	b0068	[pn:thiamine-binding periplasmic protein precursor] [gn:tbpa]
CONTIG499	29941042_f3_138	3766	9428	921	307	828	1.1(10)-82	Escherichia coli	b0066	[pn:hypothetical abc transporter in arac-tbpa intergenic region]
CONTIG499	10937566_f3_141	3767	9429	1770	590	2439	2.1(10)-253	Escherichia coli	b0063	[pn:l-ribulokinase] [gn:arab]
CONTIG499	15755192_f3_145	3768	9430	828	276	1193	2.2(10)-121	Escherichia coli	b0061	[pn:l-ribulose-5-phosphate 4-epimerase] [gn:arad]
CONTIG499	31765657_f3_146	3769	9431	2514	838	3674	0	Escherichia coli	b0060	[pn:dna polymerase ii] [gn:polb]

CONTIG499	3211058_c1_165	3770	9432	804	268	920	1.8(10)-92	Escherichia coli	b0065	[pn:hypothetical 26.3 kd protein in arac-tbpa intergenic region]
CONTIG499	33722680_c1_171	3771	9433	1263	421	1669	8.1(10)-172	Escherichia coli	b0070	[pn:hypothetical 42.7 kd protein in tbpa-leud intergenic region]
CONTIG499	34632808_c1_183	3772	9434	513	171	758	2.7(10)-75	Escherichia coli	b0078	[gn:yabm]
CONTIG499	15752150_c1_187	3773	9435	399	133	519	6.0(10)-50	Escherichia coli	b0083	[pn:acetolactate synthase isozyme iii small subunit] [gn:ilvh]
CONTIG499	32539093_c1_188	3774	9436	1782	594	2669	8.8(10)-278	Escherichia coli	b0084	[pn:cell division protein ftsl] [gn:fts]
CONTIG499	26256317_c1_191	3775	9437	1437	479	1871	3.2(10)-193	Escherichia coli	b0086	[pn:penicillin-binding protein 3 precursor] [gn:fts]
CONTIG499	12265765_c1_192	3776	9438	1278	426	1637	2.0(10)-168	Escherichia coli	b0089	[pn:d-alanyl] [gn:murf]
CONTIG499	832575_c1_197	3777	9439	564	188	674	2.2(10)-66	Escherichia coli	b0093	[pn:cell division protein ftsw] [gn:ftsq]
CONTIG499	6527_c2_236	3778	9440	1011	337	1318	1.3(10)-134	Escherichia coli	b0076	[pn:leuo]
CONTIG499	4492650_c2_237	3779	9441	987	329	1500	6.7(10)-154	Escherichia coli	b0082	[pn:cell division protein ftsq]
CONTIG499	16987800_c2_240	3780	9442	1509	503	2125	3.8(10)-220	Escherichia coli	b0085	[pn:hypothetical 34.9 kd protein in frur-fts intergenic region] [gn:yabc]
CONTIG499	3398507_c2_244	3781	9443	1416	472	1859	6.0(10)-192	Escherichia coli	b0088	[pn:meso-diaminopimelate-adding enzyme] [gn:mure]
CONTIG499	13869067_c2_247	3782	9444	1479	493	2196	1.2(10)-227	Escherichia coli	b0091	[pn:udp-n-acetylmuramoyl-l-alanine] [gn:murd]
CONTIG499	1172057_c3_266	3783	9445	1023	341	1299	1.3(10)-132	Escherichia coli	b0064	[pn:udp-n-acetylmuramale] [gn:murc]
CONTIG499	14485081_c3_287	3784	9446	1755	585	2612	9.6(10)-272	Escherichia coli	b0077	[pn:arabinose operon regulatory protein] [gn:arac]
CONTIG499	5897968_c3_288	3785	9447	1014	338	1684	2.1(10)-173	Escherichia coli	b0080	[pn:acetolactate synthase isozyme iii large subunit] [gn:ilvi]
CONTIG499	36016382_c3_290	3786	9448	513	171	705	1.2(10)-69	Escherichia coli	b0081	[pn:fructose repressor] [gn:frur]
CONTIG499	35333290_c3_295	3787	9449	1128	376	1620	1.3(10)-166	Escherichia coli	b0087	[pn:hypothetical 17.4 kd protein in frur-fts intergenic region] [gn:yabb]
CONTIG499	35244787_c3_298	3788	9450	1107	369	1655	2.5(10)-170	Escherichia coli	b0090	[pn:phospho-n-acetylmuramoyl-pentapeptide- transferase] [gn:mray]
CONTIG499								Escherichia coli		[pn:udp-n-acetylglucosamine] [gn:murg]

CONTIG499	2927042_c3_299	3789	9451	948	316	1322	4.7(10)-135	Escherichia coli	b0092	[pn:d-alanine] [gn:ddb]
CONTIG5	14265875_c3_6	3790	9452	465	155	225	9.3(10)-25	Escherichia coli	b0368	[pn:hypothetical protein] [gn:taud]
CONTIG50	31847506_f2_1	3791	9453	729	243	1149	1.0(10)-116	Escherichia coli	b0096	[pn:udp-3-o-3-hydroxymyristoyl n-acetylglucosamine deacetylase] [gn:lpac]
CONTIG500	16464136_f1_8	3792	9454	846	282	1294	4.5(10)-132	Escherichia coli	b3697	[pn:hypothetical 29.7 kd protein in ibpa-gyrb intergenic region]
CONTIG500	31297917_f1_10	3793	9455	978	326	1268	2.6(10)-129	Escherichia coli	b3693	[pn:hypothetical 31.4 kd protein in ibpa-gyrb intergenic region]
CONTIG500	26380382_f1_11	3794	9456	336	112	92	0.0015	Escherichia coli	b3692	[pn:hypothetical 64.0 kd protein in ibpa-gyrb intergenic region]
CONTIG500	14316958_f1_12	3795	9457	1203	401	1929	2.2(10)-199	Escherichia coli	b3692	[pn:hypothetical 64.0 kd protein in ibpa-gyrb intergenic region]
CONTIG500	1265891_f1_13	3796	9458	1398	466	2061	2.3(10)-213	Escherichia coli	b3691	[pn:hypothetical 48.8 kd protein in ibpa-gyrb intergenic region]
CONTIG500	5328280_f1_14	3797	9459	1281	427	1771	1.3(10)-182	Escherichia coli	b3689	[pn:hypothetical 46.4 kd protein in ibpa-gyrb intergenic region]
CONTIG500	24712882_f1_16	3798	9460	465	155	614	5.0(10)-60	Escherichia coli	b3686	[pn:hs1] [gn:ibpb]
CONTIG500	36455080_f1_17	3799	9461	1851	617	2260	1.8(10)-234	Escherichia coli	b3685	[pn:hypothetical 58.9 kd protein in ibpb 3'''region] [gn:yide]
CONTIG500	24254062_f1_20	3800	9462	1674	558	1724	1.2(10)-177	Escherichia coli	b3683	[pn:pts system arbutin-like iic component] [gn:glvc]
CONTIG500	9847285_f1_24	3801	9463	711	237	160	6.5(10)-12	Escherichia coli	D90866	or:escherichia coli pn:d-serine dehydratase transcriptional activator gn:dsdc le:11564 re:11818 di:complement sr:escherichia coli (strain:k12) dna, clone lib:kohara lambda minise nt:similar to [pir accession number a28674];
CONTIG500	979582_f1_26	3802	9464	954	318	1262	1.1(10)-128	Escherichia coli	b2364	[pn:d-serine deaminase activator] [gn:dsdc]
CONTIG500	24228532_f1_27	3803	9465	1116	372	93	0.098	Clostridium sp.	P23340	endoglucanase c307 precursor (ec 3.2.1.4) (endo-1,4-beta-glucanase) (cellulase).
CONTIG500	4554818_f1_45	3804	9466	462	154	598	2.5(10)-58	Escherichia coli	b3663	[pn:hypothetical 18.2 kd protein in nipa-uhpt intergenic region]

CONTIG500	2994757_f1_47	3805	9467	1233	411	1251	1.6(10)-127	Escherichia coli	b3662	[pn:hypothetical 43.6 kd protein in nlpa 3 ^{'''} region] [gn:yicm]
CONTIG500	4551942_f2_55	3806	9468	1125	375	1762	1.1(10)-181	Escherichia coli	b3700	[pn:protein] [gn:recf]
CONTIG500	24417336_f2_60	3807	9469	1038	346	333	3.1(10)-30	Bacillus subtilis	yogA	[pn:hypothetical protein]
CONTIG500	33750965_f2_61	3808	9470	717	239	556	7.2(10)-54	Escherichia coli	b3695	[pn:hypothetical transcriptional regulator in ibpa-gyrb intergenic region] [gn:yidw]
CONTIG500	3210443_f2_63	3809	9471	630	210	669	7.5(10)-66	Escherichia coli	b3692	[pn:hypothetical 64.0 kd protein in ibpa-gyrb intergenic region]
CONTIG500	15806417_f2_73	3810	9472	378	126	371	2.8(10)-34	Escherichia coli	b3676	[pn:hypothetical 12.8 kd protein in ybl-ibpb intergenic region]
CONTIG500	6362807_f2_79	3811	9473	459	153	97	3.1(10)-5	Escherichia coli	D90866	or escherichia coli pn:d-serine dehydratase transcriptional activator gn:dsdc [c:10864 re 11133 di:complement sr:escherichia coli (strain.k12) dna, clone_lib:kohara lambda minise nt:similar to [pir accession number a28674];
CONTIG500	4898593_f2_86	3812	9474	429	143	390	2.7(10)-36	Escherichia coli	b3082	[pn:hypothetical 15.0 kd protein in cbgc-exut intergenic region] [gn:ygjm]
CONTIG500	32541507_f2_87	3813	9475	1731	577	2464	4.7(10)-256	Escherichia coli	b3671	[pn:acetoxyhydroxy acid synthase i, small subunit] [gn:ilvb]
CONTIG500	24790908_f2_88	3814	9476	291	97	435	4.7(10)-41	Escherichia coli	b3670	[pn:acetoxyhydroxy acid synthase i, small subunit] [gn:ilvn]
CONTIG500	4822086_f2_90	3815	9477	1515	505	1640	9.6(10)-169	Escherichia coli	b3668	[pn:sensor protein uhpbl] [gn:uhpb]
CONTIG500	29430341_f2_96	3816	9478	1017	339	167	2.0(10)-10	Bacillus subtilis	yfhM	[pn:hypothetical protein]
CONTIG500	22462782_f2_99	3817	9479	531	177	94	9.5(10)-5	Helicobacter pylori	HP0641	[pn:h]
CONTIG500	14316406_f3_105	3818	9480	1110	370	1669	8.1(10)-172	Escherichia coli	b3701	[pn:dna polymerase iii beta-subunit] [gn:dnan]
CONTIG500	26432887_f3_106	3819	9481	2430	810	3700	0	Escherichia coli	b3699	[pn:dna gyrase, subunit b] [gn:gyrb]
CONTIG500	22870125_f3_120	3820	9482	429	143	607	2.7(10)-59	Escherichia coli	b3687	[pn:hsltl] [gn:ibpa]

CONTIG500	34156516_f3_129	3821	9483	1479	493	1696	1.1(10)-174	Bacillus subtilis	glvA	[pn:6-phospho-alpha-glucosidase] [gn:glvg]
CONTIG500	30707515_f3_130	3822	9484	363	121	287	2.2(10)-25	Escherichia coli	b3675	[pn:hypothetical 13.8 kd protein in ivbl-ibpb intergenic region]
CONTIG500	15085840_f3_141	3823	9485	342	114	349	6.2(10)-32	Escherichia coli	b3083	[pn:hypothetical 12.1 kd protein in cbgc-exut intergenic region] [gn:ygjn]
CONTIG500	14930291_f3_143	3824	9486	768	256	932	1.0(10)-93	Escherichia coli	b3669	[pn:transcriptional regulatory protein uhpA] [gn:uhpa]
CONTIG500	4333318_f3_145	3825	9487	1320	440	1875	1.2(10)-193	Escherichia coli	b3667	[pn:regulatory protein uhpC] [gn:uhpc]
CONTIG500	12582291_f3_146	3826	9488	1524	508	2073	1.3(10)-214	Escherichia coli	b3666	[pn:hexosephosphate transport protein] [gn:uhpt]
CONTIG500	5116067_c1_160	3827	9489	315	105	223	1.3(10)-18	Bacillus subtilis	licA	[pn:phosphotransferase system] [gn:celc]
CONTIG500	24226552_c1_161	3828	9490	1407	469	190	3.7(10)-12	Escherichia coli	b4036	[pn:phage lambda receptor protein] [gn:lamb]
CONTIG500	24101517_c1_162	3829	9491	1050	350	1083	1.0(10)-109	Escherichia coli	b3660	[pn:hypothetical 33.1 kd protein in nlpa 5''' region] [gn:yicI]
CONTIG500	4332811_c1_168	3830	9492	912	304	426	4.2(10)-40	Pseudomonas putida	P10183	transcriptional activator protein nahr.
CONTIG500	10837763_c1_190	3831	9493	1341	447	1507	1.2(10)-154	Escherichia coli	b2365	[pn:dstdx permease] [gn:dstdx]
CONTIG500	34557265_c1_199	3832	9494	756	252	928	2.7(10)-93	Escherichia coli	b3684	[pn:hypothetical transcriptional regulator in ilvo- ibpb intergenic region] [gn:yidp]
CONTIG500	17004052_c1_215	3833	9495	342	114	99	5.5(10)-5	Escherichia coli	U27192	or:escherichia coli pn.modd gn.modd lc:5360 rc:6055 di:direct
CONTIG500	25878136_c2_226	3834	9496	1368	456	1543	1.8(10)-158	Bacillus subtilis	ydhP	[pn:hypothetical protein]
CONTIG500	23940636_c2_255	3835	9497	855	285	100	0.00839	Haemophilus influenzae	HI1538	[pn:lic-1 operon protein] [gn:licb]
CONTIG500	34415953_c2_277	3836	9498	336	112	448	2.0(10)-42	Escherichia coli	b3688	[pn:o135] [gn:yidq]
CONTIG500	10626535_c2_291	3837	9499	948	316	407	4.4(10)-38	Escherichia coli	b0208	[pn:hypothetical transcriptional regulator in rmh- dnir intergenic region] [gn:yalc]
CONTIG500	33729167_c2_292	3838	9500	1446	482	291	4.5(10)-28	Haloflex sp.	P21562	hypothetical 80.2 kd protein in the 5' region of gyra and gyrb (orf 4).

CONTIG500	31273568_c2_293	3839	9501	1059	353	349	5.0(10)-31	Haloferax sp.	P21562	hypothetical 80.2 kd protein in the 5' region of gyra and gyrb (orf 4).
CONTIG500	13677158_c3_326	3840	9502	291	97	136	2.2(10)-9	Escherichia coli	U70214	or:escherichia coli le:84358 re:84669
CONTIG500	1984555_c3_330	3841	9503	1230	410	1118	2.0(10)-113	Escherichia coli	b3673	di:complement nt:hypothetical
CONTIG500	4859538_c3_336	3842	9504	1389	463	1854	2.0(10)-191	Escherichia coli	b2366	[pn:multidrug resistance protein d] [gn:emrd]
CONTIG501	34093886_f1_3	3843	9505	1983	661	3188	0	Escherichia coli	b4069	[pn:d-serine dehydratase] [gn:dsda]
CONTIG501	10039711_f1_4	3844	9506	1680	560	2193	2.3(10)-227	Escherichia coli	b4067	[pn:acetyl-coa synthetase] [gn:acs]
CONTIG501	26306592_f1_52	3845	9507	1203	401	1883	1.7(10)-194	Escherichia coli	b4034	[pn:hypothetical 59.2 kd protein in soxr-acs intergenic region] [gn:yjcg]
CONTIG501	17074051_f1_56	3846	9508	909	303	1253	9.9(10)-128	Escherichia coli	b4032	[pn:periplasmic maltose-binding protein] [gn:male]
CONTIG501	21501708_f1_63	3847	9509	282	94	99	0.0006	Streptomyces ambofaciens	Z46913	[pn:maltose transport inner membrane protein] [gn:malg]
CONTIG501	14554662_f2_71	3848	9510	348	116	366	9.8(10)-34	Escherichia coli	b4068	or:streptomyces ambofaciens
CONTIG501	4977000_f2_75	3849	9511	897	299	540	3.6(10)-52	Bacillus subtilis	ywbl	pn:polyketide synthase le:<1 re:>3596 di:direct nt:putative
CONTIG501	3409812_f2_83	3850	9512	240	80	204	1.3(10)-16	Escherichia coli	b4062	[pn:hypothetical 11.7 kd protein in soxr-acs intergenic region] [gn:yjch]
CONTIG501	898566_f2_89	3851	9513	333	111	356	1.1(10)-32	Escherichia coli	b4060	[pn:hypothetical protein] [gn:ipa-24d]
CONTIG501	5267327_f2_91	3852	9514	2823	941	4604	0	Escherichia coli	b4058	[pn:regulatory protein soxs] [gn:soxs]
CONTIG501	26421891_f2_94	3853	9515	303	101	175	1.7(10)-13	Escherichia coli	Z26592	[pn:hypothetical 13.0 kd protein in ssb-soxs intergenic region] [gn:yjcb]
CONTIG501	2552281_f2_100	3854	9516	1110	370	1519	6.5(10)-156	Escherichia coli	b4051	[pn:excision nuclease] [gn:uvra]
CONTIG501	14569216_f2_109	3855	9517	2502	834	3793	0	Escherichia coli	b4041	or:escherichia coli pn:dna binding protein sp:p36558 le:1086 re:1376
CONTIG501	12307842_f2_120	3856	9518	1557	519	2116	3.5(10)-219	Escherichia coli	b4033	di:direct
								Escherichia coli		[pn:quinone oxidoreductase] [gn:qor]
								Escherichia coli		[pn:glycerol-3-phosphate acyltransferase] [gn:pls]
								Escherichia coli		[pn:maltose transport inner membrane protein] [gn:mal]

CONTIG501	16147918_f3_151	3857	9519	552	184	150	5.9(10)-10	Pseudomonas aeruginosa	U50396	or:pseudomonas aeruginosa pn:wbpn gn:wbpn lc:22302 re:23693 di:direct
CONTIG501	15680438_f3_152	3858	9520	522	174	248	1.2(10)-20	Pseudomonas aeruginosa	U50396	or:pseudomonas aeruginosa pn:wbpn gn:wbpn lc:22302 re:23693 di:direct
CONTIG501	276642_f3_161	3859	9521	552	184	849	6.4(10)-85	Escherichia coli	b4046	[pn:hypothetical 21.7 kd protein in dinf-qor intergenic region] [gn:yjbk]
CONTIG501	35242955_c1_184	3860	9522	216	72	93	0.00259	Saccharomyces cerevisiae	YJR151C	[pn:similarity to mucin proteins, yk224c, stalp] [gn:j2223]
CONTIG501	11883290_c1_189	3861	9523	2139	713	3366	0	Escherichia coli	b4029	[pn:hypothetical 78.5 kd protein in pgi-xyle intergenic region] [gn:yjbh]
CONTIG501	14113277_c1_190	3862	9524	468	156	475	2.7(10)-45	Escherichia coli	b4030	[pn:hypothetical 15.6 kd protein in pgi-xyle intergenic region] [gn:yjba]
CONTIG501	5868877_c1_202	3863	9525	570	190	756	4.5(10)-75	Escherichia coli	b4039	[pn:chorismate lyase] [gn:ubic]
CONTIG501	24821088_c1_203	3864	9526	882	294	1175	1.8(10)-119	Escherichia coli	b4040	[pn:4-hydroxybenzoate-octaprenyl transferase] [gn:ubia]
CONTIG501	16087_c1_206	3865	9527	381	127	416	4.9(10)-39	Escherichia coli	b4042	[pn:diacylglycerol kinase] [gn:dgka]
CONTIG501	22298201_c1_207	3866	9528	633	211	949	1.6(10)-95	Escherichia coli	b4043	[pn:lexa] [gn:lexa]
CONTIG501	33753275_c1_208	3867	9529	1380	460	1701	3.2(10)-175	Escherichia coli	b4044	[pn:dna-damage-inducible protein f] [gn:dinf]
CONTIG501	4425037_c1_212	3868	9530	1005	335	1606	3.8(10)-165	Escherichia coli	b4049	[pn:hypothetical 38.4 kd protein in dinf-qor intergenic region] [gn:yjbn]
CONTIG501	4859693_c1_216	3869	9531	1089	363	1628	1.8(10)-167	Escherichia coli	b4053	[pn:alanine racemase] [gn:alr]
CONTIG501	12579812_c1_221	3870	9532	447	149	631	8.0(10)-62	Escherichia coli	b4056	[pn:hypothetical 15.7 kd protein in tyrb-uvra intergenic region]
CONTIG501	11958316_c1_225	3871	9533	225	75	98	2.5(10)-5	Escherichia coli	J01721	or:escherichia coli lc:124 re:300 di:complement sr:escherichia coli, pdr1996 plasmid dna nt:single- stranded dna-binding protein (ssb)
CONTIG501	3908567_c1_231	3872	9534	468	156	749	2.5(10)-74	Escherichia coli	b4063	[pn:soxr protein] [gn:soxr]
CONTIG501	32453126_c1_236	3873	9535	1794	598	2089	2.6(10)-216	Escherichia coli	b4065	[pn:hypothetical 60.5 kd protein in soxr-acs intergenic region] [gn:yjce]
CONTIG501	17036340_c1_240	3874	9536	736	252	257	3.5(10)-22	Bacillus subtilis	ywbG	[pn:hypothetical protein] [gn:ipa- 22r]

CONTIG501	24035252_c1_248	3875	9537	1260	420	1530	4.4(10)-157	Escherichia coli	b4077	[pn:glutamate- aspartate carrier] [gn:gltP]
CONTIG501	36343956_c2_251	3876	9538	840	280	805	3.0(10)-80	Escherichia coli	b4028	[pn:hypothetical 26.3 kd protein in pgi-xyle intergenic region] [gn:yjbg]
CONTIG501	23884712_c2_273	3877	9539	369	123	350	4.9(10)-32	Escherichia coli	b4050	[pn:hypothetical 17.4 kd protein in dnf-qor intergenic region] [gn:yjbo]
CONTIG501	22477280_c2_278	3878	9540	1209	403	1795	3.7(10)-185	Escherichia coli	b4054	[pn:tyrosine aminotransferase] [gn:tyrb]
CONTIG501	9932188_c2_284	3879	9541	549	183	531	3.2(10)-51	Escherichia coli	b4059	[pn:single-strand dna-binding protein] [gn:ssb]
CONTIG501	2236375_c2_285	3880	9542	1476	492	220	5.0(10)-15	Escherichia coli	b1285	[pn:hypothetical protein] [gn:ycir]
CONTIG501	1581_c2_288	3881	9543	738	246	305	2.8(10)-27	Saccharomyces cerevisiae	P40582	hypothetical 26.8 kd protein in hyr1 3'region
CONTIG501	35287516_c2_289	3882	9544	1419	473	1796	2.8(10)-185	Escherichia coli	b4064	[pn:hypothetical 45.7 kd protein in sox-r-acs intergenic region] [gn:yjcd]
CONTIG501	13958261_c3_305	3883	9545	1893	631	2763	9.6(10)-288	Escherichia coli	b4025	[pn:glucose-6-phosphate isomerase] [gn:pgi]
CONTIG501	35551431_c3_307	3884	9546	681	227	961	8.6(10)-97	Escherichia coli	b4027	[pn:hypothetical 25.0 kd lipoprotein in pgi-xyle intergenic region]
CONTIG501	24824066_c3_316	3885	9547	1125	375	1774	6.0(10)-183	Escherichia coli	b4035	[pn:cytoplasmic membrane protein for maltose uptake] [gn:mak]
CONTIG501	956308_c3_317	3886	9548	1353	451	1872	2.5(10)-193	Escherichia coli	b4036	[pn:phage lambda receptor protein] [gn:lamb]
CONTIG501	32547893_c3_318	3887	9549	996	332	1128	1.8(10)-114	Escherichia coli	b4037	[pn:maltose operon periplasmic protein] [gn:malm]
CONTIG501	14276661_c3_329	3888	9550	225	75	355	1.3(10)-32	Escherichia coli	b4045	[pn:hypothetical protein] [gn:yjbj]
CONTIG501	12315630_c3_336	3889	9551	1452	484	2320	8.5(10)-241	Escherichia coli	b4052	[pn:replicative dna helicase] [gn:dnab]
CONTIG501	20516561_c3_341	3890	9552	738	246	973	4.7(10)-98	Escherichia coli	b4055	[pn:hypothetical 26.1 kd protein in tyrb-uvra intergenic region]
CONTIG501	24079387_c3_343	3891	9553	384	128	515	1.6(10)-49	Escherichia coli	b4057	[pn:hypothetical 13.4 kd protein in tyrb-uvra intergenic region] [gn:yjbr]
CONTIG501	31895161_c3_349	3892	9554	588	196	155	6.9(10)-10	Micrococcus luteus	JQ0406	hypothetical protein 1246 (uvra region) - micrococcus luteus(fragment)
CONTIG501	32212775_c3_354	3893	9555	1650	550	1657	1.5(10)-170	Escherichia coli	b4061	[pn:hypothetical 60.8 kd protein in ssb-soxs intergenic region] [gn:yjcc]

CONTIG501	6719025_c3_363	3894	9556	477	159	145	2.6(10)-10	Bacillus subtilis	ywbH	[pn:hypothetical protein] [gn:ipa-23r]
CONTIG502	4093891_f1_14	3895	9557	1533	511	1600	1.7(10)-164	Escherichia coli	b0621	[pn:hypothetical protein] [gn:dcuc]
CONTIG502	19792580_f1_16	3896	9558	354	118	372	2.2(10)-34	Escherichia coli	b2387	[pn:hypothetical protein]
CONTIG502	11897505_f1_17	3897	9559	1275	425	1432	1.1(10)-146	Escherichia coli	b2386	[pn:hypothetical protein]
CONTIG502	15908192_f1_18	3898	9560	1122	374	1339	7.7(10)-137	Escherichia coli	b2384	[pn:hypothetical protein]
CONTIG502	5941376_f1_32	3899	9561	984	328	780	1.3(10)-77	Escherichia coli	b0603	[pn:hypothetical protein]
CONTIG502	14882962_f1_38	3900	9562	621	207	306	2.2(10)-27	Bacillus subtilis	ykrY	[pn:hypothetical protein]
CONTIG502	6040765_f1_44	3901	9563	1311	437	763	8.3(10)-76	Bacillus subtilis	ykrT	[pn:hypothetical protein]
CONTIG502	24243791_f1_53	3902	9564	1113	371	1416	5.2(10)-145	Escherichia coli	b0599	[pn:hypothetical protein in csta 3'' region] [gn:ybdh]
CONTIG502	32286450_f1_54	3903	9565	801	267	419	2.3(10)-39	Escherichia coli	b4249	[pn:hypothetical 24.6 kd protein in pyrI-argI intergenic region] [gn:yjg]
CONTIG502	4971937_f1_55	3904	9566	372	124	101	1.2(10)-5	Methanococcus jannaschii	MJ1103	[pn:conserved hypothetical protein]
CONTIG502	34178885_f2_75	3905	9567	891	297	1078	3.5(10)-109	Escherichia coli	b0611	[pn:ribonuclease i precursor] [gn:rna]
CONTIG502	12370750_f2_77	3906	9568	447	149	441	1.1(10)-41	Escherichia coli	b2385	[pn:hypothetical protein]
CONTIG502	26250966_f2_80	3907	9569	2457	819	2860	5.0(10)-298	Escherichia coli	b2383	[pn:hypothetical protein]
CONTIG502	6923316_f2_82	3908	9570	426	142	501	4.7(10)-48	Escherichia coli	b0610	[pn:regulator of nucleoside diphosphate kinase] [gn:rmk]
CONTIG502	16490807_f2_92	3909	9571	684	228	758	2.7(10)-75	Escherichia coli	b0601	[pn:hypothetical protein]
CONTIG502	3301088_f2_103	3910	9572	582	194	121	3.7(10)-6	Hordeum vulgare	S35221	globulin beg1 precursor - barley
CONTIG502	994032_f3_134	3911	9573	831	277	798	1.6(10)-79	Escherichia coli	b2385	[pn:hypothetical protein]
CONTIG502	14664811_f3_146	3912	9574	444	148	642	5.5(10)-63	Escherichia coli	b0607	[pn:hypothetical protein] [gn:ybdq]

CONTIG502	21932056_f3_149	3913	9575	261	87	124	2.1(10)-13	Burkholderia cepacia	Q02940	beta-lactamase precursor (ec 3.5.2.6) (penicillinase).
CONTIG502	4095150_f3_151	3914	9576	1281	427	1792	7.5(10)-185	Escherichia coli	b0602	[pn:hypothetical protein]
CONTIG502	15820827_f3_156	3915	9577	723	241	943	7.0(10)-95	Klebsiella oxytoca	A49101	enolase-phosphatase e-1 - klebsiella oxytoca
CONTIG502	11036262_c1_190	3916	9578	528	176	591	1.3(10)-57	Escherichia coli	b0597	[pn:hypothetical 15.0 kd protein in enta-csta intergenic region] [gn:ybdb]
CONTIG502	14479186_c1_199	3917	9579	1644	548	803	4.7(10)-80	Bacillus subtilis	rbsA	[pn:ribose abc transporter]
CONTIG502	24415937_c1_200	3918	9580	1068	356	114	0.00046	Escherichia coli	b2548	[pn:hypothetical protein]
CONTIG502	22297582_c1_202	3919	9581	1083	361	555	9.1(10)-54	Methanococcus jannaschii	MJ0454	[pn:translation initiation factor eif-2b, subunit alpha]
CONTIG502	5320781_c1_211	3920	9582	621	207	970	9.6(10)-98	Escherichia coli	b0605	[pn:alkyl hydroperoxide reductase c22 protein] [gn:ahpc]
CONTIG502	24109377_c1_216	3921	9583	732	244	277	2.6(10)-24	Bacillus subtilis	ywrF	[pn:hypothetical protein]
CONTIG502	29970066_c1_233	3922	9584	1596	532	630	1.0(10)-61	Escherichia coli	b0574	[pn:hypothetical protein] [gn:yld]
CONTIG502	16975677_c1_236	3923	9585	996	332	832	4.0(10)-83	Escherichia coli	b0622	[pn:hypothetical protein in cspe 5'''region] [gn:ybeg]
CONTIG502	1462634_c2_237	3924	9586	1310	436	1591	1.5(10)-163	Escherichia coli	b0593	[pn:isochorismate synthase entc] [gn:entc]
CONTIG502	4319068_c2_238	3925	9587	1620	540	2268	2.7(10)-235	Escherichia coli	b0594	[pn:2,3-dihydroxybenzoate-amp ligase] [gn:ente]
CONTIG502	15830125_c2_239	3926	9588	822	274	978	1.3(10)-98	Escherichia coli	b0596	[pn:2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase] [gn:enta]
CONTIG502	6135002_c2_263	3927	9589	1098	366	999	8.1(10)-101	Escherichia coli	b2382	[pn:hypothetical protein]
CONTIG502	26343841_c2_274	3928	9590	1305	435	125	5.5(10)-5	Alcaligenes sp.	JC4698	divalent cation resistant determinant protein c - alcaligenessp. this protein is a cation/proton antiporter protein, which determines the resistance for cadmium, zinc, cobalt.
CONTIG502	21768943_c2_278	3929	9591	2124	708	2082	1.3(10)-215	Escherichia coli	b0575	[pn:hypothetical protein in phep 5'''region] [gn:ybde]

CONTIG502	29786337_c3_285	3930	9592	1035	345	1312	5.5(10)-134	Escherichia coli	b0595	[pn:isochorismatase] [gn:entb]
CONTIG502	5972011_c3_288	3931	9593	2139	713	2899	3.7(10)-302	Escherichia coli	b0598	[pn:hypothetical protein] [gn:csta]
CONTIG502	14629386_c3_289	3932	9594	312	104	270	1.5(10)-23	Escherichia coli	b4353	[pn:hypothetical 7.7 kd protein in mtr-tsrl intergenic region] [gn:yjix]
CONTIG502	13786067_c3_295	3933	9595	1035	345	317	1.5(10)-28	Bacillus subtilis	rbsC	[pn:ribose abc transporter]
CONTIG502	32610082_c3_305	3934	9596	1242	414	1693	2.3(10)-174	Escherichia coli	b0600	[pn:hypothetical protein]
CONTIG502	22661668_c3_310	3935	9597	1605	535	2447	3.0(10)-254	Escherichia coli	b0606	[pn:alkyl hydroperoxide reductase f52a protein] [gn:ahpf]
CONTIG502	22363758_c3_312	3936	9598	1266	422	1759	2.3(10)-181	Escherichia coli	b0608	[pn:hypothetical protein]
CONTIG502	33722793_c3_313	3937	9599	234	78	128	1.6(10)-8	Escherichia coli	b0609	[pn:hypothetical protein]
CONTIG502	203525_c3_328	3938	9600	336	112	96	4.0(10)-5	Escherichia coli	b0573	[pn:hypothetical protein] [gn:yloc]
CONTIG502	35673516_c3_332	3939	9601	1188	396	1204	1.5(10)-122	Escherichia coli	b0575	[pn:hypothetical protein in phep 5''' region] [gn:ybde]
CONTIG503	34069387_fl_6	3940	9602	1002	334	732	1.6(10)-72	Escherichia coli	b0147	[pn:hypothetical protein in sfss-mrcb intergenic region] [gn:yadp]
CONTIG503	33994165_fl_7	3941	9603	477	159	689	5.7(10)-68	Escherichia coli	b0145	[pn:dosage-dependent dnaK suppressor protein] [gn:dksa]
CONTIG503	261403_fl_14	3942	9604	903	301	1134	4.0(10)-115	Escherichia coli	b0133	[pn:pantoate] [gn:panc]
CONTIG503	87812_fl_15	3943	9605	615	205	140	8.6(10)-10	Escherichia coli	b0141	[pn:hypothetical fimbrial-like protein in ecpd-folk intergenic region] [gn:yadn]
CONTIG503	12944680_fl_16	3944	9606	627	209	183	2.3(10)-14	Escherichia coli	b0138	[pn:hypothetical 20.3 kd protein in panb-htr intergenic region] [gn:yadm]
CONTIG503	32035766_fl_18	3945	9607	1122	374	197	7.5(10)-16	Escherichia coli	b0135	[pn:hypothetical fimbrial-like protein in panb-htr intergenic region] [gn:yadc]
CONTIG503	22380131_fl_45	3946	9608	1803	601	1054	1.2(10)-106	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-sclc intergenic region] [gn:yicj]
CONTIG503	35282686_fl_50	3947	9609	987	329	1201	3.2(10)-122	Escherichia coli	b0109	[pn:micoinate-nucleotide pyrophosphorylase] [gn:nadc]

CONTIG503	24692676_f1_53	3948	9610	1224	408	1007	1.2(10)-101	Escherichia coli	b0106	[pn:protein transport protein hofc] [gn:hofc]
CONTIG503	10835150_f1_55	3949	9611	639	213	684	2.0(10)-67	Escherichia coli	b0103	[pn:hypothetical 22.5 kd protein in mutt-guac intergenic region precursor] [gn:yacc]
CONTIG503	13023261_f2_62	3950	9612	585	195	114	7.2(10)-5	Homo sapiens	Q15428	[GN:SAP62] [SR.:HUMAN] [DE:SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)] [SP:Q15428]
CONTIG503	5097193_f2_67	3951	9613	714	238	956	3.0(10)-96	Escherichia coli	b0146	[pn:sugar fermentation stimulation protein] [gn:sfsa]
CONTIG503	4582717_f2_71	3952	9614	489	163	620	1.2(10)-60	Escherichia coli	b0142	[pn:2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase]
CONTIG503	34166637_f2_72	3953	9615	831	277	1237	4 9(10)-126	Escherichia coli	b0134	[pn:3-methyl-2-oxobutanoate hydroxymethyltransferase] [gn:panb]
CONTIG503	6444212_f2_74	3954	9616	393	131	506	1 3(10)-48	Escherichia coli	b0131	[pn:aspartate 1-decarboxylase] [gn:panb]
CONTIG503	23713380_f2_76	3955	9617	840	280	568	3.7(10)-55	Escherichia coli	b0140	[pn:chaperone protein ecpd precursor] [gn:ecpd]
CONTIG503	806542_f2_77	3956	9618	2598	866	1852	3.2(10)-191	Escherichia coli	b0139	[pn:outer membrane usher protein hire precursor] [gn:hire]
CONTIG503	21754165_f2_79	3957	9619	651	217	159	8.4(10)-12	Escherichia coli	b0136	[pn:hypothetical 21.1 kd protein in panb-hire intergenic region] [gn:yadk]
CONTIG503	14462840_f2_91	3958	9620	897	299	1402	1.6(10)-143	Escherichia coli	b0121	[pn:spermidine synthase] [gn:spec]
CONTIG503	3320325_f2_92	3959	9621	795	265	1327	1.3(10)-135	Escherichia coli	b0120	[pn:s-adenosylmethionine decarboxylase proenzyme] [gn:sped]
CONTIG503	14241436_f2_112	3960	9622	1392	464	1968	1.7(10)-203	Escherichia coli	b0112	[pn:aromatic amino acid transport protein arop] [gn:arop]
CONTIG503	33625332_f2_113	3961	9623	999	333	90	0.37	Selenomonas ruminantium	AF040720	[de:selenomonas ruminantium xylosidase/arabinosidase (xsa) gene, complete cds] [pn:xylosidase/arabinosidase] [gn:xsa]
CONTIG503	24645887_f2_121	3962	9624	213	71	95	0.00259	Turnip yellow mosaic virus	AF035403	[de:turnip yellow mosaic blue lake isolate, complete genome.] [pn:replicase protein]

CONTIG503	2230418_f3_138	3963	9625	924	308	1271	1.2(10)-129	Escherichia coli	b0144	[pn:hypothetical 29.3 kd protein in penb-dksa intergenic region] [gn:yadb]
CONTIG503	129175_f3_139	3964	9626	1440	480	1951	1.1(10)-201	Escherichia coli	b0143	[pn:poly] [gn:penb]
CONTIG503	32048127_f3_147	3965	9627	606	202	268	2.3(10)-23	Escherichia coli	b0137	[pn:hypothetical 21.0 kd protein in panb-htr intergenic region]
CONTIG503	13695127_f3_151	3966	9628	768	256	1029	5.4(10)-104	Escherichia coli	b0126	[pn:hypothetical protein in hpt-pand intergenic region] [gn:yadf]
CONTIG503	23475311_f3_153	3967	9629	2424	808	3386	0	Escherichia coli	b0124	[pn:glucose dehydrogenase] [gn:gcd]
CONTIG503	32448952_f3_156	3968	9630	636	212	625	3.5(10)-61	Escherichia coli	b0122	[pn:hypothetical protein in spee-gcd intergenic region] [gn:yacc]
CONTIG503	22916285_f3_162	3969	9631	1554	518	807	1.8(10)-80	Escherichia coli	b0117	[pn:hypothetical protein in lpda-sped intergenic region] [gn:yach]
CONTIG503	4507318_f3_179	3970	9632	447	149	499	7.9(10)-48	Escherichia coli	b0108	[pn:prepilin peptidase dependent protein d precursor] [gn:ppdd]
CONTIG503	15089211_f3_180	3971	9633	1392	464	1500	6.7(10)-154	Escherichia coli	b0107	[pn:protein transport protein hofb] [gn:hofb]
CONTIG503	33708341_f3_185	3972	9634	837	279	1007	1.2(10)-101	Escherichia coli	b0102	[pn:hypothetical protein in mut-guac intergenic region] [gn:yacf]
CONTIG503	5181693_f3_186	3973	9635	204	68	312	5.2(10)-28	Escherichia coli	b0101	[pn:yacg]
CONTIG503	10052077_c1_190	3974	9636	2739	913	4104	0	Escherichia coli	b0098	[pn:preprotein translocase seca subunit] [gn:seca]
CONTIG503	24017063_c1_191	3975	9637	450	150	538	5.7(10)-52	Escherichia coli	b0099	[pn:mutator mutt protein] [gn:mutt]
CONTIG503	34613891_c1_195	3976	9638	1098	366	1681	4.4(10)-173	Escherichia coli	b0104	[pn:gmp reductase] [gn:guac]
CONTIG503	10042802_c1_201	3977	9639	579	193	839	7.4(10)-84	Escherichia coli	b0110	[pn:ampd protein] [gn:ampd]
CONTIG503	12367317_c1_221	3978	9640	2643	881	4131	0	Escherichia coli	b0118	[pn:aconitate hydratase 2] [gn:acnb]
CONTIG503	7032637_c1_228	3979	9641	555	185	872	2.3(10)-87	Escherichia coli	b0125	[pn:phoxanthine phosphoribosyltransferase] [gn:hpt]
CONTIG503	4304753_c1_229	3980	9642	936	312	1453	6.4(10)-149	Escherichia coli	b0127	[pn:hypothetical abc transporter in hpt-pand intergenic region]
CONTIG503	2594632_c1_230	3981	9643	468	156	560	2.7(10)-54	Escherichia coli	b0129	[pn:hypothetical protein in hpt-pand intergenic region] [gn:yadi]

CONTIG503	837557_c1_231	3982	9644	1311	437	1647	1.8(10)-169	Escherichia coli	b0130	[pn:hypothetical 46.3 kd protein in hpt-pand intergenic region precursor] [gn:yade]
CONTIG503	34661686_c1_248	3983	9645	519	173	131	7.7(10)-9	Haemophilus influenzae	L20805	or:haemophilus influenzae le.< re:172 di:direct nt:truncated sequence, 32.6% identity and 67%
CONTIG503	35244781_c2_277	3984	9646	1929	643	2436	4.2(10)-253	Escherichia coli	b0115	[pn:c2 of pyruvate dehydrogenase] [gn:acef]
CONTIG503	16970218_c2_286	3985	9647	483	161	594	6.7(10)-58	Escherichia coli	b0119	[pn:hypothetical protein in lpda-sped intergenic region] [gn:yac]
CONTIG503	81953_c2_315	3986	9648	2430	810	3244	0	Escherichia coli	b0148	[pn:atp-dependent helicase hrpb] [gn:hrpb]
CONTIG503	34634452_c2_316	3987	9649	1956	652	2530	9.8(10)-275	Escherichia coli	b0149	[pn:peptidoglycan synthetase] [gn:mrcb]
CONTIG503	22742711_c3_322	3988	9650	522	174	116	2.0(10)-6	Pseudomonas aeruginosa	P24564	hypothetical 19.5 kd protein in pilt region (orf6).
CONTIG503	4486068_c3_325	3989	9651	864	288	1164	2.7(10)-118	Escherichia coli	b0111	[pn:ampe protein] [gn:ampe]
CONTIG503	24355151_c3_332	3990	9652	795	265	1105	4.7(10)-112	Escherichia coli	b0113	[pn:pyruvate dehydrogenase complex repressor] [gn:pdhr]
CONTIG503	13870927_c3_333	3991	9653	2679	893	4352	0	Escherichia coli	b0114	[pn:pyruvate dehydrogenase e1 component] [gn:acee]
CONTIG503	5112963_c3_334	3992	9654	1434	478	2284	5.5(10)-237	Escherichia coli	b0116	[pn:diacylglycerol kinase] [gn:lpda]
CONTIG503	16145137_c3_343	3993	9655	447	149	199	4.9(10)-16	Xanthomonas campestris	P22264	hypothetical protein in clp 5'region (orf1) (fragment).
CONTIG503	22393826_c3_345	3994	9656	1764	588	1537	3.2(10)-210	Escherichia coli	b0123	[pn:hypothetical protein in spee-gcd intergenic region precursor] [gn:yack]
CONTIG503	12692811_c3_351	3995	9657	834	278	1000	6.4(10)-101	Escherichia coli	b0128	[pn:hypothetical 28.5 kd protein in hpt-pand intergenic region]
CONTIG504	24645388_fl_1	3996	9658	237	79	377	6.7(10)-35	Escherichia coli	b2741	[pn:rna polymerase sigma subunit rpos] [gn:rpos]
CONTIG504	5086577_fl_5	3997	9659	603	201	543	1.7(10)-52	Bacillus subtilis	yclB	[pn:hypothetical protein]
CONTIG504	24652343_fl_12	3998	9660	357	119	524	1.8(10)-50	Escherichia coli	b2732	[pn:hypothetical 13.9 kd protein in flha-muts intergenic region] [gn:ygba]

CONTIG504	32041625_f1_31	3999	9661	624	208	474	3.5(10)-45	Escherichia coli	b2725	[pn:formate hydrogenlyase regulatory protein] [gn:hycal]
CONTIG504	26074191_f1_32	4000	9662	1827	609	1828	1.2(10)-188	Escherichia coli	b2723	[pn:formate hydrogenlyase subunit 3] [gn:hycb]
CONTIG504	1032706_f1_38	4001	9663	807	269	1176	1.3(10)-119	Escherichia coli	b2719	[pn:formate hydrogenlyase subunit 7] [gn:hycg]
CONTIG504	6407943_f1_39	4002	9664	465	155	687	9.4(10)-68	Escherichia coli	b2717	[pn:hydrogenase 3 maturation protease] [gn:hyci]
CONTIG504	26618750_f1_65	4003	9665	1111	371	1295	3.5(10)-132	Escherichia coli	b2701	[pn:membrane-bound lytic transglycosylase b precursor] [gn:mltb]
CONTIG504	10166031_f2_71	4004	9666	1521	507	1636	2.6(10)-168	Bacillus subtilis	ycIC	[pn:hypothetical protein]
CONTIG504	2038467_f2_76	4005	9667	495	165	288	1.8(10)-25	Escherichia coli	b2848	[pn:hypothetical protein]
CONTIG504	26272556_f2_96	4006	9668	630	210	749	2.5(10)-74	Escherichia coli	b2724	[pn:formate hydrogenlyase subunit 2] [gn:hycb]
CONTIG504	21491325_f2_97	4007	9669	948	316	1094	7.0(10)-111	Escherichia coli	b2722	[pn:formate hydrogenlyase subunit 4] [gn:hycd]
CONTIG504	6917175_f2_98	4008	9670	1725	575	2877	8.0(10)-300	Escherichia coli	b2721	[pn:formate hydrogenlyase subunit 5] [gn:hycf]
CONTIG504	4425068_f2_99	4009	9671	552	184	905	7.5(10)-91	Escherichia coli	b2720	[pn:formate hydrogenlyase subunit 6] [gn:hycf]
CONTIG504	12525131_f2_108	4010	9672	2373	791	2325	2.5(10)-241	Escherichia coli	b2712	[pn:transcriptional regulatory protein hypf] [gn:hypf]
CONTIG504	16304657_f2_113	4011	9673	1071	357	205	1.3(10)-16	Escherichia coli	U03846	or:escherichia coli lc:<1 re:183 di:direct nt:putative orf >60aa
CONTIG504	33709461_f3_124	4012	9674	906	302	320	7.2(10)-29	Haemophilus influenzae	HI1364	[pn:hypothetical protein]
CONTIG504	29930206_f3_126	4013	9675	258	86	189	5.5(10)-15	Bacillus subtilis	ycID	[pn:hypothetical protein]
CONTIG504	14855436_f3_130	4014	9676	900	300	563	1.3(10)-54	Escherichia coli	b2847	[pn:hypothetical protein]
CONTIG504	11885418_f3_160	4015	9677	423	141	592	1.1(10)-57	Escherichia coli	b2718	[pn:formate hydrogenlyase maturation protein] [gn:hych]
CONTIG504	32444642_f3_166	4016	9678	1053	351	1336	1.6(10)-136	Escherichia coli	b2714	[pn:asc operon repressor protein] [gn:ascg]
CONTIG504	32501052_f3_167	4017	9679	582	194	850	5.0(10)-85	Escherichia coli	b2713	[pn:4fe-4s iron-sulfur protein] [gn:hydn]

CONTIG504	33260958_f3_170	4018	9680	1239	413	570	2.3(10)-55	Ralstonia eutropha	P23516	high-affinity nickel transport protein.
CONTIG504	4863165_f3_175	4019	9681	1599	533	2152	5.4(10)-223	Escherichia coli	b2709	[pn:hypothetical sigma-54-dependent transcriptional regulator in gutq-hypf intergenic region] [gn:ygaa]
CONTIG504	10050718_c1_191	4020	9682	849	283	1166	1.6(10)-118	Escherichia coli	b2705	[pn:sorbitol-6-phosphate 2-dehydrogenase] [gn:srld]
CONTIG504	4349193_c1_221	4021	9683	360	120	407	4.4(10)-38	Escherichia coli	b2726	[pn:hypa protein] [gn:hypa]
CONTIG504	33447142_c1_222	4022	9684	867	289	1153	3.8(10)-117	Escherichia coli	b2727	[pn:hydrogenase isoenzymes formation protein hypb] [gn:hypb]
CONTIG504	16252_c1_226	4023	9685	2109	703	2883	1.8(10)-300	Escherichia coli	b2731	[pn:transcriptional activator of the formate hydrogenlyase system] [gn:fhla]
CONTIG504	13672291_c1_235	4024	9686	330	110	92	0.00011	Escherichia coli	b4347	[pn:hypothetical 14.6 kd protein in mcrb-hsds intergenic region] [gn:yjiw]
CONTIG504	11992307_c2_247	4025	9687	990	330	1231	2.1(10)-125	Escherichia coli	b2703	[gn:srla_2]
CONTIG504	15728588_c2_248	4026	9688	375	125	475	2.7(10)-45	Escherichia coli	b2704	[pn:pts system, glucitol/sorbitol-specific iia component] [gn:srlb]
CONTIG504	25914811_c2_249	4027	9689	372	124	385	9.5(10)-36	Escherichia coli	b2706	[pn:gutm] [gn:gutm]
CONTIG504	25627000_c2_250	4028	9690	837	279	1202	2.5(10)-122	Escherichia coli	b2707	[pn:srlr] [gn:srlr]
CONTIG504	35739757_c2_258	4029	9691	1152	384	1525	1.5(10)-156	Escherichia coli	b2711	[pn:hypothetical protein in hyda 3'''region] [gn:ygbd]
CONTIG504	31894511_c2_262	4030	9692	342	114	103	6.5(10)-5	Plasmid pSB24.2	M32513	or:plasmid psb24.2 pn:neomycin resistance protein le:1443 re:2756 di:direct sr:plasmid psb24.2 dna
CONTIG504	14259667_c2_293	4031	9693	1014	338	1359	5.7(10)-139	Escherichia coli	b2730	[pn:hydrogenase isoenzymes formation protein hylp] [gn:hylp]
CONTIG504	4572178_c2_298	4032	9694	765	255	409	2.7(10)-38	Escherichia coli	b4287	[pn:ironiii dicitrate transport atp-binding protein fecf] [gn:fecf]
CONTIG504	5195253_c2_299	4033	9695	1230	410	263	1.3(10)-22	Escherichia coli	b1065	[pn:hypothetical protein]
CONTIG504	22548313_c2_302	4034	9696	2583	861	3763	0	Escherichia coli	b2733	[pn:dna mismatch repair protein] [gn:mutS]

CONTIG504	7156875_c2_303	4035	9697	264	88	99	0.00013	Salmonella typhi	Q56132	rna polymerase sigma factor rpos (sigma-38).
CONTIG504	24335932_c3_316	4036	9698	594	198	697	8.1(10)-69	Escherichia coli	b2702	[pn:pts system, glucitol/sorbitol-specific iibc component] [gn:srla_1]
CONTIG504	24495456_c3_320	4037	9699	978	326	1287	2.5(10)-131	Escherichia coli	b2708	[pn:gutq] [gn:gutq]
CONTIG504	15682878_c3_324	4038	9700	1461	487	2252	1.3(10)-233	Escherichia coli	b2710	[pn:hypothetical protein]
CONTIG504	11730162_c3_333	4039	9701	1497	499	1768	2.7(10)-182	Escherichia coli	b2715	[pn:phosphotransferase enzyme iabc-asc]
CONTIG504	26054757_c3_334	4040	9702	1443	481	2295	3.7(10)-238	Escherichia coli	b2716	[pn:6-phospho-beta-glucosidase] [gn:ascb]
CONTIG504	22753805_c3_344	4041	9703	243	81	95	0.00033	Homo sapiens	U31468	[de:homo sapiens homeobox protein (gbx2) gene, complete cds.] [pn:homeobox protein] [gn:gbx2]
CONTIG504	35282013_c3_346	4042	9704	342	114	409	2.7(10)-38	Escherichia coli	b2728	[pn:hydrogenase isoenzymes formation protein hycp] [gn:hycp]
CONTIG504	19790911_c3_347	4043	9705	1125	375	1709	4.7(10)-176	Escherichia coli	b2729	[pn:hydrogenase isoenzymes formation protein hypd] [gn:hypd]
CONTIG504	24646891_c3_352	4044	9706	1005	335	106	2.3(10)-8	Bacillus subtilis	yvrC	[pn:hypothetical protein]
CONTIG504	29869067_c3_353	4045	9707	747	249	268	2.3(10)-23	Bacillus subtilis	fhuB	[pn:ferrichrome abc transporter]
CONTIG504	167342_c3_369	4046	9708	435	145	128	1.6(10)-8	Bacillus subtilis	yybA	[pn:hypothetical protein]
CONTIG504	14181462_c3_372	4047	9709	1416	472	220	1.7(10)-15	Escherichia coli	b2367	[pn:multidrug resistance protein y] [gn:emry]
CONTIG505	3208137_fl_23	4048	9710	1215	405	1418	3.2(10)-145	Escherichia coli	b3124	[pn:hypothetical 42.1 kd protein in mpb-soha intergenic region] [gn:yhad]
CONTIG505	4082005_fl_33	4049	9711	1437	479	1983	4.4(10)-205	Escherichia coli	b3110	[pn:hypothetical 46.6 kd protein in exur-tdec intergenic region] [gn:yhao]
CONTIG505	34007882_fl_48	4050	9712	1515	505	2290	1.3(10)-237	Escherichia coli	b3091	[pn:altronate hydrolase] [gn:uxaa]
CONTIG505	282138_fl_57	4051	9713	1395	465	1887	6.5(10)-195	Escherichia coli	b3084	[pn:hypothetical 43.4 kd protein in ebac-exut intergenic region] [gn:ygio]

CONTIG505	13144378_f1_66	4052	9714	938	313	602	9.5(10)-59	Escherichia coli	b1514	[pn:hypothetical protein]
CONTIG505	23712803_f2_76	4053	9715	774	258	1052	2.0(10)-106	Escherichia coli	b3126	[pn:hypothetical 27.4 kd protein in rmpb-soha intergenic region] [gn:yha]
CONTIG505	34381931_f2_77	4054	9716	912	304	1312	5.5(10)-134	Escherichia coli	b3125	[pn:hypothetical 31.0 kd protein in rmpb-soha intergenic region] [gn:yhae]
CONTIG505	4104583_f2_80	4055	9717	933	311	1248	3.3(10)-127	Escherichia coli	b3118	[pn:bc operon transcriptional activator] [gn:tdca]
CONTIG505	24630001_f2_81	4056	9718	1029	343	1249	2.6(10)-127	Escherichia coli	b3117	[pn:catabolic threonine dehydratase] [gn:tdcb]
CONTIG505	24416526_f2_99	4057	9719	1509	503	2319	1.1(10)-240	Escherichia coli	b3092	[pn:uronate isomerase] [gn:uxac]
CONTIG505	35728280_f2_119	4058	9720	1575	525	1521	4.0(10)-156	Escherichia coli	b1513	[pn:hypothetical protein]
CONTIG505	4157318_f3_135	4059	9721	813	271	1216	8.3(10)-124	Escherichia coli	b3131	[pn:putative aga operon transcriptional repressor] [gn:agar]
CONTIG505	24103376_f3_140	4060	9722	1335	445	1803	5.2(10)-186	Escherichia coli	b3116	[pn:threonine-serine permease] [gn:tdcc]
CONTIG505	21617157_f3_141	4061	9723	1239	413	1388	4.9(10)-142	Escherichia coli	b3115	[pn:hypothetical protein in exur-tdcc intergenic region] [gn:yhaa]
CONTIG505	2151667_f3_142	4062	9724	2307	769	3452	0	Escherichia coli	b3114	[pn:probable formate acetyltransferase 3] [gn:yhas]
CONTIG505	16048967_f3_144	4063	9725	1398	466	720	3.0(10)-71	Escherichia coli	b3108	[pn:hypothetical 19.4 kd protein in exur-tdcc intergenic region] [gn:yham]
CONTIG505	32313842_f3_147	4064	9726	972	324	1419	2.6(10)-145	Escherichia coli	b3105	[pn:hypothetical transcriptional regulator in exur-tdcc intergenic region] [gn:yhai]
CONTIG505	24117711_c1_190	4065	9727	1611	537	2058	4.9(10)-213	Escherichia coli	b1511	[pn:hypothetical protein] [gn:ydev]
CONTIG505	5109457_c1_194	4066	9728	1005	335	1405	7.7(10)-144	Escherichia coli	b3087	[pn:ygr]
CONTIG505	14337766_c1_195	4067	9729	1245	415	1456	3.1(10)-149	Escherichia coli	b3089	[pn:hypothetical 43.5 kd protein in ebgc-exut intergenic region] [gn:ygu]
CONTIG505	6375378_c1_200	4068	9730	1347	449	1783	6.7(10)-184	Escherichia coli	b3093	[pn:hexuronate transporter] [gn:exut]

CONTIG505	14261275_c1_204	4069	9731	414	138	430	1.6(10)-40	Escherichia coli	b3097	[pn:hypothetical 14.5 kd protein in exur-tdcc intergenic region]
CONTIG505	26056653_c1_206	4070	9732	300	100	428	2.6(10)-40	Escherichia coli	b3100	[pn:hypothetical protein]
CONTIG505	23886067_c1_211	4071	9733	717	239	1030	4.2(10)-104	Escherichia coli	b3106	[pn:hypothetical 25.9 kd protein in exur-tdcc intergenic region]
CONTIG505	25915932_c1_227	4072	9734	1575	525	2421	1.7(10)-251	Escherichia coli	b3128	[pn:hypothetical 56.4 kd protein in mpb-soha intergenic region]
CONTIG505	12616452_c1_229	4073	9735	1326	442	1876	9.5(10)-194	Escherichia coli	b3132	[pn:putative tagatase 6-phosphate kinase agaz] [gn:agaz]
CONTIG505	29925955_c1_230	4074	9736	942	314	1003	3.1(10)-101	Vibrio furnissii	U65015	or:vibrio furnissii pn:pts permease for mannose subunit iibman gn:manz le:1604 re:2485 di:direct nt:manz
CONTIG505	10937880_c2_243	4075	9737	1050	350	996	1.7(10)-100	Escherichia coli	b1512	[pn:hypothetical protein]
CONTIG505	12753401_c2_245	4076	9738	2064	688	2834	2.8(10)-295	Escherichia coli	b3081	[pn:probable nadh-dependent flavin oxidoreductase] [gn:ygil]
CONTIG505	2238537_c2_259	4077	9739	519	173	403	1.2(10)-37	Escherichia coli	b3096	[pn:hypothetical 14.2 kd protein in exur-tdcc intergenic region]
CONTIG505	35759530_c2_260	4078	9740	471	157	282	7.7(10)-25	Escherichia coli	b3099	[pn:hypothetical 15.1 kd protein in exur-tdcc intergenic region]
CONTIG505	2424140_c2_261	4079	9741	414	138	486	1.8(10)-46	Escherichia coli	b3101	[pn:hypothetical 17.2 kd protein in exur-tdcc intergenic region]
CONTIG505	13833558_c2_262	4080	9742	1059	353	1589	2.5(10)-163	Escherichia coli	b3102	[pn:hypothetical 37.4 kd protein in exur-tdcc intergenic region]
CONTIG505	24432937_c2_289	4081	9743	489	163	764	6.5(10)-76	Escherichia coli	b3133	[pn:pts system, n-acetylglactosamine-specific iib component 2] [gn:agav]
CONTIG505	3239382_c2_293	4082	9744	1176	392	704	1.5(10)-69	Escherichia coli	b3135	[pn:putative n-acetylglactosamine-6-phosphate deacetylase] [gn:agaa]
CONTIG505	22369003_c2_294	4083	9745	1146	382	1610	1.5(10)-165	Escherichia coli	b3136	[pn:protein] [gn:agas]
CONTIG505	3395463_c2_295	4084	9746	885	295	1348	8.5(10)-138	Escherichia coli	b3137	[pn:tagatase-bisphosphate aldolase] [gn:agay]
CONTIG505	2395842_c2_296	4085	9747	546	182	377	6.7(10)-35	Escherichia coli	b1621	[pn:pts system, maltose and glucose-specific ii abc component] [gn:malx]

CONTIG505	1270053_c3_309	4086	9748	537	179	770	1.5(10)-76	Escherichia coli	b3085	[pn:hypothetical 20.9 kd protein in ebgo-exut intergenic region] [gn:ygjp]
CONTIG505	1171956_c3_311	4087	9749	999	333	1142	5.7(10)-116	Escherichia coli	b3088	[pn:hypothetical 35.8 kd protein in ebgo-exut intergenic region]
CONTIG505	31284686_c3_322	4088	9750	810	270	1229	3.5(10)-125	Escherichia coli	b3094	[pn:exu regulon regulator] [gn:exur]
CONTIG505	23577_c3_324	4089	9751	663	221	883	1.6(10)-88	Escherichia coli	b3095	[pn:hypothetical protein] [gn:yqia]
CONTIG505	21570341_c3_326	4090	9752	330	110	345	1.6(10)-31	Escherichia coli	b3098	[pn:hypothetical 11.1 kd protein in exur-tdec intergenic region]
CONTIG505	34562826_c3_329	4091	9753	387	129	444	5.2(10)-42	Escherichia coli	b3103	[pn:hypothetical 14.3 kd protein in exur-tdec intergenic region] [gn:yhah]
CONTIG505	26667717_c3_358	4092	9754	864	288	578	3.3(10)-56	Vibrio furnissii	U65015	or: vibrio furnissii pn:pts permease for mannose subunit iipman gn:many le:838 re:1614 di:direct nt:many; pel; iidman
CONTIG505	2822002_c3_360	4093	9755	471	157	363	2.0(10)-33	Vibrio furnissii	U65015	or: vibrio furnissii pn:pts permease for mannose subunit iipman n gn:manw le:2543 re:2983 di:direct nt:manw; iipman
CONTIG506	33726666_f1_2	4094	9756	1842	614	3110	0	Escherichia coli	b2286	[pn:chain d] [gn:nadh dehydrogenase i chain c]
CONTIG506	36225631_f1_5	4095	9757	996	332	1393	1.5(10)-142	Escherichia coli	b2282	[pn:nadh dehydrogenase i chain h] [gn:nuoh]
CONTIG506	31697625_f1_6	4096	9758	693	231	589	2.2(10)-57	Escherichia coli	b2280	[pn:nadh dehydrogenase i chain j] [gn:nuoj]
CONTIG506	7242961_f1_22	4097	9759	1311	437	1167	1.3(10)-118	Escherichia coli	b2265	[pn:isochorismate synthase] [gn:menf]
CONTIG506	26302091_f1_23	4098	9760	822	274	904	9.5(10)-91	Escherichia coli	b2263	[pn:yfbb]
CONTIG506	25520283_f1_27	4099	9761	1617	539	1589	2.5(10)-163	Escherichia coli	b2260	[pn:o-succinylbenzoic acid--coa ligase] [gn:mene]
CONTIG506	22477163_f1_31	4100	9762	513	171	130	3.1(10)-8	Agrobacterium vitis	U32375	or: agrobacterium vitis pn:unknown le:10379 re:1221 di:complement sr:plasmid ptwab3
CONTIG506	2532787_f1_34	4101	9763	729	243	843	2.7(10)-84	Salmonella typhimurium	P22104	transcriptional regulatory protein tctd.

CONTIG506	22845841_f1_36	4102	9764	366	122	327	1.3(10)-29	Salmonella typhi	AF029846	[de:salmonella typhi tctd and tcte genes, complete cds.] [pn:tcte] [gn:tcte]
CONTIG506	822702_f1_37	4103	9765	672	224	710	3.5(10)-70	Escherichia coli	b2250	[pn:hypothetical protein]
CONTIG506	26676087_f1_45	4104	9766	1371	457	1962	7.2(10)-203	Escherichia coli	b2240	[pn:glycerol-3-phosphatase transporter] [gn:gpt]
CONTIG506	4181558_f2_57	4105	9767	444	148	700	4.0(10)-69	Escherichia coli	b2288	[pn:nadh dehydrogenase i chain a] [gn:nuoa]
CONTIG506	24117711_f2_58	4106	9768	690	230	1142	5.7(10)-116	Escherichia coli	b2287	[pn:nadh dehydrogenase i chain b] [gn:nuob]
CONTIG506	16688506_f2_61	4107	9769	1356	452	2268	2.7(10)-235	Escherichia coli	b2284	[pn:nadh dehydrogenase i chain f] [gn:nuof]
CONTIG506	9822541_f2_62	4108	9770	2760	920	4322	0	Escherichia coli	b2283	[gn:nuog]
CONTIG506	5322878_f2_66	4109	9771	1851	617	2758	3.2(10)-287	Escherichia coli	b2278	[pn:nadh dehydrogenase i chain l] [gn:nuol]
CONTIG506	1207277_f2_67	4110	9772	1536	512	2262	1.2(10)-234	Escherichia coli	b2277	[pn:nadh dehydrogenase i chain m] [gn:nuom]
CONTIG506	14879150_f2_68	4111	9773	1464	488	1829	9.0(10)-189	Escherichia coli	b2276	[pn:nadh dehydrogenase i chain n] [gn:nuon]
CONTIG506	29900800_f2_72	4112	9774	339	113	279	1.6(10)-24	Escherichia coli	b2266	[pn:hypothetical protein] [gn:elab]
CONTIG506	13859718_f2_74	4113	9775	1767	589	2446	3.7(10)-254	Escherichia coli	b2264	[pn:2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase] [gn:mend]
CONTIG506	15801416_f2_76	4114	9776	1068	356	1342	3.7(10)-137	Escherichia coli	b2261	[pn:o-succinylbenzoate-coa synthase] [gn:menc]
CONTIG506	16929206_f2_89	4115	9777	1122	374	1024	1.8(10)-103	Salmonella typhi	AF029846	[de:salmonella typhi tctd and tcte genes, complete cds.] [pn:tcte] [gn:tcte]
CONTIG506	30275056_f2_91	4116	9778	1221	407	1644	3.7(10)-169	Escherichia coli	b2249	[pn:hypothetical protein]
CONTIG506	2552202_f2_109	4117	9779	2637	879	3740	0	Escherichia coli	b2231	[pn:dna gyrase subunit a] [gn:gyra]
CONTIG506	32680156_f2_110	4118	9780	2871	957	3706	0	Escherichia coli	b2218	[pn:sensor protein rscs] [gn:rscc]
CONTIG506	29305135_f3_117	4119	9781	537	179	844	2.2(10)-84	Escherichia coli	b2285	[pn:nadh dehydrogenase i chain e] [gn:nuoe]

CONTIG506	16605040_f3_122	4120	9782	423	141	374	1.3(10)-34	Escherichia coli	D90859	or:escherichia coli pn:nadh dehydrogenase i chain g (ec 1.6.5.3) gn:nuog le:9026 re:9565 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [swissprot accession number]
CONTIG506	6049181_f3_126	4121	9783	651	217	897	5.2(10)-90	Escherichia coli	b2281	[pn:nadh dehydrogenase i chain i] [gn:nuoi]
CONTIG506	26041441_f3_128	4122	9784	336	112	319	9.4(10)-29	Escherichia coli	b2279	[pn:nadh dehydrogenase i chain k] [gn:nuok]
CONTIG506	5129635_f3_134	4123	9785	498	166	630	1.0(10)-61	Escherichia coli	b2267	[pn:hypothetical protein] [gn:claa]
CONTIG506	14459708_f3_136	4124	9786	207	69	144	3.2(10)-10	Escherichia coli	D90857	or:escherichia coli pn:mend protein gn:mend le:10698 re:10907 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [pir accession number a33860]
CONTIG506	11067041_f3_137	4125	9787	969	323	1438	2.5(10)-147	Escherichia coli	b2262	[pn:naphthoate synthase] [gn:menb]
CONTIG506	3375126_f3_158	4126	9788	1191	397	1545	1.1(10)-158	Escherichia coli	b2239	[pn:glycerophosphoryl diester phosphodiesterase periplasmic precursor] [gn:glpq]
CONTIG506	24494150_c1_169	4127	9789	741	247	1051	2.5(10)-106	Escherichia coli	b2217	[pn:regulator of capsule synthesis b component] [gn:rcsb]
CONTIG506	20605418_c1_178	4128	9790	2328	776	3678	0	Escherichia coli	b2234	[pn:ribonucleoside-diphosphate reductase 1 alpha chain] [gn:nrda]
CONTIG506	14156906_c1_179	4129	9791	1221	407	1844	2.2(10)-190	Escherichia coli	b2235	[pn:ribonucleoside-diphosphate reductase 1 beta chain] [gn:nrdb]
CONTIG506	22869676_c1_197	4130	9792	1530	510	766	4.0(10)-76	Agrobacterium vitis	U32375	[PN:unknown] [SR:plasmid pTrAB3] [DE:Agrobacterium vitis plasmid pTrAB3 tartrate utilization gene region, including LysR-like regulator (ttuA), membrane protein (ttuB), tartrate dehydrogenase (ttuC and ttuC''), enzyme degrading primary ta

CONTIG506	33464808_c1_211	4131	9793	1050	350	1143	4.5(10)-116	Escherichia coli	b2268	[pn:hypothetical protein] [gn:elac]
CONTIG506	16600443_c2_242	4132	9794	744	248	1177	1.1(10)-119	Escherichia coli	b2232	[pn:3-demethylubiquinone-9 3-methyltransferase] [gn:ubig]
CONTIG506	14469587_c2_244	4133	9795	201	67	96	0.00076	Escherichia coli	K02672	or:escherichia coli gn:nrd b le:3505 re:5835 di:direct sr:escherichia coli k12 dna, clone pps2 nt:ribonucleoside diphosphate reductase b1 subunit
CONTIG506	34470790_c2_245	4134	9796	288	96	183	3.7(10)-13	Escherichia coli	K02672	or:escherichia coli gn:nrd b le:3505 re:5835 di:direct sr:escherichia coli k12 dna, clone pps2 nt:ribonucleoside diphosphate reductase b1 subunit
CONTIG506	24412702_c2_250	4135	9797	1659	553	2303	5.4(10)-239	Escherichia coli	b2241	[pn:anaerobic glycerol-3-phosphate dehydrogenase subunit a] [gn:glpa]
CONTIG506	32031937_c2_252	4136	9798	1320	440	1716	8.5(10)-177	Escherichia coli	b2243	[pn:anaerobic glycerol-3-phosphate dehydrogenase subunit c] [gn:glpc]
CONTIG506	4566712_c2_274	4137	9799	1032	344	334	2.3(10)-30	Helicobacter pylori	HP0393	[pn:chemotaxis protein chev]
CONTIG506	29956660_c3_303	4138	9800	546	182	755	5.9(10)-75	Escherichia coli	b2216	[pn:probable sensor protein yojn]
CONTIG506	7267876_c3_313	4139	9801	1053	351	223	2.6(10)-16	Mycobacterium smegmatis	X84077	[gn:yojn]
CONTIG506	22067707_c3_314	4140	9802	1095	365	108	0.00619	Mycobacterium smegmatis	X84077	or:mycobacterium smegmatis gn:orf617 le:3075 re:4925 di:complement nt:val start codon
CONTIG506	31820142_c3_321	4141	9803	291	97	383	1.5(10)-35	Escherichia coli	b2236	or:mycobacterium smegmatis gn:orf617 le:3075 re:4925 di:complement nt:val start codon
CONTIG506	35286582_c3_328	4142	9804	1329	443	1061	2.2(10)-107	Escherichia coli	b2242	[pn:hypothetical 9.3 kd protein in nrd b 5'''region] [gn:yfae]
CONTIG506	24415957_c3_336	4143	9805	984	328	232	1.6(10)-19	Bacillus subtilis	yflP	[pn:anaerobic glycerol-3-phosphate dehydrogenase subunit b] [gn:glpb]
CONTIG507	26738791_fl_3	4144	9806	768	256	146	6.4(10)-9	Haemophilus influenzae	HI0575	[pn:hypothetical protein]
CONTIG507	4693763_fl_5	4145	9807	348	116	180	5.0(10)-14	Bacillus subtilis	yvaE	[pn:gb]
CONTIG507	913562_fl_6	4146	9808	2463	821	835	2.0(10)-83	Escherichia coli	b3951	[pn:hypothetical protein]
CONTIG507										[pn:formate acetyltransferase 2] [gn:pfld]

CONTIG507	4584643_f1_7	4147	9809	234	78	208	5.4(10)-17	Escherichia coli	b2833	[pn:hypothetical protein]
CONTIG507	7320391_f1_11	4148	9810	1149	383	428	2.6(10)-40	Escherichia coli	b1486	[pn:hypothetical protein]
CONTIG507	16916450_f1_12	4149	9811	966	322	489	9.0(10)-47	Haemophilus influenzae	HI1185	[pn:dipeptide transport atp-binding protein] [gn:dppd]
CONTIG507	25391038_f1_18	4150	9812	894	298	949	1.6(10)-95	Klebsiella terrigena	P52666	bud operon transcriptional regulator.
CONTIG507	33724033_f1_25	4151	9813	495	165	95	0.0061	Saccharomyces cerevisiae	YDL037C	[pn:strong similarity to glucan 1,4-alpha-glucosidase]
CONTIG507	24416090_f2_71	4152	9814	807	269	183	7.0(10)-13	Escherichia coli	b1464	[pn:hypothetical 32.3 kd protein in rhse-narv intergenic region] [gn:ydde]
CONTIG507	30745308_f2_78	4153	9815	975	325	437	2.8(10)-41	Escherichia coli	b0824	[pn:hypothetical protein]
CONTIG507	24001537_f2_81	4154	9816	1602	534	436	3.7(10)-41	Escherichia coli	b1487	[pn:hypothetical protein]
CONTIG507	7300265_f2_87	4155	9817	864	288	477	1.7(10)-45	Bacillus subtilis	ykfD	[pn:hypothetical protein]
CONTIG507	33806966_f2_96	4156	9818	273	91	270	1.5(10)-23	Escherichia coli	b0581	[pn:hypothetical protein] [gn:ybdk]
CONTIG507	11209657_f2_97	4157	9819	537	179	233	1.2(10)-19	Vibrio cholerae	S81006	or:vibrio cholerae pn:hcp gn:hcp le:690 re:1208 di:direct sr:vibrio cholerae o17 nt:28 kda secreted hydrophilic protein; this sequence
CONTIG507	16884836_f2_117	4158	9820	753	251	129	1.8(10)-8	Saccharomyces cerevisiae	X85757	or:saccharomyces cerevisiae pn:unknown gn:internal orf g1669 le:6964 re:7365 di:direct sr:baker's yeast
CONTIG507	1300636_f2_126	4159	9821	663	221	106	0.00051	Haemophilus influenzae	HI0955	[pn:protein homolog] [gn:ttk]
CONTIG507	6923416_f2_130	4160	9822	1452	484	301	5.7(10)-25	Bacillus subtilis	mmr	[pn:methylenomycin a resistance protein]
CONTIG507	4141926_f3_151	4161	9823	429	143	146	2.0(10)-10	Escherichia coli	b0543	[pn:hypothetical protein] [gn:cmrc]
CONTIG507	12754381_f3_159	4162	9824	879	293	495	2.1(10)-47	Escherichia coli	b1485	[pn:hypothetical protein]
CONTIG507	26679086_f3_180	4163	9825	1140	380	1556	7.7(10)-160	Escherichia coli	b0581	[pn:hypothetical protein] [gn:ybdk]

CONTIG507	23479076_f3_190	4164	9826	267	89	178	8.1(10)-14	Escherichia coli	b0580	[pn:hypothetical protein] [gn:ybdj]
CONTIG507	26063750_f3_193	4165	9827	2181	727	1814	3.5(10)-187	Erwinia chrysanthemi	Q47162	ferrichrysoactin receptor precursor.
CONTIG507	10007212_f3_195	4166	9828	579	193	397	5.0(10)-37	Escherichia coli	b0579	[pn:hypothetical protein in nifb 5'''region] [gn:ybdf]
CONTIG507	10206325_f3_196	4167	9829	774	258	1084	8.0(10)-110	Enterobacter cloacae	Q01234	oxygen-insensitive nad(p)h nitroreductase (ec 1.-.-.-).
CONTIG507	4723752_f3_199	4168	9830	1302	434	1644	3.7(10)-169	Escherichia coli	b0577	[pn:hypothetical protein in phep-entd intergenic region] [gn:ybdg]
CONTIG507	1197041_f3_212	4169	9831	786	262	125	3.2(10)-5	Escherichia coli	b0457	[pn:hypothetical protein] [gn:y/lab]
CONTIG507	34065925_c1_214	4170	9832	297	99	265	4.9(10)-23	Escherichia coli	b0329	[pn:hypothetical protein] [gn:yaho]
CONTIG507	16148586_c1_217	4171	9833	1986	662	96	0.0038	Pseudomonas putida	S64724	uxpb protein - pseudomonas putida (fragment)
CONTIG507	26369168_c1_218	4172	9834	1392	464	1906	6.2(10)-197	Escherichia coli	b0576	[pn:phenylalanine-specific permease] [gn:phep]
CONTIG507	109705_c1_220	4173	9835	1296	432	669	7.5(10)-66	Escherichia coli	b2098	[pn:hypothetical protein]
CONTIG507	36225641_c1_221	4174	9836	1041	347	155	7.9(10)-9	Bacillus subtilis	iolE	[pn:hypothetical protein] [gn:yxdc]
CONTIG507	14582660_c1_234	4175	9837	420	140	499	7.9(10)-48	Klebsiella pneumoniae	Q48413	transcriptional activator rama.
CONTIG507	13867217_c1_241	4176	9838	2721	907	1360	4.5(10)-139	Bacillus subtilis	yloB	[pn:hypothetical protein]
CONTIG507	14570343_c1_242	4177	9839	1092	364	480	8.0(10)-46	Escherichia coli	b2074	[pn:hypothetical protein]
CONTIG507	4332318_c1_243	4178	9840	3165	1055	807	1.8(10)-80	Escherichia coli	b0462	[pn:acriflavin resistance protein b] [gn:acrb]
CONTIG507	7083293_c1_247	4179	9841	306	102	185	1.5(10)-14	Mycobacterium tuberculosis	Q50648	hypothetical 26.2 kd protein cy227.28c.
CONTIG507	25474036_c1_248	4180	9842	723	241	906	5.9(10)-91	Haemophilus influenzae	H10882	[pn:hypothetical protein]
CONTIG507	24620302_c1_252	4181	9843	804	268	1353	2.5(10)-138	Enterobacter aerogenes	P05361	alpha-acetolactate decarboxylase (ec 4.1.1.5).

CONTIG507	25516656_c1_256	4182	9844	834	278	1194	1.8(10)-121	Klebsiella pneumoniae	D86412	or:klebsiella pneumoniae pn:meso-2,3-butanediol dehydrogenase (d-acetoin gn:bude le:319 re:1089 di:direct sr:klebsiella pneumoniae (strain:iam1063) dna
CONTIG507	12994562_c2_290	4183	9845	258	86	93	0.0015	Bacteriophage I3	S26427	structural protein, 70k - phage i3
CONTIG507	5212842_c2_298	4184	9846	1245	415	237	9.0(10)-18	Bacillus subtilis	yfil	[pn:hypothetical protein]
CONTIG507	33485627_c2_299	4185	9847	1020	340	427	3.3(10)-40	Escherichia coli	b3753	[pn:rbs repressor] [gn:rbsr]
CONTIG507	33786037_c2_305	4186	9848	309	103	110	1.3(10)-6	Mycobacterium tuberculosis	Z84498	or:mycobacterium tuberculosis pn:unknown gn:mtcy09f9 08c le:3775 re:4224 di complement nt:mtcy09f9 08c, unknown, len: 149 aa
CONTIG507	973760_c2_314	4187	9849	1632	544	252	2.2(10)-19	Fischerichia coli	b0585	[pn:enterochelin esterase] [gn:fes]
CONTIG507	25478406_c2_320	4188	9850	894	298	660	6.9(10)-65	Mycobacterium tuberculosis	Q50648	hypothetical 26.2 kd protein cy227.28c.
CONTIG507	12347825_c2_327	4189	9851	1779	593	1407	4.7(10)-144	Bacillus subtilis	alsS	[pn:alpha-acetolactate synthase]
CONTIG507	12992781_c2_328	4190	9852	240	80	120	2.7(10)-7	Klebsiella terrigena	Q04520	acetoin(diacetyl) reductase (ec 1.1.1.5) (acetoin dehydrogenase) (ar).
CONTIG507	2035278_c2_335	4191	9853	765	255	437	2.8(10)-41	Saccharomyces cerevisiae	P40586	hypothetical 27.4 kd protein in hyr1 3'region.
CONTIG507	3940838_c3_348	4192	9854	2193	731	1970	1.0(10)-203	Yersinia enterocolitica	Q05202	ferrichrome receptor feua precursor.
CONTIG507	14510461_c3_392	4193	9855	489	163	102	9.3(10)-6	Staphylococcus aureus	AF003592	[PN:CspB] [GN:cspB] [DE:Staphylococcus aureus CspB (cspB) gene, complete cds] [NT:similar to major cold-shock protein] [L.F:439] [RE:639] [DI:direct]
CONTIG508	33992790_f1_9	4194	9856	930	310	1402	1.6(10)-143	Escherichia coli	b2916	[pn:chromosome initiation inhibitor] [gn:icia]
CONTIG508	16285416_f1_24	4195	9857	237	79	105	4.5(10)-6	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr le:59 re:580 di:direct nt:orf2

CONTIG508	31770765_f1_36	4196	9858	369	123	93	0.003	human herpesvirus 2	Z86099	or:human herpesvirus 2 gn:rs1 le:128076 re:132032 di:complement [pn:endonuclease i] [gn:enda]
CONTIG508	36438950_f1_52	4197	9859	765	255	1142	5.7(10)-116	Escherichia coli	b2945	
CONTIG508	994036_f1_53	4198	9860	750	250	948	2.1(10)-95	Escherichia coli	b2946	[pn:hypothetical protein in endo- gshb intergenic region] [gn:yggj]
CONTIG508	24807956_f1_54	4199	9861	960	320	1498	1.1(10)-153	Escherichia coli	b2947	[pn:glutathione synthetase] [gn:gshb]
CONTIG508	35661425_f1_57	4200	9862	318	106	138	1.3(10)-9	Pseudomonas aeruginosa	P24564	hypothetical 19.5 kd protein in p1t region (orf6).
CONTIG508	15751010_f1_60	4201	9863	327	109	416	4.9(10)-39	Escherichia coli	b2953	[pn:hypothetical protein] [gn:yggj]
CONTIG508	24790907_f1_61	4202	9864	597	199	910	2.2(10)-91	Escherichia coli	b2954	[pn:hypothetical protein] [gn:yggv]
CONTIG508	29976593_f1_63	4203	9865	387	129	292	6.7(10)-26	Escherichia coli	b1289	[pn:hypothetical 14.0 kd protein in cnvm-sapf intergenic region] [gn:ycjd]
CONTIG508	107553300_f1_66	4204	9866	1071	357	1684	2.1(10)-173	Escherichia coli	b2961	[pn:a/g-specific adenine glycosylase] [gn:muty]
CONTIG508	10003757_f1_67	4205	9867	1260	420	1648	1.3(10)-169	Escherichia coli	b2963	[pn:yggz] [gn:mlc]
CONTIG508	20353462_f1_81	4206	9868	1683	561	835	2.0(10)-83	Escherichia coli	b0619	[pn:hypothetical protein] [gn:cita]
CONTIG508	10940963_f2_96	4207	9869	639	213	126	3.5(10)-8	Saccharomyce s cerevisiae	P25614	very hypothetical 22.8 kd protein in pgk1 region.
CONTIG508	3925052_f2_102	4208	9870	846	282	1050	3.2(10)-106	Escherichia coli	b2936	[pn:hypothetical 31.8 kd protein in tkta-speb intergenic region] [gn:yggg]
CONTIG508	13675250_f2_123	4209	9871	1314	438	157	1.3(10)-8	Escherichia coli	b4356	[pn:hypothetical 49.4 kd protein in tsr-mdob intergenic region]
CONTIG508	16151390_f2_124	4210	9872	696	232	726	7.0(10)-72	Escherichia coli	M32363	or:escherichia coli le:271 re:1287 di:complement sr:escherichia coli (strain k-12) (clone: ple[2-5-8-5- 14]) dna nt:orf1; putative
CONTIG508	14493937_f2_127	4211	9873	1425	475	2144	3.7(10)-222	Escherichia coli	b2943	[pn:galactose-proton symport] [gn:galp]
CONTIG508	22078760_f2_132	4212	9874	453	151	659	8.8(10)-65	Escherichia coli	b2949	[pn:hypothetical protein] [gn:yqgf]
CONTIG508	6775790_f2_133	4213	9875	420	140	118	1.7(10)-6	Volvox carteri	S22697	extensin - volvox carteri (fragment)

CONTIG508	31344632_f2_134	4214	9876	717	239	855	1.5(10)-85	Escherichia coli	b2951	[pn:hypothetical protein] [gn:ygg5]
CONTIG508	34395318_f2_135	4215	9877	585	195	797	2.1(10)-79	Escherichia coli	b2952	[pn:hypothetical protein] [gn:ygg7]
CONTIG508	29845662_f2_136	4216	9878	1173	391	1799	1.3(10)-185	Escherichia coli	b2955	[pn:hypothetical protein] [gn:yggw]
CONTIG508	2911266_f2_143	4217	9879	1344	448	1883	1.7(10)-194	Escherichia coli	b2964	[pn:nucleoside permease nupg]
CONTIG508	4039075_f2_156	4218	9880	828	276	415	6.2(10)-39	Escherichia coli	b0620	[pn:transcriptional regulator crir]
CONTIG508	489515_f3_159	4219	9881	396	132	486	1.8(10)-46	Escherichia coli	b2910	[pn:hypothetical 12.7 kD protein in pepp-ssr intergenic region] [gn:ygf6]
CONTIG508	25985662_f3_160	4220	9882	693	231	748	3.2(10)-74	Escherichia coli	b2912	[pn:hypothetical 21.1 kD protein in ssr-sera intergenic region] [gn:ygf8]
CONTIG508	13073275_f3_184	4221	9883	1041	347	159	2.5(10)-11	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr le:<1 re:588 di:direct
CONTIG508	24353412_f3_204	4222	9884	1158	386	1813	4.5(10)-187	Escherichia coli	b2942	[pn:s-adenosylmethionine synthetase] [gn:metk]
CONTIG508	14957708_f3_206	4223	9885	570	190	796	2.7(10)-79	Escherichia coli	b2944	[pn:hypothetical 19.3 kD protein in galp-enda intergenic region]
CONTIG508	35820762_f3_209	4224	9886	708	236	894	1.1(10)-89	Escherichia coli	b2948	[pn:hypothetical protein]
CONTIG508	14583376_f3_218	4225	9887	381	127	436	3.7(10)-41	Escherichia coli	b2962	[pn:hypothetical protein] [gn:yggx]
CONTIG508	4879557_c1_240	4226	9888	1389	463	960	1.1(10)-96	Bacillus subtilis	yxkJ	[pn:hypothetical protein]
CONTIG508	4567918_c1_242	4227	9889	1032	344	728	4.2(10)-72	Escherichia coli	b0618	[pn:hypothetical protein]
CONTIG508	21661682_c1_243	4228	9890	903	301	935	5.0(10)-94	Escherichia coli	b0616	[pn:hypothetical protein] [gn:cite]
CONTIG508	22520128_c1_247	4229	9891	621	207	285	3.7(10)-25	Escherichia coli	b0614	[pn:hypothetical protein]
CONTIG508	4730001_c1_259	4230	9892	771	257	1178	8.8(10)-120	Escherichia coli	b2960	[pn:hypothetical 27.3 kD protein in muty 5''' region] [gn:yggg]
CONTIG508	1382785_c1_281	4231	9893	1998	666	3068	0	Escherichia coli	b2938	[pn:biosynthetic arginine decarboxylase] [gn:spca]

CONTIG508	24015955_c1_284	4232	9894	438	146	324	2.7(10)-29	Acinetobacter calcoaceticus	AF009672	[PN:unknown] [DE:Acinetobacter calcoaceticus ADP1 vanillate demethylase region, vanillate demethylase (vanB) and vanillate demethylase (vanA) genes, complete cds.] [NT:putative ferredoxin; ORF9] [LE:12779] [RE:13084] [DI:direct]
CONTIG508	16261457_c1_285	4233	9895	1116	372	1157	1.5(10)-117	Acinetobacter calcoaceticus	AF009672	[PN:unknown] [DE:Acinetobacter calcoaceticus ADP1 vanillate demethylase region, vanillate demethylase (vanB) and vanillate demethylase (vanA) genes, complete cds.] [NT:similar to vanillate demethylase (vanA subunit);] [LE:13411] [RE:143]
CONTIG508	25500413_c1_293	4234	9896	552	184	90	0.01799	Bacillus subtilis	yrkZ	[pn:hypothetical protein]
CONTIG508	5114843_c1_294	4235	9897	780	260	120	2.3(10)-5	Bacillus subtilis	yvaM	[pn:hypothetical protein]
CONTIG508	34491313_c1_307	4236	9898	1185	395	1788	2.0(10)-184	Escherichia coli	b2926	[pn:phosphoglycerate kinase] [gn:pgk]
CONTIG508	2914202_c1_309	4237	9899	855	285	1025	1.3(10)-103	Escherichia coli	b2924	[pn:hypothetical 30.9 kd protein in sbm-fba intergenic region] [gn:yggfb]
CONTIG508	14462658_c1_312	4238	9900	783	261	780	1.3(10)-77	Escherichia coli	b2922	[pn:hypothetical 26.6 kd protein in sbm-fba intergenic region] [gn:ygge]
CONTIG508	4165941_c1_318	4239	9901	384	128	548	5.0(10)-53	Escherichia coli	b2909	[pn:hypothetical 21.5 kd protein in pepp-ssr intergenic region] [gn:ygfb]
CONTIG508	15128755_c2_328	4240	9902	600	200	194	1.6(10)-15	Haemophilus influenzae	H10024	[pn:acyl lyase subunit] [gn:citd]
CONTIG508	22917825_c2_330	4241	9903	1668	556	1715	1.1(10)-176	Escherichia coli	b0615	[pn:hypothetical protein] [gn:citf]
CONTIG508	35275330_c2_332	4242	9904	807	269	449	1.6(10)-42	Escherichia coli	b0613	[pn:hypothetical protein] [gn:citg]
CONTIG508	6072130_c2_342	4243	9905	984	328	1234	1.0(10)-125	Escherichia coli	b2950	[pn:hypothetical protein]
CONTIG508	36113775_c2_351	4244	9906	243	81	161	5.2(10)-12	Escherichia coli	b2941	[pn:hypothetical 9.5 kd protein in spea-metk intergenic region] [gn:yqgd]

CONTIG508	3261557_c2_352	4245	9907	219	73	125	3.3(10)-8	Escherichia coli	b2939	[pn:hypothetical 5.4 kd protein in spec-metk intergenic region] [gn:yqgb]
CONTIG508	16195806_c2_367	4246	9908	1227	409	467	1.8(10)-44	Escherichia coli	b2542	[pn:hypothetical protein]
CONTIG508	11750417_c2_372	4247	9909	987	329	248	3.1(10)-21	Escherichia coli	b1619	[pn:7-alpha-hydroxysteroid dehydrogenase] [gn:haha]
CONTIG508	4332693_c2_373	4248	9910	780	260	297	2.0(10)-26	Methanobacterium thermoautotrophicum	MT1973	[pn:conserved protein]
CONTIG508	5197318_c2_374	4249	9911	1479	493	931	1.3(10)-93	Saccharomyces cerevisiae	YER073W	[pn:aldehyde dehydrogenase] [gn:ald3]
CONTIG508	13756568_c2_377	4250	9912	2184	728	3323	0	Escherichia coli	b2935	[pn:transketolase] [gn:tkla]
CONTIG508	876260_c2_381	4251	9913	708	236	1009	7.0(10)-102	Escherichia coli	b2923	[pn:hypothetical protein in sbm-fba intergenic region] [gn:yggg]
CONTIG508	34394790_c2_384	4252	9914	696	232	1048	5.2(10)-106	Escherichia coli	b2914	[pn:ribose 5-phosphate isomerase] [gn:rpia]
CONTIG508	7226077_c2_385	4253	9915	1233	411	1936	4.2(10)-200	Escherichia coli	b2913	[pn:d-3-phosphoglycerate dehydrogenase] [gn:sera]
CONTIG508	32713250_c3_388	4254	9916	1122	374	1722	2.0(10)-177	Escherichia coli	b2965	[pn:ornithine decarboxylase, constitutive] [gn:spec]
CONTIG508	2128266_c3_394	4255	9917	924	308	396	6.5(10)-37	Bacillus subtilis	yisK	[pn:hypothetical protein]
CONTIG508	13135432_c3_411	4256	9918	387	129	571	1.8(10)-55	Escherichia coli	b2959	[pn:hypothetical protein in muty 5''' region] [gn:ygg]
CONTIG508	35745292_c3_412	4257	9919	771	257	942	9.0(10)-95	Escherichia coli	b2958	[pn:hypothetical protein in ansb 5''' region] [gn:ygg]
CONTIG508	597140_c3_430	4258	9920	948	316	1550	3.2(10)-159	Escherichia coli	b2937	[pn:agmatinase] [gn:spab]
CONTIG508	36069667_c3_435	4259	9921	771	257	300	9.6(10)-27	Bacillus subtilis	fabG	[pn:3-oxoacyl-acyl-carrier protein reductase] [gn:ylpf]
CONTIG508	5214643_c3_436	4260	9922	801	267	326	1.7(10)-29	Escherichia coli	b0272	[pn:hypothetical transcriptional regulator in per-argf intergenic region] [gn:yagi]
CONTIG508	17048951_c3_437	4261	9923	978	326	177	1.8(10)-11	Ralstonia eutropha	P17296	metapyrocatechase 2 (ec 1.13.11.2) (catechol 2,3-dioxygenase ii).

CONTIG508	6351031_c3_440	4262	9924	1278	426	247	1.1(10)-18	Escherichia coli	b4356	[pn:hypothetical 49.4 kd protein in sr-mdob intergenic region]
CONTIG508	26056558_c3_445	4263	9925	1644	548	374	2.2(10)-34	Escherichia coli	b3671	[pn:acetylhydroxy acid synthase i, small subunit] [gn:ilvb]
CONTIG508	34645626_c3_447	4264	9926	1035	345	1663	3.6(10)-171	Escherichia coli	b2927	[pn:d-erythrose 4-phosphate dehydrogenase] [gn:epd]
CONTIG508	22147313_c3_448	4265	9927	1179	393	1761	1.5(10)-181	Escherichia coli	b2925	[pn:fructose 1,6-bisphosphate aldolase] [gn:fba]
CONTIG509	10335127_f1_3	4266	9928	1932	644	2853	2.7(10)-297	Escherichia coli	b3846	[pn:large]
CONTIG509	15702_f1_18	4267	9929	1044	348	1362	2.7(10)-139	Escherichia coli	b3566	[pn:xylf] [gn:xylf]
CONTIG509	16536530_f1_19	4268	9930	1614	538	2319	1.1(10)-240	Escherichia coli	b3567	[pn:d-xylose transport atp-binding protein xyfg] [gn:xyfg]
CONTIG509	14156906_f1_32	4269	9931	1584	528	1928	2.8(10)-199	Escherichia coli	b3580	[pn:cryptic l-xylose kinase] [gn:lyx]
CONTIG509	15822667_f1_35	4270	9932	723	241	1080	2.1(10)-109	Escherichia coli	b3583	[pn:hypothetical 25.6 kd protein in avia-selb intergenic region] [gn:yias]
CONTIG509	22166282_f1_49	4271	9933	1953	651	2652	5.5(10)-276	Escherichia coli	b3599	[pn:mannitol-specific enzyme ii of phosphotransferase system] [gn:mtla]
CONTIG509	15656306_f1_56	4272	9934	1776	592	2236	6.7(10)-232	Escherichia coli	b3603	[pn:l-lactate permease] [gn:lldp]
CONTIG509	17058340_f2_68	4273	9935	525	175	595	5.2(10)-58	Escherichia coli	b3846	[pn:large]
CONTIG509	4800443_f2_69	4274	9936	1173	391	1796	2.8(10)-185	Escherichia coli	b3845	[pn:small] [gn:fada]
CONTIG509	19582686_f2_76	4275	9937	1140	380	1383	1.7(10)-141	Escherichia coli	b3561	[pn:hypothetical 37.6 kd protein in glyq-xyfb intergenic region]
CONTIG509	16213568_f2_82	4276	9938	1194	398	1570	2.5(10)-161	Escherichia coli	b3568	[pn:xylose transport permease protein xyfh] [gn:xyfh]
CONTIG509	25400283_f2_83	4277	9939	1182	394	1762	1.1(10)-181	Escherichia coli	b3569	[pn:xylose operon regulatory protein] [gn:xyfr]
CONTIG509	14069843_f2_87	4278	9940	1398	466	1914	9.0(10)-198	Escherichia coli	b3572	[pn:valine--pyruvate aminotransferase] [gn:avia]
CONTIG509	34645312_f2_91	4279	9941	1017	339	1599	2.2(10)-164	Escherichia coli	b3575	[pn:hypothetical protein] [gn:yiaj]
CONTIG509	178442_f2_93	4280	9942	1359	453	464	4.0(10)-44	Escherichia coli	b2246	[pn:hypothetical protein]

CONTIG509	36066655_f2_97	4281	9943	921	307	1257	3.7(10)-128	Escherichia coli	b3582	[pn:hypothetical 33.7 kd protein in avia-selb intergenic region] [gn:yiar]
CONTIG509	251562_f2_100	4282	9944	1428	476	752	1.2(10)-74	Escherichia coli	b3657	[pn:hypothetical 51.0 kd protein in glts-selc intergenic region] [gn:yic]
CONTIG509	35783391_f2_112	4283	9945	630	210	795	3.3(10)-79	Escherichia coli	b3601	[pn:mannitol operon repressor] [gn:mlr]
CONTIG509	36503135_f2_123	4284	9946	951	317	1316	2.1(10)-134	Escherichia coli	b3605	[pn:letd] [gn:lidd]
CONTIG509	188326_f3_148	4285	9947	2154	718	2820	8.8(10)-294	Escherichia coli	b3571	[pn:alpha-amylase] [gn:mals]
CONTIG509	7317883_f3_150	4286	9948	315	105	103	7.2(10)-6	Escherichia coli	P37670	hypothetical 11.9 kd protein in avia-selb intergenic region (o103).
CONTIG509	21932205_f3_152	4287	9949	663	221	673	2.8(10)-66	Escherichia coli	b3576	[pn:hypothetical 17.5 kd protein in avia-selb intergenic region] [gn:yial]
CONTIG509	12756693_f3_155	4288	9950	666	222	949	1.6(10)-95	Escherichia coli	b3581	[pn:hypothetical 23.4 kd protein in avia-selb intergenic region] [gn:yiaa]
CONTIG509	911390_f3_161	4289	9951	2007	669	172	9.0(10)-10	Bacteroides ovatus	U15179	or:bacteroides ovatus le:<1 re:1311 di:direct nt orf1
CONTIG509	29767327_f3_162	4290	9952	492	164	207	6.9(10)-17	Azospirillum brasilense	X70360	or:azospirillum brasilense gn:carr le:59 re:580 di:direct nt.orf2
CONTIG509	24020078_f3_163	4291	9953	1032	344	228	8.5(10)-19	Haemophilus influenzae	H10182	[pn:hypothetical protein]
CONTIG509	7147186_f3_174	4292	9954	1257	419	1561	2.2(10)-160	Escherichia coli	b3600	[pn:mannitol-1-phosphate dehydrogenase] [gn:mlld]
CONTIG509	260937_f3_176	4293	9955	441	147	496	1.6(10)-47	Escherichia coli	b3602	[pn:hypothetical 13.7 kd protein in mtlr-letp intergenic region] [gn:yibl]
CONTIG509	25495182_f3_186	4294	9956	849	283	1100	1.6(10)-111	Escherichia coli	b3604	[pn:iclr] [gn:lldr]
CONTIG509	3160052_c1_222	4295	9957	825	275	139	2.2(10)-7	Escherichia coli	b3906	[pn:l-rhamnose operon transcriptional activator] [gn:rhar]
CONTIG509	4692912_c1_237	4296	9958	267	89	96	0.00011	Escherichia coli	A27279	valine-pyruvate transaminase (ec 2.6.1.66) - escherichiacoli
CONTIG509	2081888_c1_242	4297	9959	891	297	1215	1.1(10)-123	Escherichia coli	b3570	[pn:hypothetical protein] [gn:bax]
CONTIG509	16220188_c1_265	4298	9960	645	215	828	1.1(10)-82	Escherichia coli	b3848	[pn:hypothetical 21.9 kd protein in pepq-trkh intergenic region]
CONTIG509	30116455_c1_267	4299	9961	663	221	662	4.2(10)-65	Escherichia coli	b3850	[pn:hypothetical protein] [gn:hmg]

CONTIG509	36538375_c2_275	4300	9962	606	202	184	1.8(10)-14	Escherichia coli	b0534	[pn:hypothetical fimbrial-like protein in fimz 5''' region] [gn:ybeg]
CONTIG509	21723250_c2_276	4301	9963	705	235	409	2.7(10)-38	Escherichia coli	b3143	[pn:hypothetical 25.7 kd fimbrial chaprone in agai- mtr intergeni] [gn:yrai]
CONTIG509	2931558_c2_286	4302	9964	612	204	834	2.5(10)-83	Escherichia coli	b3592	[pn:hypothetical protein] [gn:yibf]
CONTIG509	9822892_c2_288	4303	9965	1866	622	2493	4.0(10)-259	Escherichia coli	b3590	[pn:selb]
CONTIG509	2939513_c2_307	4304	9966	879	293	1274	5.9(10)-130	Escherichia coli	b3574	[pn:hypothetical transcriptional regulator in avta- selb intergenic region] [gn:yiaj]
CONTIG509	22072201_c2_308	4305	9967	459	153	517	9.8(10)-50	Escherichia coli	b3573	[pn:hypothetical 17.5 kd protein in avta-selb intergenic region]
CONTIG509	913427_c2_325	4306	9968	1518	506	1955	4.0(10)-202	Escherichia coli	b3564	[pn:xytucose kinase] [gn:xyib]
CONTIG509	20817037_c2_326	4307	9969	939	313	1494	2.8(10)-153	Escherichia coli	b3560	[pn:glycine-trna synthetase, alpha subunit] [gn:glyq]
CONTIG509	4432338_c2_327	4308	9970	2079	693	3204	0	Escherichia coli	b3559	[pn:glycine-trna synthetase, beta subunit] [gn:glys]
CONTIG509	23886001_c2_333	4309	9971	1362	454	2160	7.7(10)-224	Escherichia coli	b3847	[pn:xaa-pro dipeptidase] [gn:pepq]
CONTIG509	3377258_c3_345	4310	9972	2544	848	1465	3.3(10)-150	Escherichia coli	b3144	[pn:hypothetical outer membrane usher protein in agal-mtr intergenic region] [gn:yraj]
CONTIG509	4329717_c3_346	4311	9973	1104	368	144	1.5(10)-9	Escherichia coli	b4318	[pn:fimf protein precursor] [gn:fimf]
CONTIG509	32292527_c3_353	4312	9974	1644	548	1778	2.2(10)-183	Escherichia coli	b3591	[pn:l-seryl-trna] [gn:sela]
CONTIG509	4744642_c3_357	4313	9975	1641	547	2423	1.0(10)-251	Escherichia coli	b3588	[pn:aldehyde dehydrogenase b] [gn:aldb]
CONTIG509	24744803_c3_379	4314	9976	267	89	120	2.2(10)-7	Escherichia coli	A27279	valine--pyruvate transaminase (ec 2.6.1.66) - escherichiacoli
CONTIG509	650966_c3_380	4315	9977	369	123	182	3.1(10)-14	Escherichia coli	A27279	valine--pyruvate transaminase (ec 2.6.1.66) - escherichiacoli
CONTIG509	4739012_c3_392	4316	9978	1410	470	2209	4.9(10)-229	Escherichia coli	b3565	[pn:d-xylose isomerase] [gn:xyla]
CONTIG509	26750802_c3_408	4317	9979	1473	491	1941	1.2(10)-200	Escherichia coli	b3849	[pn:trkh]

CONTIG51	4892893_c1_3	4318	9980	297	99	239	2.7(10)-20	Escherichia coli	b1825	[pn:hypothetical protein]
CONTIG510	22735807_f1_2	4319	9981	516	172	424	7.0(10)-40	Escherichia coli	b3929	[pn:menaquinone biosynthesis protein meng] [gn:meng]
CONTIG510	23634682_f1_25	4320	9982	702	234	977	1.8(10)-98	Escherichia coli	b3912	[pn:transcriptional regulatory protein] [gn:cpxr]
CONTIG510	16015963_f1_28	4321	9983	1020	340	270	1.5(10)-23	Escherichia coli	M85158	or:escherichia coli gn:soda le:<1 re:225 di:direct sr:escherichia coli (strain k-12) (library: lambda from kohara et al
CONTIG510	23835200_f1_29	4322	9984	1149	383	1420	2.0(10)-145	Escherichia coli	b3907	[pn:rhannose permease] [gn:rha]
CONTIG510	7212781_f1_59	4323	9985	591	197	914	8.3(10)-92	Escherichia coli	b3894	[pn:formate dehydrogenase-o, major subunit] [gn:fdog]
CONTIG510	14555411_f1_60	4324	9986	2463	821	3796	0	Escherichia coli	b3894	[pn:formate dehydrogenase-o, major subunit] [gn:fdog]
CONTIG510	2992841_f1_61	4325	9987	915	305	1496	1.8(10)-153	Escherichia coli	b3893	[pn:formate dehydrogenase-o, iron-sulfur subunit] [gn:fdoh]
CONTIG510	5197193_f1_72	4326	9988	879	293	1225	9.1(10)-125	Escherichia coli	b3881	[pn:hypothetical 32 kd protein in glna-fdhe intergenic region]
CONTIG510	55413_f1_75	4327	9989	2037	679	3041	0	Escherichia coli	b3878	[pn:hypothetical 77.2 kd protein in glna-fdhe intergenic region]
CONTIG510	16119418_f1_76	4328	9990	1425	475	2125	3.8(10)-220	Escherichia coli	b3877	[pn:hypothetical 51.7 kd protein in glna-fdhe intergenic region]
CONTIG510	33862917_f1_80	4329	9991	783	261	840	5.7(10)-84	Escherichia coli	b3875	[pn:hypothetical protein]
CONTIG510	19782067_f1_85	4330	9992	1455	485	2353	2.7(10)-244	Escherichia coli	b3870	[pn:glutamine synthetase] [gn:glna]
CONTIG510	14875927_f2_92	4331	9993	927	309	1244	8.9(10)-127	Escherichia coli	b3930	[pn:menaquinone biosynthesis protein mena] [gn:mena]
CONTIG510	412557_f2_95	4332	9994	873	291	1060	2.7(10)-107	Escherichia coli	b3927	[pn:glycerol uptake facilitator protein] [gn:glpf]
CONTIG510	35707880_f2_96	4333	9995	1530	510	2456	3.2(10)-255	Escherichia coli	b3926	[pn:glycerol kinase] [gn:glpk]
CONTIG510	20910700_f2_97	4334	9996	1026	342	1516	1.3(10)-155	Escherichia coli	b3925	[pn:glpx protein] [gn:glpx]
CONTIG510	14664712_f2_98	4335	9997	774	258	1179	6.9(10)-120	Escherichia coli	b3924	[pn:ferredoxin--nadp reductase] [gn:fpf]

CONTIG510	32422943_f2_118	4336	9998	1272	424	1966	2.7(10)-203	Escherichia coli	b3903	[pn:l-rhamnose isomerase] [gn:rhaa]
CONTIG510	12975937_f2_119	4337	9999	927	309	1331	5.4(10)-136	Escherichia coli	b3902	[pn:rhamnulose-1-phosphate aldolase] [gn:rhad]
CONTIG510	35444752_f2_125	4338	10000	1272	424	391	2.2(10)-36	Bacillus subtilis	rbsC	[pn:ribose abc transporter]
CONTIG510	16666393_f2_127	4339	10001	342	114	507	1.1(10)-48	Escherichia coli	b3901	[pn:hypothetical 12.3 kd protein in rhad 3'''region] [gn:yiii]
CONTIG510	31283452_f2_146	4340	10002	930	310	1369	5.0(10)-140	Escherichia coli	b3891	[pn:fdhe protein] [gn:fdhe]
CONTIG510	892542_f2_147	4341	10003	954	318	329	8.1(10)-30	Escherichia coli	b0476	[pn:hypothetical protein in hemh-gsk intergenic region] [gn:ybac]
CONTIG510	36214211_f2_151	4342	10004	903	301	1165	2.1(10)-118	Escherichia coli	b3882	[pn:hypothetical 31.2 kd protein in glna-fdhe intergenic region]
CONTIG510	4416318_f2_158	4343	10005	1434	478	1907	4.9(10)-197	Escherichia coli	b3876	[pn:hypothetical protein]
CONTIG510	7225312_f2_163	4344	10006	1431	477	2103	8.4(10)-218	Escherichia coli	b3868	[pn:gling] [gn:gling]
CONTIG510	2166665_f3_165	4345	10007	303	101	413	1.0(10)-38	Escherichia coli	b3931	[pn:heat shock protein hslu] [gn:hslu]
CONTIG510	17085216_f3_174	4346	10008	615	205	666	1.6(10)-65	Escherichia coli	b3920	[pn:hypothetical 21.8 kd protein in tpia 3'''region precursor] [gn:yiiq]
CONTIG510	4964458_f3_175	4347	10009	783	261	1130	1.1(10)-114	Escherichia coli	b3919	[pn:triosephosphate isomerase] [gn:tpia]
CONTIG510	10636442_f3_188	4348	10010	1434	478	1806	2.5(10)-186	Escherichia coli	b3911	[pn:cpxa] [gn:cpxa]
CONTIG510	33796877_f3_194	4349	10011	1707	569	2017	1.1(10)-208	Escherichia coli	b3904	[pn:rhamnulokinase] [gn:rhab]
CONTIG510	23939402_f3_198	4350	10012	1083	361	491	5.5(10)-47	Escherichia coli	b1516	[pn:hypothetical protein]
CONTIG510	34632782_f3_199	4351	10013	1521	507	1076	5.7(10)-109	Escherichia coli	b3749	[pn:high affinity ribose transport protein] [gn:rsa]
CONTIG510	10422077_f3_200	4352	10014	1005	335	414	8.0(10)-39	Escherichia coli	b3750	[pn:high affinity ribose transport protein] [gn:rbsc]
CONTIG510	4964675_f3_202	4353	10015	1164	388	850	5.0(10)-85	Escherichia coli	b3589	[pn:hypothetical 40.2 kd protein in avia-selb intergenic region] [gn:yia]

CONTIG510	24642887_f3_211	4354	10016	666	222	172	3.5(10)-13	Streptomyces coelicolor	AL020958	[de:streptomyces coelicolor cosmid 4h8.] [pn:hypothetical protein sc4h8.02] [gn:sc4h8.02] [nt:sc4h8.02, possible membrane [pn:formate dehydrogenase, cytochrome b556] [gn:fdoi] [pn:hypothetical 48 kd protein in glna-fdhe intergenic region] [pn:glml] [gn:glml] [pn:oxygen-independent coproporphyrinogen iii oxidase] [gn:henn] or:transposon mini-tn3cm le:30 re:1508 di:complement sr:transposon mini-tn3cm dna; neisseria gonorrhoeae (strain ms11) dna nt:orf1 or:transposon mini-tn3cm le:30 re:1508 di:complement sr:transposon mini-tn3cm dna; neisseria gonorrhoeae (strain ms11) dna nt:orf1 [pn:hypothetical 23.5 kd protein in glna-fdhe intergenic region] [pn:hypothetical 37.1 kd protein in glna-fdhe intergenic region] or:enterobacter cloacae pn:mely gn:mely le:481 re:1758 di:direct sr:enterobacter cloacae (strain:ii977) dna [pn:l-rhamnose operon transcriptional activator] [gn:rhar] [pn:manganese superoxide dismutase] [gn:soda] [pn:hypothetical 26.6 kd protein in kdgt-cpxa intergenic region] [gn:yim]
CONTIG510	32304817_f3_221	4355	10017	657	219	999	8.1(10)-101	Escherichia coli	b3892	
CONTIG510	32283263_f3_230	4356	10018	1287	429	1880	3.6(10)-194	Escherichia coli	b3880	
CONTIG510	35272952_f3_245	4357	10019	1050	350	1609	1.8(10)-165	Escherichia coli	b3869	
CONTIG510	7166507_c1_252	4358	10020	1485	495	2205	1.3(10)-228	Escherichia coli	b3867	
CONTIG510	36203141_c1_256	4359	10021	969	323	311	1.3(10)-27	Transposon mini-Tn3Cm	M84113	
CONTIG510	31847192_c1_257	4360	10022	570	190	257	1.5(10)-21	Transposon mini-Tn3Cm	M84113	
CONTIG510	1964051_c1_271	4361	10023	654	218	813	4.2(10)-81	Escherichia coli	b3885	
CONTIG510	12978333_c1_273	4362	10024	1092	364	1480	8.8(10)-152	Escherichia coli	b3888	
CONTIG510	15829202_c1_289	4363	10025	1401	467	1892	1.8(10)-195	Enterobacter cloacae	AB000622	
CONTIG510	3963265_c1_303	4364	10026	879	293	1050	3.2(10)-106	Escherichia coli	b3906	
CONTIG510	31884586_c1_305	4365	10027	654	218	1074	9.1(10)-109	Escherichia coli	b3908	
CONTIG510	1026_c1_306	4366	10028	705	235	966	2.6(10)-97	Escherichia coli	b3910	

CONTIG510	5910626_c1_308	4367	10029	603	201	491	5.5(10)-47	Escherichia coli	b3914	[pn:hypothetical 14.4 kd protein in cpxa-pfka intergenic region]
CONTIG510	4579541_c1_309	4368	10030	909	303	1289	1.5(10)-131	Escherichia coli	b3915	[pn:hypothetical 32.9 kd protein in cpxa-pfka intergenic region]
CONTIG510	14119712_c2_326	4369	10031	282	94	198	6.2(10)-16	Escherichia coli	b3866	[pn:hypothetical 19.1 kd protein in pola-henn intergenic region]
CONTIG510	25671932_c2_346	4370	10032	948	316	1040	3.7(10)-105	Escherichia coli	b3883	[pn:hypothetical 31.9 kd protein in glna-fdhe intergenic region]
CONTIG510	34100937_c2_351	4371	10033	462	154	698	6.4(10)-69	Escherichia coli	b3887	[pn:hypothetical 15.9 kd protein in glna-fdhe intergenic region]
CONTIG510	16688543_c2_366	4372	10034	1062	354	1031	3.2(10)-104	Escherichia coli	A35160	repressor protein rafr - escherichia coli
CONTIG510	24426430_c2_367	4373	10035	2229	743	2766	4.7(10)-288	Escherichia coli	P16551	alpha-galactosidase (ec 3.2.1.22) (melibiase)
CONTIG510	4410252_c2_395	4374	10036	1095	365	1462	7.0(10)-150	Escherichia coli	b3916	[pn:6-phosphofructokinase] [gn:pfka]
CONTIG510	33260055_c2_396	4375	10037	1050	350	1469	1.3(10)-150	Escherichia coli	b3917	[pn:periplasmic sulphate binding protein] [gn:sbp]
CONTIG510	31894063_c2_397	4376	10038	819	273	941	1.1(10)-94	Escherichia coli	b3918	[pn:cdp-diglyceride hydrolase] [gn:cdh]
CONTIG510	5914043_c3_418	4377	10039	1833	611	2757	4.2(10)-287	Escherichia coli	b3871	[pn:65.4 kd gtp-binding protein in glna-fdhe intergenic region]
CONTIG510	34163512_c3_431	4378	10040	912	304	1066	6.5(10)-108	Escherichia coli	b3884	[pn:hypothetical transcriptional regulator in glna-fdhe intergenic region] [gn:yihw]
CONTIG510	20969180_c3_432	4379	10041	951	317	997	1.3(10)-100	Escherichia coli	b3886	[pn:hypothetical 32.8 kd protein in glna-fdhe intergenic region]
CONTIG510	30100280_c3_448	4380	10042	912	304	1110	1.3(10)-112	Escherichia coli	b3895	[pn:fdhd protein] [gn:fdhd]
CONTIG510	818893_c3_449	4381	10043	279	93	97	3.1(10)-5	Escherichia coli	b0802	[pn:hypothetical 8.6 kd protein in ding/rarb 3''' region] [gn:ybij]
CONTIG510	14704431_c3_452	4382	10044	642	214	168	9.4(10)-13	Escherichia coli	b1434	[pn:hypothetical protein]
CONTIG510	10156438_c3_483	4383	10045	864	288	1052	2.0(10)-106	Escherichia coli	b3905	[pn l-rhamnose operon regulatory protein rhas] [gn:rhas]
CONTIG510	22281562_c3_494	4384	10046	1326	442	204	9.0(10)-14	Methanobacterium thermoautotrophicum	MTH788	[pn:sodium/dicarboxylate or sulfate cotransporter]

CONTIG510	20570300_c3_498	4385	10047	501	167	546	8.3(10)-53	Escherichia coli	b3921	[pn:hypothetical 16.5 kd protein in tpia-fpr intergenic region] [gn:yiiir]
CONTIG510	519167_c3_509	4386	10048	273	91	362	2.6(10)-33	Escherichia coli	b3928	[pn:hypothetical 9.6 kd protein in glpf-hslu intergenic region] [gn:yiiu]
CONTIG511	31835915_fl_2	4387	10049	3219	1073	2383	1.8(10)-247	Burkholderia cepacia	U97042	ceob., ceob. similar to cytoplasmic membrane proteins of the rnd
CONTIG511	17070152_fl_9	4388	10050	855	285	159	4.7(10)-10	Escherichia coli	b1782	[pn:hypothetical protein]
CONTIG511	29320338_fl_13	4389	10051	903	301	316	1.8(10)-28	Escherichia coli	b2409	[pn:hypothetical protein]
CONTIG511	26772536_fl_30	4390	10052	1308	436	1961	9.4(10)-203	Escherichia coli	b2497	[pn:uracil permease] [gn:uraa]
CONTIG511	31647632_fl_31	4391	10053	744	248	1118	2.0(10)-113	Escherichia coli	b2496	[pn:hypothetical protein]
CONTIG511	4335802_fl_48	4392	10054	744	248	1185	1.6(10)-120	Escherichia coli	b2476	[pn:phosphoribosylaminoimidazole-succinocarboxamide synthase] [gn:purc]
CONTIG511	1229775_fl_49	4393	10055	882	294	1223	1.5(10)-124	Escherichia coli	b2475	[pn:hypothetical protein]
CONTIG511	900837_fl_52	4394	10056	804	268	1024	1.8(10)-103	Escherichia coli	b2473	[pn:hypothetical protein] [gn:ypih]
CONTIG511	31509432_fl_64	4395	10057	2058	686	2749	2.8(10)-286	Escherichia coli	b2468	[pn:hypothetical 71.8 kd protein in kktb-narq intergenic region] [gn:yffg]
CONTIG511	25648456_fl_72	4396	10058	2304	768	3460	0	Escherichia coli	b2463	[pn:hypothetical protein]
CONTIG511	23954386_fl_74	4397	10059	525	175	707	7.2(10)-70	Escherichia coli	b2434	[pn:hypothetical protein]
CONTIG511	4772706_fl_77	4398	10060	948	316	1451	1.0(10)-148	Escherichia coli	b2431	[pn:hypothetical protein]
CONTIG511	15634678_fl_79	4399	10061	837	279	1110	1.3(10)-112	Escherichia coli	b2424	[pn:sulfate transport system permease protein cyst] [gn:cysu]
CONTIG511	24878442_fl_80	4400	10062	1131	377	1677	1.2(10)-172	Escherichia coli	b2422	[pn:sulfate transport atp-binding protein cysa] [gn:cysa]
CONTIG511	792317_fl_81	4401	10063	873	291	986	2.0(10)-99	Escherichia coli	b2418	[pn:hypothetical protein] [gn:pdxk]

CONTIG511	10035957_f1_83	4402	10064	282	94	92	0.00169	Homo sapiens	U78554	[PN:mucin] [GN:MUC5B] [SR:human] [DE:Homo sapiens mucin (MUC5B) gene, 3 exons, partial cds.] [LE:U78552<1:U78553:266:U78553:733] [RE:526:447:904] [DI:directJoin]
CONTIG511	4866582_f2_85	4403	10065	1275	425	437	2.8(10)-41	Escherichia coli	b0463	[pn:acriflavin resistance protein a precursor] [gn:acra]
CONTIG511	4551528_f2_96	4404	10066	2379	793	2181	4.5(10)-226	Escherichia coli	b2503	[pn:hypothetical protein]
CONTIG511	36025316_f2_102	4405	10067	1434	478	1667	1.3(10)-171	Escherichia coli	b2901	[pn:6-phospho-beta-glucosidase bglA] [gn:bglA]
CONTIG511	22355137_f2_111	4406	10068	891	297	153	6.7(10)-9	Shewanella sp. SCRC-2738	U73935	[de:shewanella sp. scrc-2738 ecosapentaenoic acid (epa) synthesis genecluster, complete sequence] [pn:unknown] [nt:orf4]
CONTIG511	10000668_f2_120	4407	10069	906	302	1390	3.0(10)-142	Escherichia coli	b2478	[pn:dihydrodipicolinate synthase] [gn:dapa]
CONTIG511	261305_f2_139	4408	10070	291	97	117	3.5(10)-6	Escherichia coli	L34011	or:escherichia coli pn:fe-s center and glutamate synthase (gltD) gn:aeg53.0 le:239 re:2197 di:direct sr:escherichia coli (individual isolate mc4100, strain k-12) (library)
CONTIG511	864182_f2_140	4409	10071	621	207	795	3.3(10)-79	Escherichia coli	b2467	[pn:hypothetical 21.7 kd protein in tkib-narq intergenic region] [gn:yffh]
CONTIG511	24651580_f2_152	4410	10072	456	152	531	3.2(10)-51	Escherichia coli	b2433	[pn:hypothetical protein]
CONTIG511	114787_f2_153	4411	10073	639	213	700	4.0(10)-69	Escherichia coli	b2432	[pn:hypothetical protein]
CONTIG511	4817593_f2_155	4412	10074	1023	341	1482	5.4(10)-152	Escherichia coli	b2425	[pn:thiosulfate-binding protein precursor] [gn:cysp]
CONTIG511	6289053_f2_160	4413	10075	921	307	1385	1.0(10)-141	Escherichia coli	b2421	[pn:cysteine synthase b] [gn:cysm]
CONTIG511	6025325_f3_197	4414	10076	723	241	1036	9.8(10)-105	Escherichia coli	b2498	[pn:uracil phosphoribosyltransferase] [gn:upp]
CONTIG511	14070177_f3_210	4415	10077	1113	371	1299	1.3(10)-132	Escherichia coli	b2493	[pn:hypothetical protein] [gn:pcrm]

CONTIG511	5079818_f3_212	4416	10078	1044	348	1537	8.0(10)-158	Escherichia coli	b2477	[pn:lipoprotein-34 precursor] [gn:nlpb]
CONTIG511	22906410_f3_214	4417	10079	1968	656	2029	5.7(10)-210	Escherichia coli	b2474	[pn:hypothetical protein] [gn:ypfi]
CONTIG511	5173152_f3_229	4418	10080	1134	378	1351	4.0(10)-138	Escherichia coli	b2466	[pn:hypothetical protein]
CONTIG511	24344411_f3_243	4419	10081	918	306	1325	2.2(10)-135	Escherichia coli	P16702	sulfate transport system permease protein cysw.
CONTIG511	30603817_c1_249	4420	10082	456	152	719	3.7(10)-71	Escherichia coli	b2416	[pn:phosphoenolpyruvate-protein phosphotransferase] [gn:ptsi]
CONTIG511	2598451_c1_280	4421	10083	387	129	115	3.8(10)-7	Escherichia coli	P37670	hypothetical 11.9 kd protein in avian self intergenic region (o103).
CONTIG511	36130181_c1_297	4422	10084	591	197	853	2.3(10)-85	Escherichia coli	b2479	[pn:gcvi]
CONTIG511	16540667_c1_302	4423	10085	462	154	488	1.2(10)-46	Escherichia coli	b2495	[pn:hypothetical protein]
CONTIG511	4492202_c1_313	4424	10086	696	232	935	5.0(10)-94	Escherichia coli	b2500	[pn:phosphoribosylglycinamide myltransferase] [gn:purn]
CONTIG511	10268800_c1_324	4425	10087	537	179	104	3.2(10)-5	Bacillus subtilis	yhdE	[pn:hypothetical protein]
CONTIG511	4339088_c2_334	4426	10088	519	173	577	4.2(10)-56	Haemophilus influenzae	HI1711	[pn:glucose phosphotransferase enzyme iii-gl] [gn:err]
CONTIG511	16289055_c2_349	4427	10089	927	309	1468	1.6(10)-150	Escherichia coli	b2436	[pn:coproporphyrinogen iii oxidase] [gn:hemi]
CONTIG511	156276_c2_355	4428	10090	975	325	1380	3.5(10)-141	Escherichia coli	b2464	[pn:hypothetical protein] [gn:tala]
CONTIG511	34176402_c2_371	4429	10091	384	128	480	8.0(10)-46	Escherichia coli	b2471	[pn:hypothetical 13.6 kd protein in dape 5''' region] [gn:yffb]
CONTIG511	30165880_c2_372	4430	10092	1131	377	1862	2.8(10)-192	Escherichia coli	b2472	[pn:succinyl-diaminopimelate desuccinylase] [gn:dape]
CONTIG511	29900316_c2_373	4431	10093	201	67	192	2.7(10)-15	Escherichia coli	D90875	or:escherichia coli le:15855 re:16055 di:direct sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [pir accession number d42959]
CONTIG511	5109818_c2_392	4432	10094	1428	476	614	5.0(10)-60	Haemophilus influenzae	HI1705	[pn:aminopeptidase a/i] [gn:pepa]
CONTIG511	23947283_c2_399	4433	10095	1041	347	1603	8.0(10)-165	Escherichia coli	b2499	[pn:phosphoribosylformylglycinamide cyclo-ligase] [gn:purn]

CONTIG511	36366008_c2_402_4434	10096	2067	689	3137	0	Escherichia coli	b2501	[pn:polyphosphate kinase] [gn:ppk]
CONTIG511	4790881_c2_403_4435	10097	1542	514	2265	5.7(10)-235	Escherichia coli	b2502	[pn:exopolyphosphatase] [gn:ppx]
CONTIG511	12360706_c2_408_4436	10098	225	75	189	5.5(10)-15	Escherichia coli	b2504	[pn:hypothetical protein]
CONTIG511	26600312_c2_410_4437	10099	1236	412	91	0.28	Escherichia coli	b0045	[pn:hypothetical metabolite transport protein in carb-kefe intergenic region] [gn:yaau]
CONTIG511	31752035_c2_413_4438	10100	1407	469	296	1.5(10)-24	Escherichia coli	b2078	[pn:sensor protein baes] [gn:baes]
CONTIG511	14120812_c2_423_4439	10101	321	107	237	4.5(10)-20	Escherichia coli	b1531	[pn:multiple antibiotic resistance protein] [gn:mara]
CONTIG511	12323286_c3_437_4440	10102	909	303	1262	1.1(10)-128	Escherichia coli	b2435	[pn:probable n-acetylmutamoyl-L-alanine amidase] [gn:amia]
CONTIG511	31728382_c3_444_4441	10103	1992	664	3150	0	Escherichia coli	b2465	[pn:transketolase 2] [gn:tktb]
CONTIG511	23488453_c3_449_4442	10104	1695	565	1836	1.7(10)-189	Escherichia coli	b2469	[pn:nitrate/nitrite sensor protein] [gn:narq]
CONTIG511	24351016_c3_450_4443	10105	3141	1047	4723	0	Escherichia coli	b2470	[pn:acridine resistance protein d] [gn:acrd]
CONTIG511	12306553_c3_464_4444	10106	474	158	808	1.3(10)-80	Escherichia coli	b2480	[pn:bacterioferritin comigratory protein] [gn:bcp]
CONTIG511	24397576_c3_467_4445	10107	1632	544	2010	6.0(10)-208	Escherichia coli	b2494	[pn:hypothetical protein]
CONTIG511	12578456_c3_471_4446	10108	1407	469	846	1.3(10)-84	Bacillus subtilis	ywbA	[pn:hypothetical protein] [gn:ipa-16d]
CONTIG511	36572167_c3_472_4447	10109	960	320	287	2.2(10)-25	Escherichia coli	b0828	[pn:hypothetical protein in moea-grxa intergenic region] [gn:ybk]
CONTIG511	2035_c3_492_4448	10110	729	243	375	1.1(10)-34	Haemophilus influenzae	HI1708	[pn:transcriptional regulatory protein]
CONTIG512	32516252_fl_1_4449	10111	999	333	1465	3.3(10)-150	Escherichia coli	b2615	[pn:hypothetical 32.6 kd protein in grpe-recn intergenic region]
CONTIG512	2431957_fl_15_4450	10112	1290	430	146	1.3(10)-7	Bacillus subtilis	yxIH	[pn:hypothetical protein]
CONTIG512	11722677_fl_16_4451	10113	1383	461	656	1.8(10)-64	Methanobacterium thermoautotrophicum	MTH225	[pn:histidino] dehydrogenase]

CONTIG512	3244033_f1_17	4452	10114	768	256	302	5.9(10)-27	Escherichia coli	b2842	[pn:2-deoxy-d-gluconate 3-dehydrogenase] [gn:kdud]
CONTIG512	4884682_f1_37	4453	10115	921	307	431	1.3(10)-40	Escherichia coli	b0900	[pn:hypothetical protein] [gn:ycan]
CONTIG512	4567957_f1_45	4454	10116	309	103	101	0.00017	Nicotiana tabacum	P13983	extensin precursor (cell wall hydroxyproline-rich glycoprotein).
CONTIG512	13022331_f1_51	4455	10117	237	79	99	1.8(10)-5	Drosophila melanogaster	X13625	or:drosophila melanogaster sp:p13008 lc:58 re:398 di:direct sr:fruit fly nt:put. ribosomal protein
CONTIG512	4507693_f1_54	4456	10118	1413	471	166	2.5(10)-9	Escherichia coli	b3035	[pn:tolc] [gn:tolc]
CONTIG512	24323967_f1_56	4457	10119	342	114	102	2.2(10)-5	Orf virus	C34768	orf2 protein - orf virus (strain n2)
CONTIG512	6382182_f1_58	4458	10120	1251	417	293	1.3(10)-25	Bordetella pertussis	P11091	cyad protein
CONTIG512	10428883_f2_94	4459	10121	1782	594	2335	2.2(10)-242	Escherichia coli	b2616	[pn:recn] [gn:recn]
CONTIG512	29854158_f2_95	4460	10122	378	126	244	8.3(10)-21	Haemophilus influenzae	H10838	[pn:hypothetical protein]
CONTIG512	16145763_f2_114	4461	10123	834	278	302	5.9(10)-27	Escherichia coli	b2245	[pn:hypothetical protein]
CONTIG512	24847006_f2_122	4462	10124	1950	650	265	2.0(10)-27	Escherichia coli	b3533	[pn:hypothetical 101.6 kd protein in delta-dppf intergenic region]
CONTIG512	32457178_f2_127	4463	10125	2727	909	520	2.6(10)-63	Escherichia coli	b2786	[pn:sensor protein bara] [gn:bara]
CONTIG512	15822183_f2_131	4464	10126	468	156	108	6.0(10)-5	Helicobacter pylori	HP0357	[pn:short chain alcohol dehydrogenase]
CONTIG512	22738760_f2_156	4465	10127	387	129	225	8.5(10)-19	Haemophilus influenzae	H11250	[pn:hypothetical protein]
CONTIG512	12925816_f2_164	4466	10128	276	92	100	0.00033	Caenorhabditis elegans	Z81518	[de:caenorhabditis elegans cosmid f28d9, complete sequence.]
CONTIG512	16103408_f2_166	4467	10129	924	308	385	9.5(10)-36	Escherichia coli	b0254	[pn:f28d9.a] [nt:protein predicted using genefinder; preliminary]
CONTIG512	10025462_f2_170	4468	10130	891	297	95	0.016	Plasmodium falciparum	M13987	[pn:peroxide resistance protein perr] [gn:perr]
CONTIG512										or:plasmodium falciparum pn:histidine-rich protein le:<23 re:679 di:direct sr:p.falciparum (strain 7g8) dna, clone pfhrp-iii

CONTIG512	33723390_f2_178	4469	10131	984	328	1370	4.0(10)-140	Escherichia coli	b0316	[pn:hypothetical protein] [gn:yahb]
CONTIG512	13713887_f3_187	4470	10132	513	171	768	2.5(10)-76	Escherichia coli	b2620	[pn:small protein b] [gn:smpb]
CONTIG512	14164827_f3_188	4471	10133	588	196	395	8.3(10)-37	Escherichia coli	b2622	[pn:slpa integrase] [gn:inta]
CONTIG512	26589591_f3_201	4472	10134	774	258	92	0.04499	Escherichia coli	b3412	[pn:bioh] [gn:bioh]
CONTIG512	6298291_f3_209	4473	10135	306	102	90	0.00059	Aedes densovirus	C40784	hypothetical protein 2 - aedes densovirus (strain gkv 002002)
CONTIG512	4453208_f3_218	4474	10136	2277	759	110	0.0028	Escherichia coli	b1617	[pn:beta-d-glucuronidase] [gn:uida]
CONTIG512	9772307_f3_224	4475	10137	11517	3839	681	9.8(10)-77	Acinetobacter calcoaceticus	AF011339	[PN:unknown] [DE:Acinetobacter calcoaceticus unknown protein gene, partial cds] [LE:<1] [RE:2753] [DI:direct]
CONTIG512	22057062_f3_228	4476	10138	2226	742	451	2.1(10)-42	Bacillus subtilis	yknV	[pn:hypothetical protein]
CONTIG512	13864182_f3_231	4477	10139	447	149	408	3.5(10)-38	Escherichia coli	b0483	[pn:hypothetical protein]
CONTIG512	23516311_f3_238	4478	10140	681	227	431	1.3(10)-40	Synechocystis sp.	S77469	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG512	4723443_f3_266	4479	10141	528	176	448	2.0(10)-42	Escherichia coli	b2668	[pn:hypothetical protein] [gn:ygap]
CONTIG512	13726077_c1_269	4480	10142	240	80	170	5.7(10)-13	Escherichia coli	b2666	[pn:hypothetical protein]
CONTIG512	32207625_c1_270	4481	10143	1773	591	2214	1.5(10)-229	Escherichia coli	b0321	[pn:hypothetical protein] [gn:yahg]
CONTIG512	5986592_c1_278	4482	10144	1011	337	1145	2.7(10)-116	Rhizobium sp.	P55573	hypothetical transketolase family protein y4mn,
CONTIG512	32079650_c1_294	4483	10145	252	84	142	5.2(10)-10	Escherichia coli	U73857	or:escherichia coli le:5101 re:5604 di:direct nt:hypothetical protein
CONTIG512	4494082_c1_319	4484	10146	342	114	116	3.0(10)-7	Bacillus subtilis	spollAA	[pn:anti-anti-sigma factor]
CONTIG512	12948567_c1_332	4485	10147	291	97	391	2.2(10)-36	Escherichia coli	I41306	hypothetical protein (argf-lacZ region) - escherichia coli

CONTIG512	10187_c1_337	4486	10148	411	137	133	4.7(10)-9	Escherichia coli	D90888	or:escherichia coli gn:yfjc le:13589 re:13900 di:complement sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise nt:similar to [swissprot accession number p37907]
CONTIG512	3462787_c2_339	4487	10149	624	208	703	1.8(10)-69	Escherichia coli	b0318	[pn:hypothetical protein] [gn:yahd]
CONTIG512	11187791_c2_340	4488	10150	1650	550	2082	1.3(10)-215	Escherichia coli	b0320	[pn:hypothetical protein] [gn:yahf]
CONTIG512	24785843_c2_347	4489	10151	990	330	1312	5.5(10)-134	Escherichia coli	b0323	[pn:hypothetical protein] [gn:yahi]
CONTIG512	31337753_c2_352	4490	10152	1335	445	444	5.2(10)-42	Escherichia coli	b3127	[pn:hypothetical 49 0 kd protein in mpb-soha intergenic region] [gn:yhau]
CONTIG512	30267840_c2_353	4491	10153	762	254	407	4.4(10)-38	Escherichia coli	b1093	[pn:3-oxoacyl-acyl-carrier protein reductase] [gn:fabg]
CONTIG512	14954818_c2_354	4492	10154	858	286	891	2.2(10)-89	Rhizobium sp.	P55574	hypothetical transketolase family protein y4mo,
CONTIG512	15712817_c2_359	4493	10155	1185	395	432	9.9(10)-41	Bacillus subtilis	ytdD	[pn:hypothetical protein]
CONTIG512	1377152_c2_415	4494	10156	435	145	91	0.00309	Bacillus subtilis	rsbW	[pn:switch protein/serine kinase and anti-sigma factor]
CONTIG512	14082025_c2_428	4495	10157	1200	400	93	0.20999	Methanococcus jannaschii	MJ0156	[pn:acetyl-coa decarboxylase/synthase, subunit beta]
CONTIG512	21678202_c2_429	4496	10158	1296	432	720	3.0(10)-71	Escherichia coli	b2020	[pn:histidinol dehydrogenase] [gn:hisd]
CONTIG512	31725412_c2_430	4497	10159	1365	455	284	3.3(10)-23	Methanobacterium thermoautotrophicum	MTH1496	[pn:amidase]
CONTIG512	787577_c2_435	4498	10160	477	159	701	3.1(10)-69	Escherichia coli	b2619	[pn:hypothetical protein] [gn:yfig]
CONTIG512	35625788_c3_438	4499	10161	381	127	231	2.0(10)-19	Escherichia coli	b2669	[pn:dna-binding protein spa] [gn:stpa]
CONTIG512	5989812_c3_448	4500	10162	1632	544	509	6.9(10)-49	Synechocystis sp.	S76103	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803,, PCC 6803] [SR:PCC 6803,,]

CONTIG512	31350680_c3_451	4501	10163	1458	486	2018	8.5(10)-209	Escherichia coli	b0324	[pn:hypothetical protein] [gn:yahj]
CONTIG512	26818956_c3_457	4502	10164	861	287	358	6.9(10)-33	Haemophilus influenzae	HI0912	[pn:gp]
CONTIG512	31307931_c3_460	4503	10165	903	301	397	5.0(10)-37	Escherichia coli	b3243	[pn:hypothetical protein] [gn:yhes]
CONTIG512	24632632_c3_495	4504	10166	744	248	632	6.4(10)-62	Synechocystis sp.	S76993	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG512	34275752_c3_515	4505	10167	1269	423	210	1.3(10)-16	Haemophilus influenzae	HI0884	[pn:aerobic respiration control protein arcA] [gn:arca]
CONTIG512	29383255_c3_527	4506	10168	1209	403	340	5.5(10)-31	Escherichia coli	b2714	[pn:asc operon repressor protein] [gn:ascg]
CONTIG512	30347307_c3_535	4507	10169	984	328	437	2.8(10)-41	Escherichia coli	b3558	[pn:insertion element is150 hypothetical 33.3 kd protein] [gn:y15b]
CONTIG512	32660955_c3_540	4508	10170	372	124	409	2.7(10)-38	Escherichia coli	b2618	[pn:hypothetical protein]
CONTIG513	23629567_f1_1	4509	10171	2427	809	1447	2.7(10)-148	Escherichia coli	b0124	[pn:glucose dehydrogenase] [gn:gdh]
CONTIG513	7282800_f1_18	4510	10172	378	126	509	6.9(10)-49	Escherichia coli	b1599	[pn:hypothetical protein]
CONTIG513	24406285_f1_26	4511	10173	918	306	1150	8.1(10)-117	Escherichia coli	b1595	[pn:hypothetical protein] [gn:ynfl]
CONTIG513	4891293_f1_40	4512	10174	687	229	758	2.7(10)-75	Proteus mirabilis	P07641	chloramphenicol acetyltransferase (ec 2.3.1.28).
CONTIG513	25584832_f1_50	4513	10175	723	241	868	6.2(10)-87	Escherichia coli	b1585	[pn:hypothetical protein] [gn:ynic]
CONTIG513	33876063_f1_52	4514	10176	1116	372	1366	1.1(10)-139	Escherichia coli	b1580	[pn:starvation sensing protein rspb] [gn:rspb]
CONTIG513	7119082_f1_59	4515	10177	2037	679	2392	2.0(10)-248	Escherichia coli	b1538	[pn:dipeptidyl carboxypeptidase ii] [gn:dcp]
CONTIG513	23611652_f1_61	4516	10178	825	275	322	4.5(10)-29	Escherichia coli	b1790	[pn:hypothetical protein]
CONTIG513	24259677_f1_62	4517	10179	495	165	293	5.2(10)-26	Bacillus subtilis	ybbK	[pn:hypothetical protein]
CONTIG513	1048177_f1_70	4518	10180	309	103	138	1.3(10)-9	Escherichia coli	b3238	[pn:hypothetical protein] [gn:yhen]

CONTIG513	30286561_fl_76	4519	10181	1590	530	2218	5.5(10)-230	Escherichia coli	b1385	[pn:hypothetical protein] [gn:feab]
CONTIG513	24490626_fl_85	4520	10182	999	333	1487	1.6(10)-152	Escherichia coli	b1388	[pn:hypothetical protein]
CONTIG513	14539213_fl_86	4521	10183	300	100	495	2.1(10)-47	Escherichia coli	b1389	[pn:hypothetical protein]
CONTIG513	4713467_fl_91	4522	10184	798	266	1016	1.3(10)-102	Escherichia coli	b1394	[pn:hypothetical protein]
CONTIG513	12276640_fl_96	4523	10185	1332	444	2185	1.7(10)-226	Escherichia coli	b1398	[pn:hypothetical protein]
CONTIG513	26737775_fl_97	4524	10186	963	321	1260	1.8(10)-128	Escherichia coli	b1399	[pn:hypothetical protein]
CONTIG513	4198568_fl_98	4525	10187	615	205	951	1.0(10)-95	Escherichia coli	b1400	[pn:hypothetical protein]
CONTIG513	23489792_fl_104	4526	10188	1548	516	654	3.0(10)-64	Mycobacterium tuberculosis	AL021932	[de:mycobacterium tuberculosis sequence v037] [pn:putative dehydrogenase] [gn:mtv037.13c] [nt:mtv037.13c, len]
CONTIG513	14878332_fl_105	4527	10189	1227	409	495	2.1(10)-47	Escherichia coli	b1661	[pn:cyclopropane-fatty-acyl-phospholipid synthase] [gn:cfa]
CONTIG513	42312_fl_115	4528	10190	3942	1314	6025	0	Escherichia coli	b1413	[pn:atp-dependent helicase hrpa] [gn:hrpa]
CONTIG513	126541_f2_141	4529	10191	1062	354	154	1.3(10)-8	Bacillus subtilis	ywcH	[pn:hypothetical protein] [gn:ipa-44d]
CONTIG513	885766_f2_153	4530	10192	1290	430	1818	1.3(10)-187	Escherichia coli	b1594	[pn:protein] [gn:mic]
CONTIG513	23462778_f2_154	4531	10193	699	233	1033	2.0(10)-104	Escherichia coli	b1593	[pn:hypothetical protein]
CONTIG513	21579652_f2_178	4532	10194	351	117	528	6.7(10)-51	Escherichia coli	b1582	[pn:hypothetical protein]
CONTIG513	4535002_f2_179	4533	10195	1254	418	2087	4.2(10)-216	Escherichia coli	b1581	[pn:starvation sensing protein rspa] [gn:rspa]
CONTIG513	24735213_f2_180	4534	10196	1437	479	1821	6.4(10)-188	Escherichia coli	b1543	[pn:hypothetical protein]
CONTIG513	4769191_f2_181	4535	10197	1476	492	2005	2.0(10)-207	Escherichia coli	b1542	[pn:hypothetical protein] [gn:ydfi]
CONTIG513	11754183_f2_195	4536	10198	2148	716	1055	9.5(10)-107	Escherichia coli	b0124	[pn:glucose dehydrogenase] [gn:gcd]

CONTIG513	4804068_f2_202	4537	10199	201	67	208	5.4(10)-17	Escherichia coli	b1382	[pn:hypothetical protein]
CONTIG513	13808563_f2_213	4538	10200	594	198	765	5.0(10)-76	Escherichia coli	b1391	[pn:hypothetical protein]
CONTIG513	26851665_f2_216	4539	10201	783	261	774	5.7(10)-77	Escherichia coli	b1393	[pn:hypothetical protein] [gn:ydbbs]
CONTIG513	32692805_f2_217	4540	10202	1581	527	1940	1.6(10)-200	Escherichia coli	b1395	[pn:hypothetical protein] [gn:ydbu]
CONTIG513	12710012_f2_218	4541	10203	1290	430	1760	1.8(10)-181	Escherichia coli	b1397	[pn:hypothetical protein]
CONTIG513	4767043_f2_225	4542	10204	1986	662	1596	4.5(10)-164	Escherichia coli	b4083	[pn:hypothetical 73.7 kd protein in fdhf-phnp intergenic region]
CONTIG513	15676040_f2_227	4543	10205	948	316	203	1.8(10)-16	Bacillus subtilis	dliE	[pn:hypothetical protein] [gn:ipa-1r]
CONTIG513	32506457_f2_229	4544	10206	753	251	231	2.0(10)-19	Mycobacterium tuberculosis	AL021932	[de:mycobacterium tuberculosis sequence v037.] [pn:hypothetical protein mtv037.12c] [gn:mtv037.12c] [nt:mtv037.12c,
CONTIG513	26584505_f2_233	4545	10207	963	321	176	3.2(10)-13	Haemophilus influenzae	H11399	[pn:hypothetical protein]
CONTIG513	14879707_f2_238	4546	10208	546	182	632	6.4(10)-62	Escherichia coli	b0354	[pn:hypothetical protein]
CONTIG513	34194791_f2_255	4547	10209	846	282	868	6.2(10)-87	Escherichia coli	b1414	[pn:hypothetical protein in alda 5" region] [gn:ydef]
CONTIG513	22744037_f3_272	4548	10210	984	328	182	4.7(10)-12	Mycobacterium tuberculosis	Z97193	[PN:hypothetical protein MTCY180.06] [GN:MTCY180.06] [DE:Mycobacterium tuberculosis cosmid Y180.] [NT:MTCY180.06, possible oxidoreductase, Len: 334.] [LE:6203] [RE:7207] [DI:direct]
CONTIG513	38275_f3_277	4549	10211	432	144	477	1.7(10)-45	Escherichia coli	b1600	[pn:hypothetical protein]
CONTIG513	859452_f3_299	4550	10212	456	152	142	1.7(10)-9	Escherichia coli	b1328	[pn:hypothetical protein] [gn:yjz]
CONTIG513	35581281_f3_320	4551	10213	459	153	383	1.5(10)-35	Escherichia coli	b0607	[pn:hypothetical protein] [gn:ybdq]
CONTIG513	5272338_f3_339	4552	10214	183	61	168	9.4(10)-13	Escherichia coli	b1550	[pn:hypothetical protein]

CONTIG513	24644576_f3_344	4553	10215	2646	882	3438	0	Escherichia coli	b1381	[pn:hypothetical protein] [gn:ydbh]
CONTIG513	16535137_f3_345	4554	10216	348	116	299	1.2(10)-26	Escherichia coli	b1383	[pn:hypothetical protein]
CONTIG513	16657590_f3_365	4555	10217	774	258	997	1.3(10)-100	Escherichia coli	b1390	[pn:hypothetical protein]
CONTIG513	16269758_f3_366	4556	10218	1200	400	1585	6.5(10)-163	Escherichia coli	b1392	[pn:hypothetical protein]
CONTIG513	34614416_f3_371	4557	10219	513	171	569	3.0(10)-55	Escherichia coli	b1396	[pn:hypothetical protein]
CONTIG513	22117188_f3_387	4558	10220	978	326	437	2.8(10)-41	Haemophilus influenzae	HI1364	[pn:hypothetical protein]
CONTIG513	22870175_f3_406	4559	10221	483	161	597	3.2(10)-58	Escherichia coli	b1415	[pn:lactaldehyde dehydrogenase a] [gn:alda]
CONTIG513	22069212_c1_408	4560	10222	1668	556	134	1.3(10)-5	Bacillus subtilis	yhcA	[pn:hypothetical protein]
CONTIG513	6539783_c1_410	4561	10223	1452	484	420	1.8(10)-39	Escherichia coli	b0572	[pn:hypothetical protein] [gn:yicb]
CONTIG513	20214775_c1_439	4562	10224	696	232	116	4.2(10)-5	Escherichia coli	b0375	[pn:hypothetical protein] [gn:yaiv]
CONTIG513	23870400_c1_454	4563	10225	2091	697	2967	0	Escherichia coli	b1387	[pn:hypothetical protein] [gn:maoc]
CONTIG513	13944091_c1_480	4564	10226	231	77	247	4.0(10)-21	Escherichia coli	b1541	[pn:hypothetical protein]
CONTIG513	12911066_c1_491	4565	10227	939	313	138	3.1(10)-9	Homo sapiens	Q09327	beta-1,4-mannosyl-glycoprotein beta-1,4-n-acetylglucosaminyltransferase (ec 2.4.1.144) (n-glycosyl oligosaccharide-glycoprotein n-acetylglucosaminyltransferase iii) (n-acetylglucosaminyltransferase iii) (gnt-iii) (glnac-t iii).
CONTIG513	15786281_c1_492	4566	10228	348	116	323	3.5(10)-29	Escherichia coli	b1586	[pn:hypothetical protein]
CONTIG513	30361281_c1_495	4567	10229	270	90	221	3.5(10)-17	Escherichia coli	b1587	[pn:hypothetical protein]
CONTIG513	22925083_c1_502	4568	10230	783	261	97	0.006	Sinorhizobium meliloti	AF031940	[de:sinorhizobium meliloti alcohol dehydrogenase (adha) gene, completecds.] [pn:hypothetical protein] [nt:orf1]

CONTIG513	15679061_c1_504	4569	10231	672	224	291	8.6(10)-26	Bacillus subtilis	opuCB	[pn:glycine betaine/carnitine/choline abc transporter] [gn:yvbd]
CONTIG513	25961525_c1_512	4570	10232	1503	501	823	3.7(10)-82	Bacillus subtilis	ypwA	[pn:hypothetical protein]
CONTIG513	11722677_c1_521	4571	10233	1461	487	1881	2.7(10)-194	Escherichia coli	b1184	[pn:umuc protein] [gn:umuc]
CONTIG513	892531_c1_523	4572	10234	996	332	1546	8.9(10)-159	Klebsiella pneumoniae	P27504	coenzyme pqq synthesis protein b.
CONTIG513	914591_c2_541	4573	10235	1209	403	338	9.0(10)-31	Escherichia coli	b2685	[pn:multidrug resistance protein a] [gn:emra]
CONTIG513	641967_c2_549	4574	10236	858	286	422	1.1(10)-39	Escherichia coli	b0058	[pn:hypothetical 24.9 kd protein in sura-hepa intergenic region] [gn:yabo]
CONTIG513	1969212_c2_550	4575	10237	1041	347	321	5.5(10)-28	Escherichia coli	b3829	[pn:5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase] [gn:mete]
CONTIG513	32667541_c2_582	4576	10238	2502	834	3407	0	Escherichia coli	b1386	[pn:copper amine oxidase precursor] [gn:tyna]
CONTIG513	14063411_c2_583	4577	10239	2037	679	1604	6.2(10)-165	Escherichia coli	b4083	[pn:hypothetical 73.7 kd protein in fdhf-phnp intergenic region]
CONTIG513	10338967_c2_584	4578	10240	1158	386	268	1.3(10)-21	Escherichia coli	b1025	[pn:hypothetical protein] [gn:yedtl]
CONTIG513	3324025_c2_586	4579	10241	438	146	173	2.7(10)-13	Azospirillum brasilense	X70360	or-azospirillum brasilense gn:carr le:59 re:580 di:direct nt:orf2
CONTIG513	30257702_c2_588	4580	10242	951	317	982	5.2(10)-99	Escherichia coli	b1384	[pn:hypothetical protein] [gn:fear]
CONTIG513	23908516_c2_595	4581	10243	1020	340	1498	1.1(10)-153	Escherichia coli	b1380	[pn:d-lactate dehydrogenase] [gn:ldha]
CONTIG513	915887_c2_596	4582	10244	840	280	1066	6.5(10)-108	Pseudomonas pyrocinia	JN0828	chloroperoxidase (ec 1.11.1.-) precursor - pseudomonaspyrocinia this enzyme catalyzes the formation of carbon-halogen bonds in the presence of hydrogen peroxide, halide ions, and a suitable organic substrate. this enzyme is involved in the production o
CONTIG513	9823576_c2_606	4583	10245	696	232	1021	3.7(10)-103	Escherichia coli	b1931	[pn:yedg] [gn:yedk]

CONTIG513	36070465_c2_609	4584	10246	852	284	113	0.00017	Methanobacterium thermoautotrophicum	MTH882	[pn:conserved protein]
CONTIG513	3250786_c2_620	4585	10247	609	203	870	3.7(10)-87	Escherichia coli	b1584	[pn:spermidine n1-acetyltransferase] [gn:spg]
CONTIG513	25869028_c2_623	4586	10248	2325	775	3450	0	Escherichia coli	b1587	[pn:hypothetical protein]
CONTIG513	14572206_c2_624	4587	10249	621	207	1110	1.3(10)-112	Escherichia coli	b0895	[pn:anaerobic dimethyl sulfoxide reductase chain b] [gn:dmsb]
CONTIG513	13126632_c2_626	4588	10250	723	241	764	6.5(10)-76	Escherichia coli	b1591	[pn:hypothetical protein]
CONTIG513	24475938_c2_629	4589	10251	291	97	156	8.4(10)-11	Pseudomonas aeruginosa	Q01609	hypothetical 40.7 kd protein in opde 3'region (orf2).
CONTIG513	14322166_c2_631	4590	10252	738	246	305	2.8(10)-27	Bacillus subtilis	opuCB	[pn:glycine betaine/carnitine/choline abc transporter] [gn:yvbd]
CONTIG513	9899186_c2_632	4591	10253	912	304	362	2.6(10)-33	Bacillus subtilis	opuCC	[pn:osmoprotectant-binding protein] [gn:yvbc]
CONTIG513	164182_c2_641	4592	10254	1338	446	1829	9.0(10)-189	Escherichia coli	b1596	[pn:hypothetical protein] [gn:ynfm]
CONTIG513	12597675_c2_643	4593	10255	843	281	1086	4.9(10)-110	Escherichia coli	b1598	[pn:hypothetical protein]
CONTIG513	16602291_c2_658	4594	10256	438	146	424	7.0(10)-40	Klebsiella pneumoniae	P27506	coenzyme pqq synthesis protein d.
CONTIG513	14744537_c2_660	4595	10257	2298	766	2069	3.3(10)-214	Klebsiella pneumoniae	P27508	coenzyme pqq synthesis protein f (ec 3.4.99.-).
CONTIG513	21729677_c3_684	4596	10258	666	222	928	2.7(10)-93	Escherichia coli	b1412	[pn:acyl carrier protein phosphodiesterase] [gn:acpd]
CONTIG513	31502177_c3_754	4597	10259	1299	433	434	8.9(10)-49	Escherichia coli	b2796	[pn:putative serine transporter] [gn:sdac]
CONTIG513	1206557_c3_755	4598	10260	246	82	263	8.0(10)-23	Salmonella typhimurium	Q56031	virulence protein msga.
CONTIG513	1257206_c3_763	4599	10261	897	299	1144	3.5(10)-116	Escherichia coli	b1539	[pn:hypothetical oxidoreductase in dep-noha intergenic region]
CONTIG513	24813151_c3_764	4600	10262	708	236	998	1.0(10)-100	Escherichia coli	b1540	[pn:hypothetical protein]
CONTIG513	2189155_c3_775	4601	10263	372	124	408	3.5(10)-38	Escherichia coli	b1583	[pn:hypothetical protein]

CONTIG513	14473425_c3_783	4602	10264	927	309	932	1.0(10)-93	Escherichia coli	b1590	[pn:hypothetical protein]
CONTIG513	10945780_c3_785	4603	10265	453	151	236	5.7(10)-20	Escherichia coli	b1848	[pn:hypothetical 10.7 kd protein in part 5'''region] [gn:yebg]
CONTIG513	6025635_c3_790	4604	10266	1257	419	806	2.2(10)-80	Bacillus subtilis	opuBA	[pn:choline abc transporter] [gn:prov]
CONTIG513	13159433_c3_791	4605	10267	1416	472	1077	4.4(10)-109	Escherichia coli	b1592	[pn:hypothetical protein]
CONTIG513	29882802_c3_803	4606	10268	1065	355	1065	8.3(10)-108	Escherichia coli	b1601	[pn:hypothetical protein]
CONTIG513	10662961_c3_806	4607	10269	363	121	561	2.1(10)-54	Escherichia coli	b0410	[pn:yajd]
CONTIG513	36382212_c3_807	4608	10270	1038	346	1150	8.1(10)-117	Klebsiella pneumoniae	P27509	hypothetical protein in pqa 5' region (orf x) (fragment).
CONTIG513	16069816_c3_808	4609	10271	843	281	1153	3.8(10)-117	Klebsiella pneumoniae	P27505	coenzyme pqq synthesis protein c.
CONTIG513	24066262_c3_810	4610	10272	1185	395	1943	7.5(10)-201	Klebsiella pneumoniae	P27507	coenzyme pqq synthesis protein e.
CONTIG52	33807686_fl_1	4611	10273	465	155	723	1.3(10)-71	Escherichia coli	b0683	[pn:ferric uptake regulation protein] [gn:fur]
CONTIG52	4167842_c3_6	4612	10274	240	80	250	1.8(10)-21	Escherichia coli	b0682	[pn:hypothetical protein] [gn:ybfm]
CONTIG53	10359689_c2_3	4613	10275	425	141	660	6.9(10)-65	Escherichia coli	b1827	[pn:hypothetical protein]
CONTIG54	14978382_fl_1	4614	10276	356	119	192	9.4(10)-15	Thiobacillus ferrooxidans	P20085	mobilization protein mobil.
CONTIG56	4070952_f2_2	4615	10277	303	101	92	0.00021	Escherichia coli	b0530	[pn:hypothetical protein] [gn:sfma]
CONTIG58	10947127_fl_1	4616	10278	459	153	543	1.7(10)-52	Escherichia coli	b1938	[pn:flagellar basal-body m-ring protein] [gn:flif]
CONTIG58	23641281_c2_7	4617	10279	477	159	186	1.2(10)-14	Bacillus subtilis	ydff	[pn:hypothetical protein]
CONTIG59	36350016_c2_5	4618	10280	744	248	1104	6.0(10)-112	Escherichia coli	b3232	[pn:hypothetical 43.1 kd protein in rplm-hhaa intergenic region] [gn:yhem]
CONTIG6	29877090_c2_8	4619	10281	339	113	92	0.00067	Bacillus subtilis	ccpA	[pn:transcriptional regulator] [gn:grar]
CONTIG6	32494527_c3_9	4620	10282	426	142	217	6.0(10)-18	Haemophilus influenzae	H10522	[pn:sp]

CONTIG60	29322524_c1_3	4621	10283	385	128	325	2.2(10)-29	Bacteriophage phi-80	P14819	repressor protein ci.
CONTIG61	35550041_c2_6	4622	10284	1290	430	1593	9.3(10)-164	Escherichia coli	b0955	[pn:hypothetical protein]
CONTIG62	33261442_fl_1	4623	10285	1028	343	101	0.034	Thiobacillus ferrooxidans	AF032884	[de:thiobacillus ferrooxidans n-acetylglucosamine-1-phosphateuridylyltransferase (glmu) gene, partial cds; glucosamine synthase(glms) and recg (recg) genes, complete cds; and transposon tn5468,complete sequence"] [pn:tnsd]
CONTIG63	13071907_f2_3	4624	10286	246	82	339	7.0(10)-31	Escherichia coli	b0957	[pn:outer membrane protein a]
CONTIG63	22276682_c1_6	4625	10287	483	161	709	4.4(10)-70	Escherichia coli	b0956	[pn:hypothetical protein in ompa 3"" region] [gn:yebg]
CONTIG64	22847502_c1_6	4626	10288	198	66	100	8.0(10)-5	Escherichia coli	b1987	[pn:transcriptional regulator] [gn:ebi]
CONTIG64	26453393_c3_7	4627	10289	822	274	1178	8.8(10)-120	Escherichia coli	b1987	[pn:transcriptional regulator] [gn:ebi]
CONTIG65	25838388_c1_1	4628	10290	219	73	269	1.8(10)-23	Escherichia coli	b0958	[pn:cell division inhibitor] [gn:sula]
CONTIG66	4866552_f2_2	4629	10291	426	142	120	1.1(10)-7	Escherichia coli	L43373	or-escherichia coli pn:pilin le-22 re-567 di:direct sr-escherichia coli (strain 31a/o6) dna
CONTIG67	13175643_fl_1	4630	10292	1026	342	135	1.7(10)-8	Haemophilus influenzae	III1488	[pn:e16 protein] [gn:mue16]
CONTIG7	31267540_f2_2	4631	10293	282	94	326	1.7(10)-29	Escherichia coli	b1734	[pn:phospho-beta-glucosidase b] [gn:celf]
CONTIG7	11729152_f3_3	4632	10294	345	115	138	1.1(10)-8	Escherichia coli	b1734	[pn:phospho-beta-glucosidase b] [gn:celf]
CONTIG70	22066625_f3_2	4633	10295	687	229	961	8.6(10)-97	Escherichia coli	b0055	[pn:hypothetical 30.6 kd protein in sura-hepa intergenic region] [gn:yabh]
CONTIG71	23880458_f2_2	4634	10296	579	193	962	6.7(10)-97	Escherichia coli	b0675	[pn:nagd protein] [gn:nagd]
CONTIG71	16251037_f3_4	4635	10297	345	115	370	5.7(10)-34	Escherichia coli	b0674	[pn:asparagine synthetase b] [gn:asnb]

CONTIG72	3943817_c1_3	4636	10298	684	228	104	0.00289	Yersinia enterocolitica (type 0:8)	U46859	or:yersinia enterocolitica (type 0:8) pn:rfbx gn:rfbx le:6526 re:7815 di:direct
CONTIG73	33719031_c3_4	4637	10299	594	198	1003	3.1(10)-101	Escherichia coli	b0223	[pn:hypothetical protein in gmha- fhia intergenic region] [gn:yafj]
CONTIG74	431332_f3_1	4638	10300	987	329	94	0.07	Bacillus subtilis	yvrC	[pn:hypothetical protein]
CONTIG77	32145043_c2_7	4639	10301	222	74	235	7.5(10)-20	synthetic construct	M15619	or:artificial sequence le:29 re:>232 di:direct sr:e.coli (strain se5000) synthetic dna, clone pkb1 nt:orf16- lacZ fusion protein
CONTIG78	31901556_c2_6	4640	10302	1035	345	1101	1.3(10)-111	Escherichia coli	X05874	or:escherichia coli pn:mature receptor protein le:244 re:2367 di:direct nt.author-given protein sequence is in conflict with
CONTIG80	23629716_f3_2	4641	10303	614	205	909	2.7(10)-91	Escherichia coli	b0054	[pn:organic solvent tolerance protein precursor] [gn:imp]
CONTIG82	14570453_c3_4	4642	10304	366	122	159	8.4(10)-12	Escherichia coli	b1160	[pn:hypothetical protein]
CONTIG83	22166288_f3_3	4643	10305	801	267	1289	1.5(10)-131	Escherichia coli	b0432	[pn:cytochrome o ubiquinol oxidase subunit ii] [gn:cvoa]
CONTIG84	35663506_c1_7	4644	10306	441	147	419	2.3(10)-39	Escherichia coli	b3344	[pn:hypothetical protein] [gn:yhem]
CONTIG84	12203427_c2_8	4645	10307	441	147	396	6.5(10)-37	Escherichia coli	b3345	[pn:hypothetical 13.6 kd protein in rpsl-fkpa intergenic region]
CONTIG85	26573386_f3_3	4646	10308	615	205	328	1.0(10)-29	Escherichia coli	b1025	[pn:hypothetical protein] [gn:ycdt]
CONTIG85	2080192_c3_7	4647	10309	390	130	545	1.1(10)-52	Escherichia coli	b1642	[pn:hypothetical protein] [gn:slya]
CONTIG86	36150166_c1_2	4648	10310	468	156	100	0.00064	Haemophilus influenzae	H10676	[pn:integrase-recombinase protein] [gn:xerc]
CONTIG87	12308130_c1_4	4649	10311	402	134	334	2.3(10)-30	Escherichia coli	b1090	[pn:plsx protein] [gn:plsx]
CONTIG87	20738833_c1_5	4650	10312	519	173	762	1.1(10)-75	Escherichia coli	b1091	[pn:3-oxoacyl-acyl-carrier-protein synthase iii] [gn:fabh]
CONTIG88	6362961_c1_4	4651	10313	789	263	1231	2.1(10)-125	Escherichia coli	b0931	[pn:nicotinate phosphoribosyltransferase] [gn:pncb]
CONTIG89	22078757_c2_4	4652	10314	522	174	259	2.1(10)-22	Escherichia coli	b1374	[pn:hypothetical protein]

CONTIG90	2150290_fl_1	4653	10315	651	217	781	1.0(10)-77	Escherichia coli	b0212	[pn:hypothetical protein] [gn:glob]
CONTIG90	4538138_c3_6	4654	10316	420	140	511	4.2(10)-49	Escherichia coli	b0213	[pn:hypothetical protein] [gn:yafs]
CONTIG91	135805_c2_5	4655	10317	849	283	853	1.6(10)-104	Escherichia coli	b2581	[pn:hypothetical 37.8 kd protein in ung 3''' region] [gn:yfif]
CONTIG92	117202_fl_1	4656	10318	429	143	734	9.9(10)-73	Escherichia coli	b3231	[pn:50s ribosomal subunit protein 113] [gn:rplm]
CONTIG92	25525308_fl_2	4657	10319	396	132	645	2.7(10)-63	Escherichia coli	b3230	[pn:30s ribosomal subunit protein s9] [gn:rpsl]
CONTIG93	32478807_fl_1	4658	10320	609	203	849	6.4(10)-85	Escherichia coli	b1818	[pn:pts system, mannose-specific ic component] [gn:many]
CONTIG93	26056711_fl_2	4659	10321	474	158	748	3.2(10)-74	Escherichia coli	b1819	[pn:pts system, mannose-specific nd component] [gn:manz]
CONTIG94	3412917_c1_4	4660	10322	414	138	313	4.0(10)-28	Escherichia coli	b1678	[pn:hypothetical protein]
CONTIG96	128251_c2_4	4661	10323	648	216	958	1.8(10)-96	Escherichia coli	b0222	[pn:phosphoheptose isomerase] [gn:gmha]
CONTIG98	10161416_c1_4	4662	10324	870	290	152	9.5(10)-9	Escherichia coli	b1959	[pn:hypothetical 32.2 kd protein in vsr 5'''region] [gn:yeda]
CONTIG99	13867212_fl_1	4663	10325	270	90	326	1.7(10)-29	Haemophilus influenzae	H11713	[pn:phosphohistidinoprotein-hexose phosphotransferase] [gn:ptsh]
CONTIG99	3964643_fl_2	4664	10326	845	282	1035	1.3(10)-104	Escherichia coli	b2416	[pn:phosphoenolpyruvate-protein phosphotransferase] [gn:ptsi]
CONTIG99	12298262_c1_4	4665	10327	357	119	269	1.8(10)-23	Salmonella typhimurium	S04160	[pn:hypothetical protein k - salmonella typhimurium (fragment)]
CONTIG103	26692751_f3_2	4666	10328	192	64					
CONTIG104	4086013_fl_1	4667	10329	231	77					
CONTIG107	2461718_f3_2	4668	10330	426	142					
CONTIG107	160902_c2_4	4669	10331	198	66					
CONTIG108	16922530_f2_1	4670	10332	369	123					
CONTIG109	10550041_f3_3	4671	10333	258	86					
CONTIG112	24298378_c2_2	4672	10334	411	137					
CONTIG112	267327_c3_3	4673	10335	483	161					
CONTIG114	24328157_c2_2	4674	10336	924	308					
CONTIG116	32086557_c3_10	4675	10337	348	116					
CONTIG118	24508568_c3_17	4676	10338	183	61					
CONTIG12	24883437_c2_3	4677	10339	240	80					
CONTIG123	15647957_c2_8	4678	10340	189	63					

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CONTIG211	2456516_f3_10	4757	10419	243	81							
CONTIG212	9875632_f3_5	4758	10420	186	62							
CONTIG213	34032182_f3_5	4759	10421	630	210							
CONTIG214	1268757_c3_13	4760	10422	459	153							
CONTIG216	23613160_f1_2	4761	10423	189	63							
CONTIG216	5197128_f3_8	4762	10424	939	313							
CONTIG216	34382017_c2_15	4763	10425	291	97							
CONTIG219	4589680_f1_1	4764	10426	597	199							
CONTIG219	23948453_c1_5	4765	10427	453	151							
CONTIG219	20349040_c1_6	4766	10428	414	138							
CONTIG219	35390888_c1_7	4767	10429	222	74							
CONTIG221	882808_f3_3	4768	10430	228	76							
CONTIG221	1407886_c3_7	4769	10431	930	310							
CONTIG222	34385156_f2_3	4770	10432	792	264							
CONTIG222	10750925_f2_5	4771	10433	399	133							
CONTIG224	7235025_f3_9	4772	10434	252	84							
CONTIG228	22850390_f1_1	4773	10435	405	135							
CONTIG228	24329555_f2_3	4774	10436	306	102							
CONTIG228	3378181_f2_5	4775	10437	309	103							
CONTIG229	5317907_c3_10	4776	10438	222	74							
CONTIG230	1447201_f1_1	4777	10439	561	187							
CONTIG231	29878930_f3_10	4778	10440	210	70							
CONTIG232	10439637_f2_3	4779	10441	201	67							
CONTIG233	34469636_c1_11	4780	10442	354	118							
CONTIG233	35833587_c2_16	4781	10443	399	133							
CONTIG233	24220308_c3_19	4782	10444	282	94							
CONTIG233	31437882_c3_20	4783	10445	267	89							
CONTIG234	12207001_f1_1	4784	10446	288	96							
CONTIG234	11751391_f2_4	4785	10447	249	83							
CONTIG235	19698591_f2_3	4786	10448	576	192							
CONTIG235	29803965_f2_4	4787	10449	924	308							
CONTIG235	6053417_f3_5	4788	10450	1353	451							
CONTIG235	155_f3_7	4789	10451	345	115							
CONTIG235	10398388_c1_8	4790	10452	327	109							
CONTIG239	26049067_c1_17	4791	10453	564	188							
CONTIG239	25397328_c2_20	4792	10454	342	114							
CONTIG239	10266657_c2_21	4793	10455	198	66							
CONTIG239	4016936_c2_23	4794	10456	270	90							
CONTIG239	20506592_c3_26	4795	10457	309	103							

CONTIG239	20080082_c3_28	4796	10458	237	79						
CONTIG24	22831586_c3_7	4797	10459	498	166						
CONTIG241	33882055_f3_13	4798	10460	201	67						
CONTIG242	32130002_f3_7	4799	10461	264	88						
CONTIG243	12791092_c1_12	4800	10462	690	230						
CONTIG243	13680433_c3_18	4801	10463	591	197						
CONTIG245	36589693_c2_15	4802	10464	198	66						
CONTIG249	22682137_c3_19	4803	10465	312	104						
CONTIG25	21620388_f3_3	4804	10466	372	124						
CONTIG250	31275789_c1_13	4805	10467	257	85						
CONTIG250	36379838_c3_18	4806	10468	378	126						
CONTIG251	5334456_f2_10	4807	10469	183	61						
CONTIG252	24619412_f1_4	4808	10470	321	107						
CONTIG252	25401076_f1_6	4809	10471	186	62						
CONTIG252	14632816_c1_30	4810	10472	747	249						
CONTIG252	10720376_c2_36	4811	10473	240	80						
CONTIG252	10333376_c2_40	4812	10474	243	81						
CONTIG252	14492307_c2_41	4813	10475	663	221						
CONTIG252	2213887_c3_49	4814	10476	249	83						
CONTIG253	21739402_f2_2	4815	10477	249	83						
CONTIG257	32213278_f1_1	4816	10478	195	65						
CONTIG257	12313528_c2_9	4817	10479	363	121						
CONTIG259	20963558_f1_1	4818	10480	195	65						
CONTIG26	35267665_c1_4	4819	10481	432	144						
CONTIG260	6455338_f2_6	4820	10482	225	75						
CONTIG260	4394036_c3_33	4821	10483	432	144						
CONTIG261	10195340_c3_27	4822	10484	210	70						
CONTIG262	5900260_f3_14	4823	10485	201	67						
CONTIG262	3957016_f3_16	4824	10486	315	105						
CONTIG262	25939586_c2_23	4825	10487	438	146						
CONTIG263	35944827_f1_1	4826	10488	249	83						
CONTIG263	24412582_f1_2	4827	10489	450	150						
CONTIG263	22850400_f3_9	4828	10490	363	121						
CONTIG263	34411305_f3_11	4829	10491	357	119						
CONTIG263	20003_c2_18	4830	10492	537	179						
CONTIG263	11020251_c3_25	4831	10493	198	66						
CONTIG267	25662886_f2_10	4832	10494	216	72						
CONTIG269	34664677_f2_4	4833	10495	942	314						
CONTIG269	25517202_f2_6	4834	10496	1671	557						

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CONTIG318	6814128_f3_13	4913	10575	213	71						
CONTIG318	26363308_f3_18	4914	10576	309	103						
CONTIG318	30579507_c2_25	4915	10577	195	65						
CONTIG319	14957657_f1_2	4916	10578	186	62						
CONTIG319	10440713_f1_6	4917	10579	381	127						
CONTIG319	30339027_f1_7	4918	10580	555	185						
CONTIG319	19776557_f3_26	4919	10581	225	75						
CONTIG319	45245692_c2_30	4920	10582	333	111						
CONTIG319	22459705_c2_32	4921	10583	186	62						
CONTIG32	1979167_c1_2	4922	10584	186	62						
CONTIG320	4348250_f3_14	4923	10585	198	66						
CONTIG320	36378428_c1_22	4924	10586	228	76						
CONTIG322	20941652_c3_44	4925	10587	207	69						
CONTIG324	36022916_f1_1	4926	10588	249	83						
CONTIG326	16225827_f2_12	4927	10589	192	64						
CONTIG326	4094687_f2_13	4928	10590	273	91						
CONTIG326	6839662_f3_23	4929	10591	900	300						
CONTIG326	2346907_f3_29	4930	10592	198	66						
CONTIG326	21579680_c1_41	4931	10593	219	73						
CONTIG326	22345463_c1_43	4932	10594	417	139						
CONTIG326	26847916_c2_54	4933	10595	288	96						
CONTIG326	33790916_c3_56	4934	10596	342	114						
CONTIG327	34666516_f1_8	4935	10597	732	244						
CONTIG327	5117968_f1_9	4936	10598	597	199						
CONTIG327	32313591_f3_18	4937	10599	378	126						
CONTIG327	6119561_c2_37	4938	10600	219	73						
CONTIG329	31900713_c3_35	4939	10601	255	85						
CONTIG330	16015787_f1_7	4940	10602	432	144						
CONTIG330	786402_f3_17	4941	10603	267	89						
CONTIG330	22477305_c1_29	4942	10604	228	76						
CONTIG330	9975431_c1_31	4943	10605	525	175						
CONTIG330	11891652_c1_32	4944	10606	1206	402						
CONTIG330	5976381_c1_33	4945	10607	282	94						
CONTIG330	20006305_c1_36	4946	10608	441	147						
CONTIG330	26753427_c1_37	4947	10609	714	238						
CONTIG330	14844816_c2_38	4948	10610	1635	545						
CONTIG330	6719787_c2_42	4949	10611	291	97						
CONTIG330	26292592_c2_44	4950	10612	333	111						
CONTIG330	24663201_c3_47	4951	10613	801	267						

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CONTIG369	23531258_c1_33	5030	10692	198	66
CONTIG369	3207208_c1_38	5031	10693	237	79
CONTIG369	12363916_c1_41	5032	10694	567	189
CONTIG369	24330056_c1_42	5033	10695	216	72
CONTIG369	19631640_c2_43	5034	10696	726	242
CONTIG369	24651077_c2_53	5035	10697	432	144
CONTIG369	26587501_c3_54	5036	10698	633	211
CONTIG369	12595667_c3_61	5037	10699	294	98
CONTIG37	14709456_f1_2	5038	10700	228	76
CONTIG37	4692027_c2_7	5039	10701	327	109
CONTIG370	10634580_f2_21	5040	10702	279	93
CONTIG370	19587651_f3_26	5041	10703	195	65
CONTIG370	2868876_c1_38	5042	10704	549	183
CONTIG370	34472152_c1_41	5043	10705	459	153
CONTIG370	2515956_c2_53	5044	10706	528	176
CONTIG370	5115877_c3_58	5045	10707	546	182
CONTIG370	32597762_c3_64	5046	10708	186	62
CONTIG370	12303966_c3_65	5047	10709	315	105
CONTIG370	4375015_c3_66	5048	10710	246	82
CONTIG371	29300800_f2_17	5049	10711	249	83
CONTIG371	36368932_c1_45	5050	10712	189	63
CONTIG371	30756575_c1_55	5051	10713	345	115
CONTIG371	14063790_c1_59	5052	10714	756	252
CONTIG371	11213517_c2_61	5053	10715	726	242
CONTIG373	25500292_f3_26	5054	10716	1917	639
CONTIG373	30191284_c1_30	5055	10717	296	98
CONTIG373	3261258_c1_34	5056	10718	372	124
CONTIG374	6439203_f1_2	5057	10719	405	135
CONTIG374	5158567_c3_102	5058	10720	279	93
CONTIG375	30275201_f2_11	5059	10721	291	97
CONTIG375	23839830_f3_38	5060	10722	183	61
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CLAIMS

1. An isolated nucleic acid comprising a nucleotide sequence encoding an *E. cloacae* polypeptide selected from the group consisting of SEQ ID NO: 5663 -
5 SEQ ID NO: 11324.
2. A recombinant expression vector comprising the nucleic acid of claim 1 operably linked to a transcription regulatory element.
- 10 3. A cell comprising a recombinant expression vector of claim 2.
4. A method for producing an *E. cloacae* polypeptide comprising culturing a cell of claim 3 under conditions that permit expression of the polypeptide.
- 15 5. An isolated nucleic acid comprising a nucleotide sequence encoding an *E. cloacae* polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1 - SEQ ID NO: 5662.
- 20 6. A recombinant expression vector comprising the nucleic acid of claim 5 operably linked to a transcription regulatory element.
7. A cell comprising a recombinant expression vector of claim 6.
8. A method for producing an *E. cloacae* polypeptide comprising culturing
25 a cell of claim 7 under conditions that permit expression of the polypeptide.

9. A probe comprising a nucleotide sequence consisting of at least 8 nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 - SEQ ID NO: 5662.

5 10. An isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length, wherein the sequence is hybridizable to a nucleic acid having a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 - SEQ ID NO: 5662.

10 11. A vaccine composition for prevention or treatment of an *E. cloacae* infection comprising an effective amount of a nucleic acid of claim 5 and a pharmaceutically acceptable carrier.

12. A vaccine composition of claim 11, further comprising an adjuvant.

15

13. A vaccine composition of claim 11, further comprising one or more additional active ingredients.

14. A method of treating a subject for *E. cloacae* infection comprising
20 administering to a subject a vaccine composition of claim 11, such that treatment of *E. cloacae* infection occurs.

15. A method of claim 14, wherein the treatment is a prophylactic treatment.

25

16. A method of claim 14, wherein the treatment is a therapeutic treatment.

17. A recombinant or substantially pure preparation of an *E. cloacae* polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 5663 - SEQ ID NO: 11324.

5 18. A vaccine composition for prevention or treatment of an *E. cloacae* infection comprising an effective amount of an *E. cloacae* polypeptide of claim 17 and a pharmaceutically acceptable carrier.

10 19. A vaccine composition of claim 18, further comprising an adjuvant.

20. A vaccine composition of claim 18, further comprising one or more additional active ingredients.

15 21. A method of treating a subject for *E. cloacae* infection comprising administering to a subject a vaccine composition of claim 18, such that treatment of *E. cloacae* infection occurs.

20 22. A method of claim 21, wherein the treatment is a prophylactic treatment.

23. A method of claim 21, wherein the treatment is a therapeutic treatment.

24. A method for detecting the presence of a *Enterobacter* nucleic acid in a sample comprising:

(a) contacting a sample with a nucleic acid of claim 5 under conditions in which a hybrid can form between the probe and a *Enterobacter* nucleic acid in the sample; and

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Enterobacter* nucleic acid in the sample.

25. A computer readable medium having recorded thereon the nucleotide sequences depicted in SEQ ID NO: 1 - SEQ ID NO: 5662 or fragments thereof.

10 26. A computer based system for identifying fragments of the *Enterobacter* genome of commercial importance comprising the following elements;

a) a data storage means comprising the nucleotide sequences SEQ ID NO: 1 - SEQ ID NO: 5662 or fragments thereof,

15 b) a search means for comparing a target sequence to the nucleotide sequences of the data storage means of step (a) to identify homologous sequences, and;

c) a retrieval means for obtaining said homologous sequences(s) of step (b).

20 27. A method of identifying commercially important nucleic acid fragments of the *Enterobacter* genome comprising the step of comparing a database comprising the nucleotide sequences SEQ ID NO: 1 - SEQ ID NO: 5662 or fragments thereof with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target
25 sequence is not randomly selected.

28. A method for identifying an expression modulating fragment of the *Enterobacter* genome comprising the step of comparing a database comprising the nucleotide sequences SEQ ID NO: 1 - SEQ ID NO: 5662 or fragments thereof with a target sequence to obtain a nucleic acid molecule comprised of a complementary
- 5 nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known regulate gene expression.

ABSTRACT OF THE DISCLOSURE

The invention provides isolated polypeptide and nucleic acid sequences derived from *Enterobacter cloacae* that are useful in diagnosis and therapy of pathological conditions; antibodies against the polypeptides; and methods for the production of the
5 polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

SEQUENCE LISTING

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gcctgcggct	tgccggcgat	aacgggtata	agaccatggc	gttccccgcc	attagcaccg	480
gggtgttcgg	ctatccaaag	gaagcggcag	ctacgatcgc	cgtgaatacc	gtttatcaat	540
acctttccct	caaaccocat	ccggaaaaag	tcatttttgt	ctgtttcgat	gagcacaccg	600
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<210> 8

<211> 924

<212> DNA

<213> Enterobacter cloacae

<400> 8

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tggtcgatcc	tgctgctgat	tgctctttat	aagctcggcg	acgctttcgc	catgagtctg	180
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cgtctgtcgc	tgttccgtgc	tctgctgatc	ttcggcatcc	ttcagggcgc	ttcgaatgcc	360
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tttgaaaatc	tgtgcggagg	tatgggcaca	gcggcatttg	tcgccctgct	gatgacgctg	480
tgcaataagt	cattttccgc	caccacagtt	gcccctgctc	ctgccctctc	agccgtcggg	540
cgcgtgtacg	taggtcccgt	cgccgggctg	tttgttgaag	cccacggctg	gccgacattt	600
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gcaggcgtgt	ttctcgccat	cgtgggtatc	ctgaccgggtg	ggatgctgga	tttcatgtca	900
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<210> 9

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (997)

<400> 9

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ctcaaccgtg	cattcacacc	aaaggggtgat	tttggaagag	taattttctt	agcaaataac	180
gcatacaaac	aaattaaccg	tgcattttca	aagagcatga	attttgatga	agctggtaaa	240
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tatcaggacg	cttacggggc	ttaaaggaaa	ggccgctcaa	atccaccagc	agccggaaag	360
ccacaaggca	gaggtctcga	tttaacagcc	gctaattcaa	tccgttccact	cgctaatact	420
cagttctatt	cgaatctgac	aagacgctta	gaggggtatg	gttcaactgg	acaagcaagg	480
gcgatgaaat	tacgccagca	ggttcacgga	ttgagagatg	atgcttttag	caatccctca	540

gccagtttga	atcaattccg	tttagcatta	cgtgcagcca	ctgatagcgc	gtctaaatgg	600
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accttgaaac	agtacactgg	ctttgctgcg	ggtagctcaga	attcgttagg	ctatcagggt	900
acacaggact	tctataagaa	tgtgctgta	ttcggtcgta	ttcgtgggct	tgatgctgaa	960
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<210> 10

<211> 1170

<212> DNA

<213> Enterobacter cloacae

<400> 10

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atctttttct	gtcagaagct	ggtcaggatc	ctcggcgcg	cggttgatgg	cgaaatccca	180
acgaatctgg	tgttttccct	gctcgggctt	ggcgtgcgg	aaatggcgca	gcttatcctg	240
ccgttaagcc	tgttccttgg	tctgctgatg	accctgggta	agctctatac	cgaaagtga	300
atcacctga	tgcattgctg	cggcctcagt	aaagccgtac	tggtaaaagc	agccatgggtg	360
ctggcgctgt	ttacgggcat	tgttgccgcg	gttaacgtca	tgtggcgggg	gccgacctcc	420
tctcgctc	aggatgaggt	gctggcgga	gcaaaagcta	accgggggct	ggcgcgctg	480
gcgcaggggc	agttccagca	ggcgaccgac	ggtaactccg	tgtgtttat	cgaaagcgtc	540
gatggcaacc	gcttcaatga	cgtgtttctt	gctcaactgc	gcccgaaagg	taacgctcgg	600
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gatactgagc	agatggatat	gcgcacctta	atgaataccg	ataccgatcg	tgcgcgtgct	840
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ccgctgagcg	tgggtgaacc	gcgcaggggc	cgcgtgctgt	cgatgctgcc	agcgatgctg	960
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attgaccoga	tgatctggac	ctgggtcgtg	aatggtttgt	atctgctgct	ggcagtcgga	1080
ctcaacttgt	gggacacggt	gcctgtgcgt	cgtcttcgtg	cccggtttac	gcgtaaagga	1140
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<210> 11

<211> 756

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (672)

<400> 11

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atggcccggc	actacaccga	gctgcaaaaa	tatctgctgg	ctccggaagt	ggccggactg	180
ctgcactttg	ttcaggactg	gggtcagcac	gcttttttta	atacgttatg	gaataccggg	240
gcacgcctga	acgaaggcct	tgccttgaga	cggcgtgact	ttcaccttaa	cgagagcatt	300
ccgcatgtcg	ttcttcgcac	cgccaaacag	cggcgtgccg	gcggcgcccg	tcgcgtaag	360
ggaaaaagtg	ccaaccgggt	ggtagcgtta	tcggaccggg	cctatgtcga	tgagatgcgc	420
cggctgttcg	ccagcacgaa	ggagcagttt	gaagatgatc	cgattacagg	cgaacgtcgc	480
gcgcaaccgg	tgtggaatgt	ttccgaccgg	acgggtgcgt	actggctggg	ccgggcgact	540
gatgcccgcg	atcgtgacgg	cgtcagactg	agcatcgacg	tcagccccc	taccttccgg	600
cacagttttg	caatgcacct	tttatatggc	cacgttcacc	ctaaggta	ccagggtctg	660
ctggggcatg	anaagtttga	gagtactgag	gtctatacga	aaatatttgc	gctcgacgtg	720
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<210> 12

<211> 951
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(937)

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 cttcttttccc cggatgttat aaagttaaaa cattatgtgg ataaaagggtga gtatcttttta 180
 gttctagcaa aggacctttt tggatttcca gaaatggatc caaagatggc tgtgcctgtt 240
 ttcaaaaacta aaacctcgta tcgagctccg ctgaacaaag actacatacc aaatccccga 300
 atacttgaac aagtgggttaa actgcttatc agtccggata tagatttaag tgtgtgtctt 360
 aaaggtgagt ccggttcttg caagactgaa atggtaatgt acattagcca catgatgaat 420
 tggccgctga caattaagca gatcaacagc aatattcgag ttgatgagct tgaaggtgag 480
 cgcagtcctta atgggtggtaa tacaggtttt gtacacagcg atttggtaac gggatttcgt 540
 aatggtcacc tcattcttct ggatgaagtg gacaaaaatc atcctgatac ggcagcaaaa 600
 cttcacatgc ccattgaacg taagccctgg tcaactcagt ctaatgggtg tgaggttata 660
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 cgccggttcg tttcttctca acgtcaagat gcagctttta taaagcgggt cttgatagtt 780
 gaaatggaga agcccgacaa agttgcttta accaatgtgc ttactaaacg atatagctct 840
 ttgccttttc aggtcattga gaagttcgta agagttagcg ttgcagtaaa tgactctggt 900
 acagaagaca gtgtgatgga tattcgtcaa ttagtancct gggttggcac g 951

<210> 13
 <211> 519
 <212> DNA
 <213> Enterobacter cloacae

<400> 13
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 caacagcaat ccgccgcact tggcagaacg gcaacgcaac cggcaaacca gaaagcgatc 180
 gccaatctgg tatacgggtg tgagtgggga aaagaacacc ttggcaatca ggctcgctggt 240
 gatggctgga aatatcgcgg tcgtgggctg aaacagatta ccggcctgag caactatcgc 300
 agttgtggcc aggcgttgaa actggacctt gttactcatc cggagctgct tgaaaaggat 360
 gaatacgccg cgcgctcagc cgcattggtt tatgcctccc gcggttgcct gcttcattcc 420
 ggcgacgtgg agcgcgtgac gcttcttata aatgggtggc gaaacgggct ggataaacgc 480
 cgcgcgctgt ttaacctggc gaaatcagtt ctggtgtga 519

<210> 14
 <211> 345
 <212> DNA
 <213> Enterobacter cloacae

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 <221>unsure
 <222>(98)

<220>
 <221>unsure
 <222>(99)

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<400> 14

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nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nggtccggca	ggccatggcg	180
gcgctacact	atgtgcccaa	ccgtggcgcg	cagcagctgg	ccgggaaacg	caccgcgacg	240
ctggggctga	tgaccagcga	tctggcgcta	catgcgccgt	cgcaaatcgc	ctcagctgta	300
aaatcccgtc	ttcaccacgg	ggctggcagg	ttccgcgcta	agcgt		345

<210> 15

<211> 342

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(40)

<400> 15

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aacgcccttg	ccaccgggat	gtatatcggc	gcgggttttg	gcgcaggccc	gcgcgacggc	120
ctgatgaccg	gcatacacgc	ccggtcgggc	tggtcgatcc	gcagcgtgcg	taccgcgatac	180
gaggtgactg	tggtgatcgt	cggctacctc	ctcgggggag	cgttttggcg	tggaaccgtg	240
ctgtatgcat	taaccatcgg	cccgctgata	cagctctgtt	tgcggtgggt	tgcgagagaga	300
ccgcgcattc	agaaagctgc	acagccggag	cggattgttt	aa		342

<210> 16

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(1022)

<400> 16

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cttgaaaaga	tcgccctcgt	tggtcagcgc	atgaaaagcg	agcagatttc	tctaaaggaa	120
tctctgatgg	cttcatcaag	agtatctgtt	tctgatgata	gtgttgatgg	tggtgataga	180
ctgatctata	accactgttt	gaataaaaaa	aatctctctg	attttttttg	gaagtcacga	240
gtaacgttca	ataaaaatact	ttcggactta	gaagaaaaag	aacttggttg	tgacacctatt	300
tatcaaaaaca	aaaatcatct	ttacacccgc	tgggatgttc	aaaaaataat	ggatgccctg	360
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ggcggtagac	ggaaaagcac	tacatctgta	gcttttagcag	tagcagctgc	tttagatcta	480
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atgattcaaa	gtgtctcaga	agatgatgtc	ttccttacag	caattgatgc	aatccttgga	600
atttatgaag	aaaattctga	gtataaaaaa	tatttagatt	caggattctc	tgaagaagaa	660
atcatcacta	atatgccttt	ttcaacgcac	ctgccaaact	tggaacgta	aacggctttt	720
ccgacagatg	ctcgttttta	agataaatac	tggaacgtgt	ctagagaaga	acgtacgtct	780
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cttacaataa	gtgaaagggt	taaacaatca	ccaagtaagg	gcgacaattt	aaaatgggtc	1020
anagttcttg	ctgtcaatgt	aatgacaaa	agtcacatag	aaagaatagt	tttgataaaa	1080
ttaatcaaaa	ctgttcaagg	acccttttga				1110

<210> 17

<211> 1056

<212> DNA

<213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(1030)

<400> 17

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gcgaagctgg	gtattgctac	cggaaaaaac	ctggcggagc	aaatccgcga	tcattatcca	180
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gactttgacc	aggcttacct	gacgctggag	cggttgctga	gtcatgccgc	tgccactatt	780
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caggtgggtga	tgcagggggt	cgtacgtttc	catattccgc	tgtgggttcg	ccgctcggtc	900
acaatgctgc	cttcctttgt	tgtgatcctg	atggggctgg	atccgaccgc	cattctggtg	960
atgagtcagg	tgctgctgag	tttcgggatt	gcgctggcgc	tggtgccgct	gctgatattc	1020
gacgtcatcn	cgcccggaat	ggaaggtagc	gcgctc			1056

<210> 18
 <211> 1071
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(1061)

<400> 18

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ctgatcgctca	ctgaccgtgt	tttggtctgac	acgggactgg	ttaacaaact	gacagatgag	180
cttgaggcgc	ataaaattag	ttatgcaata	tttgatggtg	ttcaacctaa	tccaacagag	240
aaaaatatgt	atgacgggtt	agccttgctt	gcaaaaagta	atgctgattt	tgtcattttcc	300
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gggcatattc	gggattactc	gaaagggtgtg	catctgtcca	aaaaaccaca	attaccatta	420
gttactgtaa	atacgacagc	gggtacggca	tcggaaatga	cogtatttgc	aatcgctact	480
aaccaggaag	atgaaactaa	atacccggtg	gtggataagc	actttacgcc	tatcattgcg	540
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aaaaaggttc	cogatcgttt	tgttgaaatc	gcccgggcaa	tggggattga	tgtctcaaca	960
atgactcagg	agcaggccat	taattctgct	atcgaagcaa	ttgagatggt	gtcgcacaaa	1020
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<210> 19
 <211> 537
 <212> DNA
 <213> Enterobacter cloacae

<400> 19

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gtcattggtg	atgttcgcat	ggccgatgat	gtcagcatct	ggccactcgt	cgcgatccgg	120
ggcgatgtta	actatgttgc	aatcgggtga	cgcaccaata	ttcaggacgg	cagcgtgctg	180
catgtgactc	ataagtcata	ttataacctt	gagggcaatc	cgtcatcat	tggggaagat	240
gttaccgtcg	gtcataaagt	aatgctccac	ggctgcacaa	tggtaacag	ggttctcggt	300
gggatgggat	cgatcttgct	ggatggcgct	atagtagaag	atgacgtaat	gattggcgca	360
ggaagcctag	ttccgcaaaa	caaacgcctg	gaaagtggct	atctctatct	aggcagtcgg	420
attaaacaga	tccgccccct	aaaggaggcg	gagatcgaag	gattgaaata	ctcagcgaac	480
aattacgtta	aatggaagaa	tgactatctg	gatcaggata	accagaccca	gccctga	537

<210> 20

<211> 199

<212> DNA

<213> Enterobacter cloacae

<400> 20

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acaacagggg	gcaaaacatg	tggtgatgg	tctgggcatg	ctggtggggc	aggcggctca	120
tgcggtgcta	ctctggcatg	gcgtgttacc	tgctgtagaa	ccggtgatcg	aaaagctgaa	180
aaaggaactg	atggtatga					199

<210> 21

<211> 357

<212> DNA

<213> Enterobacter cloacae

<400> 21

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attcattttc	cgcacagaga	aatctgggat	gaaaacaagc	aagcgggtgtg	tttcccggtg	180
ctgggtgcatg	gaatgcagct	cacctgtgctg	attaaagggg	agacggttgc	tcagcgtttt	240
ggtggttcag	atccgttagc	ggtcttttgt	gaaaatcgct	gggatctgga	agaggaagcc	300
agcgatttga	tccgcgtaca	gcaggaagac	gatcagggct	gggtctggtt	atcctga	357

<210> 22

<211> 198

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (142)

<400> 22

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tatctggtcg	cgatcttcgc	ccatattcat	aacctgtggt	cggatgaagat	tttatcccct	120
cagccggtoa	tttacgccct	gntggccctg	gcccttttag	cgtggcgcta	caagaagttc	180
cgccagtggg	tgcatag					198

<210> 23

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 23

aagggtgaca	attgcgcttt	gagggtatat	gttggttttt	acccgaaaat	cgcaggagat	60
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ctcggcacc	gtgagccaga	gaagtacggc	acgctaacat	tgagcgaaat	tgtaaacgt	180
ctgagtaagg	aagcagcgct	gctgaatgtg	gatttggaac	attttcagtc	taacgcggag	240
tacgcaatca	tcgaccgtat	tcatacggct	aaagacactg	tggaactatat	cctgatcaat	300
ccggccgcgt	ttacgcacac	cagtgttgct	atacgcgaac	cactgctcgc	ggtgagtatc	360
ccgttttatcg	agatccacct	gagtaacgtg	cacgcccag	agccgttcgc	ccaccactcc	420

tacctgtcag atatcgccgc tggcgtgatt tgtgggctgg gtgcagacgg ctattcatac 480
gctttacaga cagcggtaaa acgcttgta caatcacact aa 522

<210> 24
<211> 591
<212> DNA
<213> Enterobacter cloacae

<400> 24
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cagcgttac cggcacgcta tttcgaaca gggggcaaca tgaacttaag acgactgaaa 120
tacttcgtaa aaatcgtaga tatcggcagc ctgaccagc cggctgaagt gctgcatatc 180
gcgagcctg cgtgagcca gcaggcgcg actctggaag gcgaaatgga ccagcaactg 240
ttgatccga ccaagcgcgg cgtaacgcct accgaagcgg gaaaaatttt atatacccat 300
gcccgcacga tcttgcgtca gtgtgaacaa gcgcagctgg ccgtgcacaa tgtgggtcag 360
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aacagtgggt cgtgctcaa tgacaaactg ctcaacggtc agctggatat gggcgggtg 540
gtacgatcgc tcccgggtg ccgggatcac cagccagccg ctgctgaatg a 591

<210> 25
<211> 240
<212> DNA
<213> Enterobacter cloacae

<400> 25
cttatcgatc agcccgtaaa agtgaccacg gagccggacg gtagccgttg ggtagagggtt 60
cacgagccgc tttcacgcaa tcgcgcggaa tttgaatcga caaataaggt gccgtgccc 120
atttcagccg caciaaggac gcagctgata agtgaagggg cgggcgctga actggaacgg 180
cggtcgggga tgccggtgaa gcttgctatg actggtagcg cttcgcttgc cgggccttga 240

<210> 26
<211> 342
<212> DNA
<213> Enterobacter cloacae

<400> 26
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agaacagtgg ttcgtgctc aatgacaaac tgctcaacgg tcagctggat atgggcgggtg 120
ctgtacgac gtcctccggt tgccgggac accagccagc cgtgctgaa tgaagatctt 180
tatctggtcg gtaccgtga ttgccctggc cagagcattg atttaaccgc tgtggcacag 240
atgaacctgt ttcttgccg cgactacagt gccctgcgcc ttctgcttga cgaaaccccc 300
tcgctgcgcc ctctgaacgc gaataatttt ctgttagaat ga 342

<210> 27
<211> 492
<212> DNA
<213> Enterobacter cloacae

<400> 27
ccagtataca ctccgctagc gctacgtgac tggttcaggg ctgcgccccg aaacccgcta 60
aaaccactgc cgcgtctgcg gcttgtccaa caccgtgccg accgggaaaa gatttcccg 120
ccgtcccggc gttatcagga ggccggattg gcagacaaac gcagcaaat gtcaccatg 180
tgggtgactg aggacgagca ccggcgctctg ctggagcgct gcgagggtaa gcaactcgcg 240
gcttggatgc ggcagacgtg cctggaacag aagcccgcac gcgccggcaa acttccgtcg 300
atctgcggcg cgtgcttcg tcagcttgcc ggcattggga acaaccttaa ccagattgcc 360
cgccagggtt acgcgggtgg tgggaagcga cagcaccg cgccgctg tgcagattgt cgcgcgctg 420
atggccatcg atgcgggact cgagcgggtt cggcatgccg tactggaaaa ggggtgctgat 480
gatgatcggt aa 492

<210> 28

<211> 696
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (418)

<400> 28
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 ctgggttaaag atcgccagcg cgacggcgcc agcgttctgc aggggaagcc ggatgaagtc 180
 cgggagctta tcgacgcctc gccctacgcc aaaaagtaca cttccggcgt tctgtctttt 240
 gccgaacagg atttaccgcc cggccagcgc gaaaagctga tggcgagttt cgagcggggt 300
 ctgatgcccc gactcgataa agaccagtac agcgtgctgt gggttgagca ccgggacaag 360
 gggcggttg agctgaactt cctgatcccc aacacggagc ttctgaccgg caagcggnta 420
 cagcgttatt acgaccgcgc cgaccgtccg cgcacgatg cctggcagac catagtgaac 480
 ggcaggcttg ggctgcatga cccgaacgcg ccggagaacc ggcgggtgct ggtctcgcc 540
 tcgcgcgtgc cgggaagcga gcaggaagcc gccaggcgga ttacgagcgg cctgcttgcc 600
 cttgcctcat ccggggagct gaaaacgcgt caggacgtca ctgaggcgct ggaaagcgca 660
 ggttttgagg tgggtgcgcac cacacaaggc cgcac 696

<210> 29
 <211> 1392
 <212> DNA
 <213> Enterobacter cloacae

<400> 29
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 gtcgccgttg accaggaggt caccgtgcgc ggatgggtgc gtactcgccg agattctaaa 180
 gctggcatct ccttctctgc cgtctatgac ggttccgtgt ttgatccgtg acaggccgtc 240
 attaataatt ctctgcccaa ttacaatgat gacgttctgc aactgacaac cggttgttcc 300
 gtgatcgta ccggtgtagt ggtggcctct ccggggccagg gtcagagcta cgaaattcag 360
 gcgacctcgg tggaaagtac cggctgggtt gaagatccgg acacctaccc gatggctgca 420
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 attgggtcgg ttgcccgcgt gogtcatacg ctggcgcagg cgtctgcatc cttctttgac 540
 gagcagggtt acttctgggt ttctactccg ctgatccagg catccgatac cgaaggcgca 600
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 ccggcggact acagctggta tcgcgatctg tcttcaccta cgggagctgg caggatccgc 1380
 gcttacttaa cc 1392

<210> 30
 <211> 567
 <212> DNA
 <213> Enterobacter cloacae

<400> 30
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 tgggttccga cccgtaaaac gaattttatt caccgggagc ctctccgagg cgttattacc 120

caatcagagg	atTTtagaat	ggctaagaaa	gtacaagcct	acgtcaagct	gcaggttgca	180
gcaggtatgg	cgaacccaag	tccaccagtt	ggTccagctc	tgggtcagca	gggtgtgaac	240
atcatggaat	tctgtaaagc	gttcaacgcc	aaaactgaat	ccatggagaa	aggtctgcc	300
atcccagttg	taatcactgt	ttacgctgac	cgttctttca	ctttcgttac	caaaaccct	360
ccagcagcag	ttctgctgaa	gaaagcagcg	ggcatcaagt	ctggttccgg	taagccgaac	420
aaagacaaag	tgggtaaaat	ttcccgcgct	cagttgcagg	aaatcgcgca	gaccaaagct	480
gccgacatga	ctggttccga	cattgaagcg	atgactcgct	ccatcgaagg	tactgcacgt	540
tccatggggc	tggtagtgga	ggactaa				567

<210> 31

<211> 708

<212> DNA

<213> Enterobacter cloacae

<400> 31

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cagtacgaca	tcaacgaagc	tatcgctctg	ctgaaagaac	tggctaccgc	taagttcggt	120
gaaagcggtg	acgttgccgt	taacctgggc	atcgacgctc	gtaaatccga	tcagaacggt	180
cgtggcgcaa	ctgtactgcc	acacggtact	ggcggttccg	tacgcgtaac	tgtatttgc	240
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ccgaaagtgg	gtactgtaac	ccctaactgt	gctgaagcgg	ttaagaacgc	taaagcaggt	480
caggttcggt	atcgtaacga	caaaaacggc	atcatccaca	ccaccatcgg	taaagtggac	540
tttgacgctg	acaaactgaa	agaaaacctg	gaagctctgc	tggttgcgct	gaaaaaagca	600
aaaccaactc	aggcgaaagg	cgtgtacatc	aagaaagtta	gcattctccac	caccatgggt	660
gcaggtgttg	cagttgacca	ggctggcctg	agcgtctgct	caaaactaa		708

<210> 32

<211> 315

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (294)

<400> 32

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gcagtagtgg	cggattcccc	tggcggtact	gtagacaaaa	tgactgaact	gcgtaaagca	180
ggtcgtgaag	ctggcggtata	catgcgtgtt	gttcgtaaca	ccctgctgcg	tcgcgtagtt	240
gaaggtactc	agttcgagtg	cctgaaagac	acgcttggtg	gtcttcacca	cagngcggcg	300
caaggaccag	caata					315

<210> 33

<211> 384

<212> DNA

<213> Enterobacter cloacae

<400> 33

cggagcacta	aaatgatcca	agaacagact	atgctgaacg	tcgccgacaa	ctccggtgca	60
cgtcgcgtaa	tgtgtatcaa	ggttctgggt	ggctcgcacc	gtcgtctacgc	aggcgtaggc	120
gacatcatca	agatcaccat	caaggaagca	attccacgtg	gtaaggtcaa	aaaagtgat	180
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attcgtctcg	atggtaatgc	atgcgttatt	ttaaacaata	acagcgagca	gcctatcggc	300
acgcgtatct	ttggggccgt	aactcgtgaa	cttcgtactg	agaagttcat	gaaaattatc	360
tctctggcac	cagaagtact	ctaa				384

<210> 34

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 34

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gacgaagtag	ttaacaaact	catgactgag	tttaactaca	attctgtcat	gcaagtcctt	120
cgggtcgaga	agatcaccct	gaacatgggt	gttgggtgaag	cgatcgctga	caagaaactg	180
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gcacgcaaat	ctgttgcagg	cttcaaaaatc	cgtcagggct	atccgatcgg	ctgtaaagta	300
actctgcgtg	gcgaacgcat	gtgggagttc	cttgagcgcc	tgatcactat	tgctgttcca	360
cgtatccgtg	acttccgtgg	cttgctccgt	aagtctttcg	acggtcgtgg	taactacagc	420
atgggtgtcc	gtgagcagat	catcttccca	gaaatcgact	acgataaagt	cgaccgcgtg	480
cgtggttttg	atattaccat	taccactact	gggaaatctg	atgaaaaagg	ccgtgctctg	540
ctggctgcct	ttgaattccc	cgttccgcaa	gttaaggtaa	ggtttaccga	aatggcttaa	600

<210> 35

<211> 357

<212> DNA

<213> Enterobacter cloacae

<400> 35

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cgtgatgacg	aagttatcgt	gttaaccggt	aaagataaag	gtaaacgcgg	taaagtaaaa	120
aatgttctgt	cttccggcaa	actcgtcgtt	gaaggatatca	acctgggtta	gaaacatcag	180
aagccggttc	cggccctgaa	ccaaccaggc	ggcatcgttg	aaaaagaagc	tgctattcag	240
gtttctaacg	ttgcaatctt	caatgcggct	accggttaagg	ctgaccgtgt	aggctttaga	300
ttcgaagacg	gtaaaaaagt	ccgtttcttc	aagtctaaca	gcgaaactat	caagtaa	357

<210> 36

<211> 1055

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (832)

<400> 36

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cctatgaaaa	ccatgaaaat	tgccgtcagc	cgcgagctgg	tatccaaagt	ttctacgcat	180
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gttgttgaaa	gtacacagcg	cattctcgcg	ttgctgaagc	gtacgggctt	tcagctaccg	300
gtatttatgt	tctcaacaga	gccaggagag	gtgccagagg	gtgtcacggc	gatcatctcg	360
ggtaaagcac	aggaattgct	ggaactggaa	tctgcccgtt	gccggtatga	agagaacctg	420
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tgtccgggtc	accagcacgg	cgcttttttc	aaaaaacacc	cggcggggcg	gcagttctac	540
gacttcttcg	gtgaaaacgt	gtttctgtgc	gatattgtgca	atgccgacgt	gaagctcggg	600
gatttgctga	tccacgaagg	ttctgccaa	cacgcgcaaa	agttcgcggc	gaaagtgttc	660
aacgcggata	aaacctactt	cgtgctgaac	ggcacgtcgg	cggccaataa	agtggtgacc	720
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ctgatccgtg	acgtcgcgcc	gcagaaagcc	gccgaggcgc	gcccgtttcc	gtctggcgat	960
cattcagctc	cgcacctacc	tatggcacga	atctacaacg	cccggtcagg	tgaatcgacc	1020
aatattcggg	cacctttgcg	actaacatcc	ctctt			1055

<210> 37

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 37
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 atttttggcc tggcgctcgtt agggattggt atccttttag tggtgaaatg cgccaacctg 180
 ccggtgatgg tactggcgac gctgctcggc gcgctgatcg gcgaattttg ctatctggaa 240
 aagggcacatc atcacgcggg aggcacagcc aaaaatctga ttgcccagacc gggcaaggcg 300
 aagcacggca cgcacgagtc gtttattcag aactacgttg cgatcattat tctgttctgc 360
 gccagcggca cggggatatt cggttcgatg caggaaggga tgaccggcga tcccagcata 420
 ttgattgcga aagcgtttct ggatttcttt actgccacca tctttgccac caccctcggc 480
 atcgccgtcg ccgcgagtc taccacggg ccggaaggac cgcgcatgcg c 531

<210> 38
 <211> 516
 <212> DNA
 <213> Enterobacter cloacae

<400> 38
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 tttctgctga tctattttgc tttatcgccc ttgcttggtc gcaccgatat tcgcaagggg 120
 cttcttcccc ataaatttct ttgcccgtcg ctatggaccg gcctgcttta ccagctctgc 180
 ctccatcctg attttttgcc gagcgcggtg gtgggtgcga tggcaggata ccgcggattc 240
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 ctcgtagccg cgttaatggc tctgctgtat ctggttgctt tctcgttggt tactcctgat 420
 aagcaggcat taaaaaaccc actgcctttt gggccatttc tggcggcagc gggtttatgc 480
 gttggctggg aaagcctgat taactttcca ctttga 516

<210> 39
 <211> 519
 <212> DNA
 <213> Enterobacter cloacae

<400> 39
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 ctccatgcaa gaatgttcaa aaactgggga ctgactcgcc tcaacgatgt tgaataccat 180
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 tatgcgga caatcacatga ctacgtcagc cgcgatatga tgatccagat cctggccgat 420
 gaagaagggc acatcgactg gcttgagacc gaactggatc tcattagcaa aattggccta 480
 cagaactacc ttcagtctca gatcaaagtg gaaagttaa 519

<210> 40
 <211> 1173
 <212> DNA
 <213> Enterobacter cloacae

<400> 40
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 ctgcccagac gtatgggtcaa tatcattggc gtgggcagct gccctctccg ttggtatggat 180
 aaagggtggg taaacgacct tgagtcgggt gtgaaatgcg ttcagcgcg cctcgaccag 240
 gctgaattga tggcagattg ccaaatttcc tctgtctatc tggcccttcc ttgtaagcat 300
 atcagctgcc agaatgaaat cgggtatggt ccgatttccg aagaagaagt gacgcaggaa 360
 gacgttgaga acgttggtcca caccggcaaa tccgtgcgtg ttcgcgacga gcaccgtgtg 420
 ctgcatgtga tcccgcagga atacgcgac gactaccagg aaggcatcaa gaatccggtc 480
 ggtctgtcgg gogtgcgtat gcaggcaaaa gtgcacctga tcacatgtca caacgatatg 540
 gcgaagaaca ttgtaaaagc cgttgaaagt tgtggcctga aagttgacca actcattttc 600
 gccggacttg ccgcgagcta ttccgtgctg accgaagacg aacgtgaact ggcgtctgt 660

```

gtgggtcgata t-ggtggtgg tacaatggac atggctgtct ataccggcgg tgcgttacgc 720
cacaccaaag tgatcccgta cgcagggaac gtcgtgacca gcgatattgc ttacgctttt 780
ggtagccac cgagcgatgc agaggcgatt aaagtgcgcc atggttgcgc gctgggctct 840
atcgctcgga aagacgagag cgttgaagtg ccgagcgtag gcggtcgacc gccgcgcagc 900
ctgcaacgcc agacgctggc agaggtaatt gagccgcgtt ataccgagct gctcaacctg 960
gtcaacgaag agattttgca gttacaggaa cagcttcgcc agcagggtgt gaaacatcat 1020
ctcgcgccgg ggattgtatt aaccggcggg gcagcgcaaa ttgaaggtct tgcggcctgc 1080
gctcagcgcg tgttccatac gcagggtcgt atcgggtgcgc cgctgaatat caccggttta 1140
acggatttct taacgcgcgg tggagtaaaa cgt 1173

```

```

<210> 41
<211> 255
<212> DNA
<213> Enterobacter cloacae

```

```

<400> 41
gcgcgcggtt cctggcagtt gaccttaacg aatggcatca agctcaacct tggccgcggc 60
gatacaatga aacgtctggc gcgttttcta gaactttacc cgtttttaca gcagcaggcg 120
cagacggatg gcaaacggat aagctacgtt gatttgcgt atgaactcagg cgcagcagtc 180
ggttgggagc cggctccggc cgaggaacct aatcagcaac aaaatcaggc acaggtacag 240
gcagaacaac aatga 255

```

```

<210> 42
<211> 657
<212> DNA
<213> Enterobacter cloacae

```

```

<400> 42
atatacctgg aggttttcat ggtgtgcgt gccacaac gttcggtaat gacgtgttt 60
tctggtccta ctgacattta tagccatcag gttcgtatcg tgcctggcga gaagggtgtc 120
agttttgaga tcgagcatgt ggaaaaggat aaccgcctc aggatctgat cgatctcaac 180
ccgagccaaa gcgtaccgac gctgggtgat ccgagcgtga cctgtggga atcccgatc 240
attatggaat acctggatga gcgtttcccg catccgcgc tgatgcctgt ttatcctgtt 300
gcgcgtgggt aaagccgcct gtacatgcag cgtatcgaga aagactggta ctgcgtgatg 360
aacgttattg tcaacggttc ctcttctgaa gcggatgctg cactaaaca gctgcgtgaa 420
gagctgctgg cgattgcgcc ggtatttggc caaaagcctt tcttctgag cgacgagttc 480
agcctggtag attgctacct ggctccgctg ctgtggcgct tgccaacct gggcgtagag 540
ttcagcggtc ctggcgcgaa agagctgaaa ggctacatga ctgcgtctt tgaacgcgac 600
tctttcctgg catccttaac tgaacgcgaa cgtgaaatgc gtctcgccg aggctaa 657

```

```

<210> 43
<211> 216
<212> DNA
<213> Enterobacter cloacae

```

```

<400> 43
aatgcgtctc ggccgaggct aatgactgtg gaaatgtcac aactttcacc acgccgtccg 60
tatatgctgc ggccttttta tgaatggctg ctggataacc agctcacgcc gcacctggtt 120
gtggatgtga cgttgccggg cgtgctggtt ccaatggaat acgcgcgcga cggacagtct 180
tcaccacgac gctggcagga tccacgctta gcgcta 216

```

```

<210> 44
<211> 333
<212> DNA
<213> Enterobacter cloacae

```

```

<400> 44
tatactgaaa ttgctttcag aaaaacatgc attgaacctc aaagtgcgtt tcttctaaca 60
cgcattaagg gggttataat ggaaaagaat agtgaagtga tccagacca tccgcttggt 120
ggctgggata tcagcacctg agacagctac gatgcgctga tgctgcgttt gcactaccag 180
accccaaate agctaaaccg tgatgaagcg gaagttggac agacgctgtg gcttacaaca 240

```

gacgtcgccc gtcagtttat ctctattttg gaagcaggca tcgcaaaaat agaatctggc 300
gactaccagg aaaatgagta taaacggcat taa 333

<210> 45
<211> 699
<212> DNA
<213> Enterobacter cloacae

<400> 45
caaagcggtta gtaaagagaa gcctatgaaa tacgatttga tcattatcgg aagcgggtcc 60
gtaggatctg ccgccggtta ttacgccacg caggcgggtc tgaatgtact gatgattgac 120
gcccacgtc ccccccactc tgaaggaagc catcacggcg ataccctct gatacgtcac 180
gcttatggcg aaggtgagcg ctatgtaccg ctggtgcttc gggctcagac gctgtgggat 240
gagctggccg ccctcaccga agaacgcatt tttgagcgca ccggggctcg taacctgggg 300
ccagccagct ccacgtttct ggcgaccgtc gaggagagcg cgaaagccta ccgctggac 360
gtcgagcgct tggatgcgaa cggcatcatg gcgcgctggc cgaaatttc tgtccctgaa 420
gactacattg ggttgtttga agccaactct ggcgtactgc acagcgaaac ggccattaac 480
acctggattg atctcgccgc caaagcgggc tgcgcgcagt tgttcaactg tccggtcacg 540
ggcatcacc accatgcaga aggttcaacc gtcaccacct ctgaaggtga atataccgcc 600
acgcgtctgc tggtagtgcc gggaacgtgg gtgacgaaac tgctgcggga cctgcccatc 660
caccgggtgc gaaaagtctt ctctgggtt ccagtctga 699

<210> 46
<211> 474
<212> DNA
<213> Enterobacter cloacae

<400> 46
caccttttcg acgtagccct aaaatttcgc gtcccatat tgtatgaggt cgttttatta 60
cgtgtttacg aagcaaaagc taaaaccagg agctatttaa tggcaacagt taaccagctg 120
gtacgcaaac cacgtgcacg caaagttgca aaaagcaacg tgcttgcgtt ggaagcctgc 180
ccgcagaaac gtggcgtatg tactcgtgta tataccacca ctctaaaaa accaaactcc 240
gcactgcgta aagtatgccg tgtgcgtttg actaacgggt ttgaagtgc ttctacatc 300
ggtggtgaag gtcacaacct tcaggagcac tccgtgatcc tgatccgtgg cggctcgtgtt 360
aaagaccttc cgggtgttcg ttaccacacc gtctcgtggt cgctggactg ctcaggtgtt 420
aaagaccgta agcaggctcg ctccaagtac ggcgtgaagc gtcttaagga ttaa 474

<210> 47
<211> 411
<212> DNA
<213> Enterobacter cloacae

<400> 47
caacggagta atcccatgcc acgtcgtcgc gtcattggtc agcgtaaaaat tcttccagat 60
ccgaaattcg gatcagaact gctggcaaaa ttgttaaata tcttgatggt agatggtaaa 120
aaatctaccg cagaagcaat cgtatacagc gcgctggaga ccttggctca gcgttctggt 180
aaaaatgaac tggaaacctt cgaagtcgct ctcgacaacg tgcgcccgac tgtagaaatt 240
aagtctcgcc gcgttggtgg ttctacttat caggttccag ttgaagttcg tccggttcgt 300
cgtaatgctc tggcaatgcg ttggatcggt gaagctgctc gtaaacgcgg tgataaatcc 360
atggctctgc gtctggcgaa cgaactttct gatgctgcgg aaaacaaagg t 411

<210> 48
<211> 339
<212> DNA
<213> Enterobacter cloacae

<400> 48
acctttgttt tccgcagcat cagaaagttc gttcgccaga cgcagagcca tggatttato 60
accgcgttta cgagcagctt caacgatcca acgcattgcc agagcattac gacgaaccgg 120
acgaacttca actggaacct gataagtaga accaccaacg cggcgagact taatttctac 180
agtggggcgc acgttgctga gagcgacttc gaaggcttcc agttcatttt taccagaacg 240

ctgagccagg gtctccagcg cgctgtatac gattgcttct gcggtagatt ttttaccatc 300
taccatcagg atatttaciaa attttgccag cagtctga 339

<210> 49
<211> 555
<212> DNA
<213> Enterobacter cloacae

<220>
<221> unsure
<222> (493)

<400> 49
aaactatacg cgagggaagc atttatgccg cggcgacaga tactgagcag tgaagagcag 60
gaacgcttac tggttatacc agatgatgaa attattctga ccggaatgtg ttttctgaac 120
gaaccggata ttgcgctcat taataagcac cgacggccag cgaatcgctt gggctttgct 180
gtattactct gttatctgcg tggacctgga tttattccgg acaaaagcag tgctcctcac 240
aatggcggtt tatccagggt tgcttcccga ctgaaacttc agcctgattt atggccggaa 300
tatgcatcca gagagcaaac ccgctgggaa catctgaccg aactttatcg ctacctggaa 360
ctatccccgt tcagccgggtc aatgcaaaaa gaatgtatcc gccatctgca accctatgcc 420
atgcgaactg acaaaagatt tatgctggcg ggaagaaatg ctacacttgg ctacataaac 480
aataatgttt atnttccccct cctgttgaaa gtgattcaaa ccgacgcctt gccgaaatcc 540
ttcacccctc gctaa 555

<210> 50
<211> 636
<212> DNA
<213> Enterobacter cloacae

<400> 50
tttcggacac acgttataat tcggacatcc atttcgtacg gaaagtttcc catgtcacgt 60
gtttttgcct actgcagggt ctcaactctg gaacagacca cagaaaacca gcgtcgtgaa 120
attgaagcgg cggtttttgc catcagatcc caacgaactta ttgaggagca tatcagtggc 180
tcggttgctg ccagcgaaacg ccccggtatt atccggttgc tagatcgcat ggaaaatggg 240
gatgtactga ttgtcaccaa acttgaccgt ctgggtcgtg atgcgatgga tatccgaaaa 300
acagttagac aactggcggc tttagatatt cgcgttcatt gtctcgcact cggaggtgtt 360
gacttgacca gtccggccgg aaaaatgact atgcaggtaa tttctgctgt agcggagtgt 420
gagcgagatt tgctgcttga gcgaacgtat tcaggatttg cgagggcaaa agcggctgga 480
aaacgcttcg gtgcgcccccc catcctgagc gaggaacaaa agcaaacagt gacagagcgc 540
ctaaatgctg gcacacgtat cagtgtctatt gcccggaat ttaataccac ccgccagatt 600
atccttcggg taaaggctgg attgctgcaa gactga 636

<210> 51
<211> 402
<212> DNA
<213> Enterobacter cloacae

<400> 51
tcccccttcg cgggtcttcg gctcttttgt gaaaagagcg atagcgttat ttgcggccac 60
tccaactgcg gcgcgatgaa ggcgattgct gacaacgcgg atctggagcc gatgccggcc 120
gtttcccaact ggctgcgcta ttctgatgcg gcaaaagcgg tgggtggagaa gaaaacctgg 180
gataagccaa tcgataaagt gaatgcgatg gtgcaggaaa acgtctttgc gcagctgagc 240
aacatcaaga cccatccgtc ggtggcggtg ggctgcgca acaatgccat tcgctgcac 300
ggctgggtat atgacatcga aagcggcaaa atccttgccc tggacaagaa cactaaatcg 360
ttcgtgtcgt tgcggaaaaa ccgggaagtc ttcttcgagt aa 402

<210> 52
<211> 909
<212> DNA
<213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(8)

<400> 52

ggggtggnat	tattcggatc	cgccgctccc	ttggtgaaga	cgagggccga	tttttactgc	60
cctatccctt	atgaaccact	gtcgggtgta	acggattgtg	tggtaggcaag	cgaaatcgac	120
aaaggcccgg	atgggctgct	tgaccgcctc	tttgcgctga	tggtagaaga	gcttgagctg	180
gcgatccgc	gatgggtgtc	ggcgatagcg	ctcggcacgc	tgaatgccga	cacgctccgt	240
gatgcctggt	ttgaggatcg	taaaaagcac	ggtcctttca	cctggggccga	agcgaatctg	300
aaagaagtgg	agcgcaacaa	gcgcgaaaaa	cgacaccgtg	cctggcgcta	taccgtgctt	360
cgtctgcatg	aagtggatca	ggccatcgct	ccttcaactc	atgagcatga	cagagagcgg	420
tttaaactcg	ggctggagcg	tgtgtttatc	gataattatg	ccgccattcc	accgcagtct	480
atccgcgggt	tactggcgct	gcgcgaggca	gggatcatta	gcgtggctgc	actcgggtgat	540
gattacgata	tggatatcgg	cagcgatcag	accgtcatca	ccacggcaaa	aaaaagttac	600
cgcttcgacg	tgtttatcga	cgcgcgcgga	caaaagccgc	tcagaaacaa	ggacattccc	660
ttccccaccc	tgcgtaaaca	gcttgcgggg	accggcgatg	acgttcggga	cgtgggggaa	720
gactatacgt	tgctggcgcc	ggcatcactg	cgggggcgta	tcgcttttgg	ggcgatcccc	780
tggtgatgcg	acgatcatcc	gtttgttcag	ggttgtctcg	agtgcgctga	aattggtaaa	840
gcgatggcga	aagcggctgg	aaaacctgcg	tcgggggtgc	gaagggaagt	accttacatg	900
gagtttttaa						909

<210> 53
 <211> 380
 <212> DNA
 <213> Enterobacter cloacae

<400> 53

aactgcttct	taatacccct	cattcaggag	aatgacacta	tgctggactg	gaacaactat	60
cgctcagagt	taatgcaacg	tttaggcgag	ttggggcaaac	tgaccccgga	gaccatgaaa	120
ggcgtgggtg	ccctgggcaa	cgcaggtaac	aaaactgacc	ttttgggcgc	aaaagtgcgt	180
gaactcattg	ccctggcgctg	cgagtcacac	accgctgcg	acggtgtgat	tgcttttcac	240
gccgacgccg	ctgtgaaagc	cggtgcaacc	gacgctgaaa	ttgctgaagc	gctgggcgtg	300
gcgattaacc	tcaacgctgg	cgcggcggtc	atttcattca	gcccgcattc	gtctacagcc	360
cgggatgaag	tagcggctcc					380

<210> 54
 <211> 357
 <212> DNA
 <213> Enterobacter cloacae

<400> 54

ctcatgcgcg	gtccggcggc	tcccttggtg	aaaactaccg	gcatgagccc	gactgaatac	60
atcatgcagg	cgctggctgg	ctgttatacc	gccaccctta	ccatgatggc	tgctgaaaaa	120
gggatcgacc	tggaagggtat	cgagctggat	cttaatttctg	atatcaacct	caacggcttc	180
cttgggctgg	acagcaacgt	gcgtaaaggt	gcgaaatcta	ttcgcgctga	tgttcacctt	240
acgagcaata	ccgccagtcg	cgaggagtta	gaagcgctgg	tcagcgaaat	gcaaaagaat	300
tcgccaatcc	acgatactct	ggctaataccg	gttgaaatga	ttacacgcct	ggcgtaga	357

<210> 55
 <211> 624
 <212> DNA
 <213> Enterobacter cloacae

<400> 55

caacaatata	atctatcaac	tagtagatta	tatggagtaa	ttatgacaac	catgacacgg	60
gaacggctgc	tcagcggaagc	agaacacctg	atgcgcgaaa	aagggtattc	agcattcagc	120
tatgctgatt	tatcaaaaat	agtgggtatc	accaaggcca	gtattcatca	ccatttcccg	180
accaaagata	ttctgggtga	gcaggtggta	atacaggcgt	tctctgatac	acaacgcgta	240
tttgagcaga	tagaggcgac	tgagaaaagc	gcggagagaa	gaattgcggc	ttacatcgat	300
atcttcgcgc	aaagccataa	agcttcgcta	ctgccactgt	gttggtgcgtt	gtcagcagag	360

accgccaatc	tgccctcaggc	aattactgta	cagacatcac	tttatttcga	tatgcaaate	420
gagtggctca	caaaagtcgt	cagggcgggc	atggagtcag	gtgagttttc	atcccatgcc	480
gaaccatcag	atattgcttt	gatgatcatt	aatgtctgtg	aaggctcaag	cgtagtggcg	540
catgcaacgg	ccagaccgga	agtcttcgcc	aacagcctta	agtatataaa	actgcttctt	600
aatacccctc	attcaggaga	atga				624

<210> 56

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 56

tcgaggttgc	accgaagaat	cgctcccttt	gaagatcatg	ctatctctgc	cacttttaaaa	60
gagtcgctta	ctaaacaggg	tggtgagttt	ttgaccgggg	cagacttaaa	acaagttaag	120
gtgggtgggtg	atthtagttat	ttgtacgggt	atcgctcggtg	aggatactca	cgtaattacg	180
gcagagaaaa	ttcttatcgc	aacagggcgc	cgccctgtga	ctgaaaaact	gaatctggac	240
gctgtcaatg	tgctgggtcg	tgcgcggtga	caggtcattg	tcgataagca	tctaatagaca	300
tcgaatccac	ggatctgggc	tgcaggtgat	gttacagggtg	aagcacaatt	tgtttaacgtc	360
gctgttgaac	aaggaagatt	agcggcaagc	aatgcacttg	ggggcgagct	ctcctctctg	420
gattacaatg	ccctccctcg	ggttaccttc	acctccctg	agttggcttc	tgtaggtttg	480
actccattgc	aagctgaaga	aagaggaatc	ccatatgaga	tccgagaact	ccctgtagct	540
tttggttttac	gtgctattgt	cagccgccat	agcgatggtt	taatcagact	ggtttctgat	600
agtcaaaacg	gaacgatttt	aggcggtcac	atgggtcagtg	aatccgcagg	tgatgtgata	660
gcagctgcga	cctatattat	ttccgccaat	atgactgtgc	atcagtttagc	aaacatttgg	720
tcgcctgagt	ttaccatgac	ggagtcactg	aagaatgttg	caaaaacttc	ccctataact	780
aactga						786

<210> 57

<211> 249

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (75)

<400> 57

ggtcacatga	gccagcaatt	aacctttgac	gacagtgagt	tttccagtaa	acgtcgccctg	60
acgaggaaaag	aaatnttctt	atcccggtatg	gatactctgc	tgccgtggcc	tcaactgctg	120
ggcaacattg	aacctgtcta	tccaaaaaca	ggtaatggcc	gccgacctta	ttcgctggaa	180
acaatgtccc	gtaatccctg	cctgcaactg	tggtacaacc	tcggtgatga	aacgatggaa	240
gacgcattg						249

<210> 58

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 58

aggagagccat	ctatgaacag	tctttttaacg	ctggcggaagg	acttagagca	gaaatcgaaa	60
gcgcagcagc	agactaccgg	cgagatgctg	aaagccgcac	tcagcgagca	cgagaagtct	120
gtcagagcgg	aactgagcga	aagcgagaag	agaatcagcg	ccgccatcct	cgaccacgac	180
cggaagctgt	cctcagccat	gagccagcgc	acgaaaggga	tgctgcgcac	ggtcagccag	240
acgtggctga	ccatcgcttc	ggtctccgcg	ctgctgatag	cgtcgagcgc	gggcattctg	300
tggtggcagg	ggcagcagat	actcgagaac	tatacgacca	tccgggagca	gaagagcacg	360
caggccatgc	tgtcagagag	gaacagcggc	gtacagctct	cgacctgcgg	cgagcagaga	420
cgccgctgcg	tgagggtgaa	cccgggaagcg	ggacagttcg	gagaggactc	gagctggatg	480
atactggcgg	ggaaatag					498

<210> 59

<211> 219

<212> DNA

<213> Enterobacter cloacae

<400> 59

cacatgacgg	agctggaaaa	acagttgctg	agcgcattag	agcagctaca	gcaggactac	60
tcgaaaaggc	tggacgagtg	ggagaacgcc	ttcgcggaat	ggcggacgat	gtctggtctt	120
attcaacggg	agaacgcggc	gctgaacgag	cgcgtcacgg	tcttgagcag	gcagggtgcag	180
agtttgagcg	agcagctgcg	ccggttgctg	aaaggctga			219

<210> 60

<211> 861

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(16)

<400> 60

ccaacattgc	cgagcncgga	cgggggggcg	aacatccgac	tgaagggagc	catctatgaa	60
cagtctttta	acgctggcga	aggacttaga	gcagaaatcg	aaagcgcagc	agcagactac	120
cggcgagatg	ctgaaagccg	cattcagcga	gcacgagaag	tctgtcagag	cggaactgag	180
cgaaagcgag	aagagaatca	gcgcgcgcac	cctcgaccac	gaccggaagc	tgctctcagc	240
catgagccag	cgcacgaaag	ggatgctgcg	catggtcagc	cagacgtggc	tgaccatcgt	300
tctggtctcc	gcgctgctga	tagcgtcgag	cgcgggcatt	ctgtggtggc	aggggcagca	360
gatactcgag	aactatacga	ccatccggga	gcagaagagc	acgcaggcca	tgctgtcaga	420
gaggaacagc	ggcgtacagc	tctcgacctg	cggcgagcag	agacgccgct	gcgtgagggg	480
gaacccggaa	gcgggacagt	tcggagagga	ctcgagctgg	atgatactgg	cggggaaata	540
gcacatgacg	gagctggaaa	aacagttgct	gagcgcatta	gagcagctac	agcaggacta	600
ctcgaaaagg	ctggacgagt	gggagaacgc	cttcgcggaa	tggcggacga	tgtctggtct	660
tattcaacgg	gagaacgcgg	cgtcgaacga	gcgcgtcacg	gtcttgagca	ggcagggtgca	720
gagtttgagc	gagcagctgc	gcgggttgct	gaaaggctga	acgcgataga	aactcaccgg	780
cagcaggagc	gggcggtgca	gcaccagaaa	gcgctggagc	tggaaacgatc	gcagtggcag	840
catcatggct	cttcgctatg	a				861

<210> 61

<211> 627

<212> DNA

<213> Enterobacter cloacae

<400> 61

tggcggcaat	ttttctcttt	ttgcttacga	ttcgttgaga	acccgaaaaat	gttaaaaaaa	60
ctcttctttc	cgttggtagc	actctttatg	ctcgccggct	gcgcgactcc	gccgacgacc	120
attgacgttt	cacaaaaaat	tacctgacct	cagcaggatc	caagcctgat	gggcgttacg	180
gtcagcatta	atggcgccga	tcagcgtcag	gaccaggcgc	tggcgaaagt	gactcgogac	240
aaccagcagg	tcacgctgac	cgcctcccg	gacctgcgct	tcctgttgca	ggaagtgtg	300
gagaaacaga	tgacctcccg	cggctacatg	attggcccaa	gcggcgcggt	tgatctgcaa	360
atcatcgtga	acaacctgta	cgtcgaacgc	tcacagggtg	acgttcgcta	caacattgct	420
actaaagccg	atatcgccat	catcgctacc	gcgaagaacg	gcaacaaaat	gaacaaaaac	480
taccgtgcga	gctattccgt	tgaaggcgca	ttccaggcct	ccaacaaaaa	tatcgctgac	540
gcggttaaca	gcgtgctgac	tgacaccatt	gcgcacatgg	cacaggacac	cagcattcac	600
gacttcattc	agcagaacgc	ccgttaa				627

<210> 62

<211> 372

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(363)

<220>
 <221>unsure
 <222>(369)

<400> 62
 ctgacccggt gcttcaccgg gtcagttcat aagaacatgt ccagtcacta cttacgcatt 60
 ttccagcaac cgaaatcagc tattttgctg atccttggtt tcgcttcggt tttgcccctt 120
 gcgctcacct ccggcacggt acaggcgtgg atgacggttg agaacatcga tcttaaaaacc 180
 attggtttct tctcgctcgt cggccaggct tacgtcttta agttcctgtg gtcgcggtg 240
 atggatcgct ataccccacc gttcctcggg cgccgtcgcg gttggtttagc gatgacgcag 300
 gcgctgctgt tgctggccat tgccgcaccg gtttccttga gctgtgaaca aagcggctca 360
 ccnaaggnt ga 372

<210> 63
 <211> 237
 <212> DNA
 <213> Enterobacter cloacae

<400> 63
 cggtgtcgga ggagtgtatt catgatgata cgtgaacaga tagaagaaaa attaagggca 60
 gogttcaacc ctgtgtttct cgaagttgtc gacgaaagct atcgtcataa cgtgccggca 120
 gggtctgaaa gccactttta agtggttctg gtcagcgatc gcttcacggg agaacgtttc 180
 ctgaaccgac accgctccat ctgtcttcac tgccgagtgc cggtagcgcg tatgtta 237

<210> 64
 <211> 765
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(757)
 <400> 64
 acggctcctg ttcactcagg agcgcgtttt acattttttaa aaacgctgcg aaagcgacgt 60
 tattttgaat tttatgaggc ttcaaacatg gtacctgtgg tcgcgcttgt cgggcgccct 120
 aacgttgga aatocactct ttttaaccgt ttaacacgca cccgtgatgc gctgggtgctg 180
 gatttcccg ggctgacgcg tgaccgtaag tacggctcgtg cagaggtgga aggacgcgag 240
 ttcatctgta tcgataccgg gggatttgac ggtacggaag acggcgtaga aaccgcgatg 300
 gcagagcaat ctctgctggc tatcgaagaa gcggatgtcg ttctgtttat ggtggatgct 360
 cgcgctggcc tgatgccgcg ggattctgct atcgctaaac atctgcgttc acgcgaaaag 420
 ccaaccttc tggtggcgaa caaaactgac ggcacgatgc ccgatcaggc cattgcggat 480
 ttctggctct taggcctggg cgatatatat cctatcgcgg cctcgcatgg ccgtggcgct 540
 accagcctgc tggaaaccgt tctgctgcg tgggttgatg aagtaaacc accggaagag 600
 gtggatgagg acgctgaata ctgggcgcag ttgaaagcc gagaagaagg agaggaagag 660
 ccggaagacg acttcaacc gcaggatctg cctatcaagc tggtatcgt gggtcgcca 720
 aacgtgggta agtctacgct tactaacgct attttcnggc gatga 765

<210> 65
 <211> 606
 <212> DNA
 <213> Enterobacter cloacae

<400> 65
 ttattttcgc ggggctgctc ctacgtagt aagacgttcg gtgccgccat tgtggggcgt 60
 gacaacggcc gagtcagcgc ggtactgat cagcagggcc agatgatctg gcagcagcgt 120
 atttcccagg cgaccggttc aactgaaatc gaccgtctga gtgacgtgga caccacgcca 180
 gttatcgtcg acggtgtggg ttacgcgctg gcgtataacg gcaacctgac ggcgctggac 240
 ctgcgtagcg gccagatcat gtgaaacgt gagctgggtt ccgtgaacga tttcatcgtc 300
 gacggcaacc gtattttat ggtggatcag aacgaccgcc tgctggcgct gagcaccgaa 360

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ggtggcgtaa cgctgtggac gcaaagcgat ctgctgcacc gtctgctgac cgcaccggca 420
ctgtataacg gcagcctggg ggtggggcag agcgaaggct atatgcactg gatcgatcca 480
gagaatggcc gcttcgtggc acagcagaaa gtggatagct caggcttctt gacggagccc 540
gttgtggctg acggcaaaact gctgattcag gcaaaaagacg gcacgctgta cgcgatcacg 600
cgtaa 606

```

```

<210> 66
<211> 462
<212> DNA
<213> Enterobacter cloacae

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<400> 66
gttatagtaa cacatcatcc ttcattatta tgtttgaaaa actctcgggt acaacccccg 60
aaaagtaccg caaaaacata taaccacacc attaaagcaa gtgactttca aatgtgtaga 120
actgacaaat ttcagcttag cgtcttaaac accatcattt ttacaataga tgcacctata 180
aaaacagggt tatcaatcaa tcattttatct attatttcag gatatagtaa atggcatctt 240
caaaaaatth tcaaacacca ttttggcatg tctttaggta catatattag acgaaaaagg 300
atagagtatg ctgctcatga aattataaat aaaaaatgca aaatcattga tgtagtgatt 360
gatttcaatt tcagcaatca atcatcgtht tgtagaacct ttaagtcaat atatggtgta 420
tcacctaaag aatttaagag tgaacatatt aaccacttat aa 462

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<210> 67
<211> 192
<212> DNA
<213> Enterobacter cloacae

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<400> 67
aaaggggaagt ggggtgtcttt ccgtgaatgg agagcaagag tgcgtttttt aaattcgcta 60
ccattattga ggacagaaaa aaccatocaa gagatatctt atttgctagg ttatagtaac 120
acatcatcct tcattattat gtttgaaaaa ctctcgggta caacccccga aaagtaccgc 180
aaaaacatat aa 192

```

```

<210> 68
<211> 360
<212> DNA
<213> Enterobacter cloacae

```

```

<400> 68
tcattgtctgt ttttgtgttt cttttgtcct tttatgttaa ttattttcaa caccatgtgc 60
gttattataa ttgccactga actggaaaaa aggtgtatca tgaaaaacgt cctctcattg 120
tcattgtctac tttttatttc aagtgggtat gcagcttcag aagtcaccta tttaaacccc 180
acacctcaag gagcggtagc aattgggtgag gtaagcttct ttaaagcagg aagtgcaacg 240
cagtcagaag taattgggtc actatcaaag aaagcagatt cattgggtgg gactcatttc 300
gaaatttcgt cacttaattc ttccgataat acgtatgcaa ccgctattgt gtacaagtag 360

```

```

<210> 69
<211> 216
<212> DNA
<213> Enterobacter cloacae

```

```

<400> 69
acgttgggaa ctgtgctgtt tctttgcttt agtatcggat tggcaatcac aatggtagct 60
atcgtgtctg ttgcagctgt aagcgtagaa caggcatcaa agcgttggga cgggttgat 120
gttttagccc gaagagcacc atatttttca agtgctttga ttgcgttagg gggaatttat 180
atgggttatc acggatggtt gggcataaca aatga 216

```

```

<210> 70
<211> 312
<212> DNA
<213> Enterobacter cloacae

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<400> 70
 ccggattttg atttaccaaa cacaacctgg caaccaccca agctggacct tgaaaatatt 60
 ctggaacctt caccagacg catctggccg gatgcttacg aacgtctgct gttggaaacc 120
 attcgtggta tccaggcgct gttcttccac cggatgaag tggaagaggc gtggaagtgg 180
 gtgcactcca tcaccgaagc gtgggcagcc gaccaggacg cgccaaaacc gtatcaggcg 240
 ggaacatggg gacctgtcgc ctccgttgcg atgatcaccg gtgatggccg ctccctggaac 300
 gagtttgaat aa 312

<210> 71
 <211> 885
 <212> DNA
 <213> Enterobacter cloacae

<400> 71
 attagaggag cttttatgaa tccgacattg ttacgcgtaa cacaacgcat tggtgaacgc 60
 tcgaaagaga cccgtgctgc ctaccttgcc cgcacgaac aggcgaagag tgaaacggtc 120
 catcgctcac agctggcctg cgggaatctg gccacaggct ttgcggcctg ccagcctggt 180
 gataaagacg cgtgaaaaag catgttgctg aacaatatcg ccatcattac ctctataac 240
 gacatgcttt cagccaccca gccgtatgag gtctaccctg ctatcatccg caatgcgctg 300
 cacagcgtga acgcgggtgg ccagggttgc ggccggcgtg cgccatgtg tgatggcgta 360
 acccagggcc aggacgggat ggagctgtcc ctgctgagcc gcgaagtgat cgccatgtca 420
 gcggcagtgg gacctgtcca caatatgttt gatggcgccg tttatctggg cgtgtgctgac 480
 aaaatcgtcc cggggctggt gatggcgccg ctgtcgtttg gccacctgcc agcgattttt 540
 gtgccgtcag gcccgatggc aagcggctct ccaacaagg aaaaagtccg tatccgccag 600
 ctgtatgccg aaggaaaagc ggaccgtcag gcaactgctg aagcgggaag cgcgctcttat 660
 cacgcgccgg gcacctgtac gttctacggt acggccaaca ccaaccagat ggtgggtggag 720
 tatatgggga tgcagctacc gggctcgtcg ttcattccagc cggatgcgcc actgcgtaaa 780
 gcgctgaccg aagccgcacg ccgtcaggtg acgcgcctga ccggtaacgg caacgagtgg 840
 atgccaatgg gcaaaatggt ggatgaaaaa gttatcgtaa aacgc 885

<210> 72
 <211> 387
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (43)

<220>
 <221> unsure
 <222> (281)

<400> 72
 caaaatggac gtcacatgct tacgtgttat gcgcttaatc atntccgcac caaaacccaa 60
 ttggcaacgg cagcaggtgt aaaactgcaa tccatttaca attggaaaga gcttgtaact 120
 gaaacccgtg ctaccggct tgaacaaccc ttccggcggg ttctgacatt ccacaaaaacc 180
 attttcgaac cacaccgtaa agcacaaaca actgggaaaa agaatacctc cccccccca 240
 agggactcga atttatgaa attccaaccg accccttcca ntgcgttctg cttggctggg 300
 gcggcggaat taaggagggg cttttccccc gaggggaatc ccgcacaaat taccocgccc 360
 agggggggcc caccttcccc tgggtgg 387

<210> 73
 <211> 423
 <212> DNA
 <213> Enterobacter cloacae

<400> 73
 aattgtotaa ctatgaaaaa tatgaacagt ctgggacagc gaatccttgc cagacgcaag 60
 gagctgaaat taactcaacg agaagccgcc aaactcgagc gcgtagcgca tgtaaccatt 120
 tcgcaatggg agcgtgacga gacgcagccg gtaggtgcaa gattatttgc gcttgcaaa 180

gctcttttct	gcaccccaac	atggctgatg	tttggtgatg	acgatcaagc	tccagttcca	240
gcagaagata	tccaattagc	gccgcaatta	tctgacaagc	acagagagtt	aattgatctc	300
tacgattccc	tgccagagtc	agagcaagag	gcacagctcg	agcaattgcg	tgctcgcggtg	360
aaaaacttca	ataagctctt	cgaagaatta	ctcaaagcca	gacagcgcca	atccaaaaaa	420
ttaa						423

<210> 74
 <211> 1260
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (44)

<400> 74						
aatggggttag	gggactcttg	cccgggatta	atggagaagg	ggcnatggat	ttctggcgaa	60
ttatttgtag	ctcttctctg	gtattttatt	ggctatcacc	tggagtcggg	ggatattatg	120
aagatgaaat	gcaataacag	gttactcaga	ttatctgcct	ccctgacctt	aatttcgttg	180
gtggtgactg	cggctaattg	aaataacggc	caggcgggga	tatctcccgt	tgccggcaatg	240
acgatgaaag	aaagtattct	tttgcctctc	gatcgcgacc	cctcgggtgag	tcagcaggcg	300
gcacagctgg	ggatcggcca	ggcacaataa	gacgaagcgc	gcagtggctg	gatgccacaa	360
atagccctga	acgggcgtac	aggtcacagc	cagaccaccg	attcaagcgg	ctcgttgcca	420
aattccgcag	cctggggcct	gagtcctgac	cagctggtgt	acgatttttg	caagaccaac	480
aacagcatca	gccagtcttc	agctcagcgt	gacagctatc	gctaccagct	gatgagcacg	540
atgtctgccc	tcgcggaata	aacggcgctc	agctatgtgg	aagtgaacgc	ctacagcgat	600
ctgttgccag	cggcaaaaag	gaacgtgcag	gcgcttaaaa	acgttgagca	gctggcaaaa	660
ctccgcgcgc	acgctggcgt	aagctccacc	tctgatgagc	ttcagaccgc	caccctgatt	720
gccgggatgc	aggcgacggg	agagcagtag	aatgcattcc	tgaacagcgc	ccgcgcgcgc	780
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gtggagccgg	attctctcaa	tcggattgat	tattcaactga	tcccaacggg	gatggccgcg	900
cagaacatgg	agcgttcagc	ccagtaacgc	gtagaaacgc	cgaagtctca	gcactggccg	960
accttaagcc	tgaagggggg	ccggacccgc	tatgagtcgg	ataatcgcg	gtactgggat	1020
gatcagatcc	agctcaatat	tgacgcaccc	ctttatcagg	gcggcgccgg	ctcggcgccg	1080
gtccgtcagg	ccgagggcgc	aagggcaatg	gcctcgctgc	aggtcgatca	ggcccgtttt	1140
gatgtcctgc	aaaaaatcct	ccgtcgcaac	ggccgactgg	accggggcgc	gtggactaat	1200
ggaagccggg	aaacgtcagc	tggaaaatgc	gttgccgcgc	cgcgatgtct	acaaaaatga	1260

<210> 75
 <211> 1197
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (1156)

<400> 75						
aggtcaggcg	gcgtaacaca	acaaagcaaa	acatcacatt	ggagcacaat	aatgagtatt	60
tccttgaaga	agtcagggat	gctgaagctt	ggtctgagtc	tggtggccat	gacogttgca	120
gcaagcgtac	aggcaaaaac	cctgggtttac	tgtcttgaag	gctctccgga	aggctttaac	180
ccacagctct	ttacctctgg	tacgacttac	gacgcaagct	ctgtaccgat	ctataaccgt	240
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cgtcagaaaa	atgccagaaa	cccgtaccat	aaagtgtctg	gcggcagcta	tgaatacttc	480
gaagggatgg	gtctgccaga	cctgatcgct	gaagtgaata	aagtggacga	taaaaccgtc	540
cagtttctgc	tgacgcgtcc	ggaagcgcca	ttcctggctg	acctggcgat	ggacttcgcc	600
tcgattctct	ctaaagagta	cgctgacaac	atgctgaaag	ccggcactcc	ggaaaaagtg	660
gacctgaacc	caatcggtac	cggcccgttc	cagctgcttc	agtaaccagaa	agattcccgt	720
attctgtata	aagccttccc	gggctactgg	ggcaccgaag	cgcagatcga	ccgtctggtc	780

ttctccatca	cgcctgacgc	atccgtgctg	tacgcaaaat	tgcagaaaaa	cgaatgtcag	840
gtgatgccgt	atccaaaccc	ggctgacatc	gcgcgcatga	agcaggacaa	aaatatcaac	900
ctgctggagc	aggcgggcct	gaacgtgggt	tatctctcct	tcaacaccga	aaagaaaccg	960
ttcgatgacg	tgaagtgcg	tcaggcgctg	acctacgcgg	tgaacaaaga	aacgatcatc	1020
aaagccgttt	accagggcgc	aggcggttgc	gccaaaaacc	tgatcccacc	aacctgtggt	1080
ggctataaca	acaaccttaa	ggactacacc	tacgatcccc	agaaaaaccg	aaccgttgct	1140
gaaaaaaacc	ggccangaac	aaggctttac	cgccaacctg	tgtgcgatgc	cgggttaa	1197

<210> 76

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 76

atggcaatcg	cagatttggga	taagcagcca	gattctgttt	cttccgtgct	gaaggtgttt	60
ggcatcttgc	aggcgctcgg	agaagagcgt	gaaatttgga	ttacagagtt	gtcgcagcgt	120
gtgatgatgt	cgaaaagcac	cgtttatcgc	tttttgcaga	cgatgaaatc	attgggttat	180
gtcgcgcagg	aaggagaatc	agaaaaatat	tctctgacgc	tgaactgttt	tgaactgggc	240
gcccgcgctt	tgcaaaacgt	ggatctgata	cgcagcgctg	acattcagat	gcgtgaactt	300
tcacgattga	cgaaagagac	aattcacctc	ggtgcg			336

<210> 77

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 77

aatagttact	ctgaaaataa	tttcacgctg	agtcattctt	ttcccatgca	aaaaaacggt	60
tctgatggcc	tgcccttacc	gcagaggtac	ggggcaattg	ccactattgt	catcggtatt	120
tcgatggctg	tccttgacgg	tgcgattgcc	aacgttgctc	ttcctaccat	tgcaaaagac	180
cttaattgctt	ctcccgcaag	ctccatctgg	attgtgaacg	cgtaccagat	agcaattgtg	240
atttccctcc	tgtaactctc	tttccctggc	gatatgtttg	gctatcgccg	ggtttaccag	300
tgccggctgg	tggtctttac	cctcacctcg	ctcttctgtg	ccctttccga	ttcactgcac	360
accctcaccc	tgccgcgtat	cgcgcagggc	tttggcgggc	cggcgcta	gagcgtgaac	420
acggccctca	tacggcttat	ctatcctcac	cgcacactgg	ggcgcgcat	gggcattaat	480
tcctttattg	tggcgtgtc	gtccgctgcc	gggcgcagca	ttgccgcgc	cattctgtcc	540
gttgectcgt	ggcagtgggt	gtttgccatt	aatgtgcgc	tgggtattgt	ggcgatcttc	600
ttcgccctgc	gctatcttcc	ggaaaatggt	cgcgaaaaca	ccatgcgcgc	ttttgacctg	660
cccagcgccg	tgatgaacgc	gctgaccttt	ggcctgctga	ttaccgcgct	gagcggattt	720
gcgcaggggc	agtctctgtc	gctcattgcc	gcagaaatcg	ttgccatgct	tatcatcgga	780
tttttcttgc	tacgacgtca	gctggcgctg	cccggtgcgt	tactgcgggt	ggatttgctg	840
cgtattccgc	tgttttcgtc	atccatttgt	acctccattt	gctcgttctg	cgcgcagatg	900
ctggcgctgg	ttgcgctgcc	gttctttttg	cagagcgctga	ctggcgcttc	ggttgtgtca	960
tcaccggcgg	tagaagtata	cctcccc				987

<210> 78

<211> 711

<212> DNA

<213> Enterobacter cloacae

<400> 78

aatgacatta	gcagccagcc	ggggagcaag	atgaaaaatat	tgatcgctga	agacgaaatt	60
aaaacagggt	aatatctcag	caaagggtct	acagaggcag	ggttcgtagt	ggatcacgct	120
gataatggtc	ttaccggata	tcctctcgcc	atgacagcgc	agtatgattt	agtcattctg	180
gatatcatgc	tacctgatgt	gaacggctgg	gatatcatcc	gcattgctgc	cactgccgga	240
aagggtatgc	cggctcttact	gctgacagcc	ctcggcacga	tcgaacatag	ggtcaaagga	300
ctggaactgg	gtgcggacga	ttatctggtt	aaaccctttg	cgtttgccga	actgctcgcc	360
cgggtgagaa	cccttctgag	gcggggaaac	acgatgatca	cggaaagcca	gtttaagggtg	420
gctgacctct	cgattgatct	cgtatccaga	aaagtcagtc	gcgcgggaaa	ccgcattgtg	480
ctcaccagta	aagagttcag	cctgctggaa	ttcttcattc	gccatcaggg	agagggtctt	540
ccccgctccc	tgattgcctc	tcaggctctg	gacatgaatt	ttgacagcga	cactaatgctg	600

atcgatgtcg cagtaaagcg actccgcgct aaaatagaca acgattacga gacaaagctg 660
atccagacag tccggggcggt gggctacatg ctggagggtcc cggatgcata g 711

<210> 79

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 79

tccagacagt	ccggggcggtg	ggctacatgc	tggagggtccc	ggatgcatag	caaacccttcc	60
agacgccctt	tctcactcgc	tctgcggctg	accctttttta	tcagcctgtc	cacgatactg	120
gcttttatcg	cattcacctg	gtttatgctg	cattctgttg	aaaatcattt	tgccgagcag	180
gatgtcagcg	atcttcaaca	aatcagcacc	acactgaacc	gtatactgca	gtccccggtg	240
gatccggatg	ataaaaaaat	aagcaaaata	aaggaatcaa	ttgccagcta	ccgcaacggt	300
gcccttttgc	tcctcaatcc	caggggggga	agtgtctctt	ag		342

<210> 80

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 80

atcatactcg	gctgtcatgg	cgagatgata	tccggtaaga	ccattatcag	cgtgatccac	60
taagaacct	gcctctgtaa	gcccttttgc	gagatattca	cctgttttta	tttcgtcttc	120
gacgatcaat	atcttcatct	tgctccccgg	ctggctgcta	atgtcattct	attgcgcccc	180
cgatcgttat	caacggatta	cagcaaaaaat	gacaacattg	tcattatcct	gtcaccgggc	240
aaacagagag	cgtttaggtaa	agtaccctta	tcaatactct	ggacttcatt	tgaaccattt	300
accagggtcg	cctggacgag	aagcggttatg	ttcaaattaa	aattactcag	cattagcacg	360
atattcatcc	tggcaggctg	cgtgtcgctt	gcgcctgaat	atcagcgggc	cgcagcaccg	420
gtaccccagc	agttttcact	gtcccataac	agcctgacgc	cagcggtaaa	tggctatcag	480
gatacgggct	ggcgtaactt	ttttgtcgat	ccccagggtta	cccggttgat	cgggtgaagct	540
ctgactaata	accgtgattt	gagaatggct	gccctgaatg	ttgaagaggc	ccgagcccag	600
ttc						603

<210> 81

<211> 1296

<212> DNA

<213> Enterobacter cloacae

<400> 81

ttttctttta	ttgttcgagt	ggagtccgcc	gtgtcacttt	cgctttggca	gcagtgtctt	60
gcccgatgac	aggatgagtt	accagccaca	gaattcagta	tgtggatccg	cccgttgcat	120
gcggaactga	gcgataaac	gctggctttg	tatggcccaa	accgtttcgt	gctcgattgg	180
gtaagggata	aataccttaa	taacatcaat	ggactgctga	atgatttctg	cgggtcagat	240
gccccacagc	tgcgttttga	agtgggcaca	aagccgggtca	cccaaaccgt	tcgtgaagtt	300
gtcaatgtgg	cagccctcgc	acaggcgggc	ccogetccag	cgctcgcgt	tgcaccggct	360
cgtcagggct	gggataacgt	tccggccccc	gctgagccta	cctaccgctc	taacgttaac	420
gtgaaacaca	cgttcgataa	cttcggttga	ggtaagtcca	accagctggc	gcgcgcggcg	480
gctcgccagg	ttgccgataa	ccccgggtgg	gcttacaacc	cgctgttcct	gtatggcggc	540
acgggtctcg	gtaaaacgca	cctgttgcat	gcgggtggga	acggcattat	ggcgcgtaag	600
cccaatgcc	aagtagtgta	tatgcactcc	gaacgcttcg	ttcaggacat	ggtaaaagcc	660
ctgcaaaaca	atgcgaccca	agagttttaa	cgctactacc	gttcggttga	tgcgctgctg	720
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gacattcgcc	tgccgggtga	agtggcggtt	tttattgcca	agcgctcgcg	ttccaacgtg	1020
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ttactgtcta	aacgtcgctt	ccgctcggtg	gcgcgtccgc	gtcagatggc	gatggcgctg	1260

gcaaaacagc taagcaacca tagcctgccg gaaatc 1296

<210> 82
<211> 288
<212> DNA
<213> Enterobacter cloacae

<400> 82
ttaaataagc ggggtccgg cagctccgtg gtgaagatcc agatggcgt cactacgctg 60
ttgcgctttg aacatgagac ggtgatgccg cctgaaatga aattcagcaa gcgtgaacgg 120
gaaattctga agtggaccgc agaagggag acgtcggcag aaatcgccat cattctttcc 180
atctcggaat ataccgtcaa ttccaccag aagaatatgc agaagaaatt caacgcaccg 240
aataagatcc agatagcgtg ttatgccggc gcgacgggac ttatctga 288

<210> 83
<211> 461
<212> DNA
<213> Enterobacter cloacae

<400> 83
accaattag cagtcagtag cgttatccct attctggaga catttccttt gatcaacgtc 60
cttcttggtg atgaccacga actgggtggc gcagggatag gacgcattct tgaagatata 120
aagggtatta aagttgccgg cgaggcgtgc tgtggcgaag atgccgtcaa atggtgtcgc 180
gctaactccg cagacgtggt gctgatggat atgaacatgc ccggtattgg cgggcttgaa 240
gccacgcgca aaatcgcgcg catgttcgtt gataccttag ttatcatgct gaccgtccat 300
accgaaaatc cgctgcctgc cagagttatg caggcgggtg ctgccgggta tctcattaaa 360
agcgccgcgc cgcaaggag tggtcaatgc gatccgccac cgtatacccc ggggcaagggt 420
tacattcctt ctgaatatgc tcaacaaaat ggctctgaat c 461

<210> 84
<211> 225
<212> DNA
<213> Enterobacter cloacae

<400> 84
atgagcacac ctgaatttgc cactgccgag aataaccagg aactggcaca ggaagtaaac 60
tgcctgaagt cgtgctgac gcttatgcta caggcgatgg gccaggctga tgctggctgt 120
gtgatcatta aaatggaaaa acagatcgcg cagatggaag accaggcgga atccgctgtt 180
tttgccaata cggttaagca aattaaacaa gcctaccgcc agtaa 225

<210> 85
<211> 366
<212> DNA
<213> Enterobacter cloacae

<400> 85
catgggtcgc atgcgatctc tctttactca caacacgctt ttgaccccag acaagaaaca 60
ctaattttta cggaaacggg gaccaccatg agtaaagcga ttatgcagca gacgtataat 120
tttgaagcct tgcacgataa aggaactggc gaacattttc ttaatgcagg aaaacatctc 180
agtggtgagg ttgaagtgtt gggctcggca atacgctgta ttatgctgac cggtgacaat 240
ctctctaata aagagattat cctgcaactg attcacgccc tcgaaattac cgaggagccc 300
gaagcctgcg atgtcattcg aaatacgtt gaaattgttg tcggttttac gcgcgatgat 360
atctga

<210> 86
<211> 888
<212> DNA
<213> Enterobacter cloacae

<400> 86
gttggtcaga taaaaccatt tatacccat agaaaagtgg ggttgataa attatatctt 60

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atcagggtgt	ggttttagcga	tgcacgtgtt	ttcagagatg	aagtctgtgc	agtaaaaaat	120
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cagatatata	gcgacatgac	gggaagggaa	tgcgttcggg	aaggcgtcga	tagcgaagaa	780
aaatttaaaa	aacttgctgc	gtaggggtt	aaacgctttc	agggatatta	tctttcccgg	840
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<210> 87

<211> 558

<212> DNA

<213> Enterobacter cloacae

<400> 87

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gatgatttca	gcccatccct	tgcagctgag	atatcagcta	tgtttgaggc	gattgcgaac	120
ggaaggaatc	attcctctgt	gtatgagtac	ccgctattaa	ccgaagtaca	ggctggctca	180
ttttgcccg	ttaatacata	cacagaacga	gacgcgaagg	aatgggtttc	aacgactgtt	240
aaagccagtg	attctgcctt	ttggcttgag	gtatcaggtc	attcgatgac	tgccccgcca	300
ggagtaaaac	cgagttttcc	tgagggaatg	cttataactca	tagatccaga	acaggatggt	360
gagcctggtg	atttctgtgt	tgcaggtatc	ttcaacgatt	cagaggtcac	ttttaaaaaa	420
tatgttcgag	aagatgggaa	gccatggctt	gaacctctaa	accccagccc	tcgctatcag	480
gccattgaat	gtaatgagaa	ttgcaggata	ataggcaaa	ttgttaaggc	ccaatggcct	540
gaaaatatct	tcgaataa					558

<210> 88

<211> 467

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (399)

<220>

<221> unsure

<222> (404)

<400> 88

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ctttgccggt	gcgtcgctgg	gttcgtcttc	ctcggcggtc	cttttctctg	tgctgttccg	120
cgtctccttc	ttcgtgtttt	gctgttttga	cgggtgtccg	gctgggtctg	tctccgcctg	180
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tgttcctgcc	cgctcggtgt	gtcccggttt	cgctgggtgc	ttttgtgggc	tttgoggcgt	300
ttgaagcgcg	gcatggagca	agctcagccg	ctctccacgt	ttctgtttta	cagcctgatg	360
ccgcagggtg	atttgagtac	ccctgtacgg	cgcgcgcanc	tcancaagct	ggcgtgcgg	420
ttaatcagcc	atgtgcccg	cgaaacgctg	cgcctctatc	tgctgtca		467

<210> 89

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 89

tttttccttt	cggcactcgg	cggtgaaaaat	cttcggggtcg	tcgatggctt	tttggatggt	60
gtcgcgctgg	cgctgttcgt	ctttttcttt	gccgttgcg	cgctgggttc	gtcctcctcg	120
gcggtccttt	tcctgctgct	gttcgcgctc	tccttcctcg	tggtttgctg	tttcgacggg	180
gtccgcgctg	gtctcgtctc	cgcttggtg	gcgttggttt	ccgcgttgcc	gtttttgtcc	240
gtcgggcgtc	ctttggtttc	gctttttgtt	cctgcccgct	ggtgttgctc	cggtttcgtc	300
ggtgcgtttt	gtgggctttg	cggcgcttga				330

<210> 90

<211> 195

<212> DNA

<213> Enterobacter cloacae

<400> 90

ggacatagaa	acagtgggtca	ttggtgtggt	acgtcatctc	gttcactcct	tcaaattccg	60
ggatgcctga	gcatgtttgc	gctggctgat	gtgaattctt	tttatgcttc	atgcgaaaacc	120
gttttcaggc	cagacctccg	tggcaaacct	gtgggtgtac	tatccaataa	tgatctgagt	180
ggtgagaagt	gtag					195

<210> 91

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 91

agtggggaca	agatgtacat	ctcagaaatt	cagattgaga	attttcggct	gttcgattcc	60
gctgaaaaag	cttttgtact	atcactcaac	cccgggctga	ccgctttggt	aggcgaaaat	120
gatgcgggaa	agacggctgt	tattgatgct	ctccggttgg	tattaggaac	ccgcgatcag	180
gagatgctgc	gtatagatat	gttaattatg	caccattggg	gggaggcaaa	atctcgaact	240
tccccctttc	gtcctatag					258

<210> 92

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 92

ggatataaca	tggcgtttaa	atttaagacc	ttcgcagcag	taggcgcact	gattggctcg	60
ctggcactgg	tgggttgctg	tcaggacgaa	aaagatocaa	accacatcaa	agtaggcgtt	120
atcgtcggtg	cagaacagca	ggttgctgag	gccgcgcaga	aaatcgctaa	agagaaatat	180
ggcctggacg	ttgaactggt	gacctcaac	gattacgttc	tgccgaacga	agcgtgagc	240
aaaggcgaca	ttgacgctaa	cgcttccag	cataaaccgt	acctggatca	gcagatcaaa	300
gatcgcggt	acaaactggt	tgctgtcggt	aacaccttcg	tttaaccgat	tgccggctac	360
tccaagaaaa	ttaaattctc	ggatgaactc	cagccggggt	cacagggttc	cgctccctaac	420
gacccaacca	accttgccg	ttccctgctt	ctgctacaga	aagtgggctt	gattaaactg	480
aaagaaggcg	ttggcctggt	accgaccgtt	ctggacgtaa	ccgaaaacc	gaaaaatctg	540
aaaattgttg	agctggaagc	accacagctg	ccagcttctc	tggacgatgc	gcagatcgcc	600
ctggccgtga	tcaacaccac	ttacgccagc	cagatcggcc	tgacccagc	gaaagatggc	660
atcttcgttg	aagataaaga	ttccccgtac	gtcaaacctga	tcgtgactcg	cgaagacaac	720
aaagacgcgg	agaatgtgaa	gaaattcata	caggcatatc	agtcctgaaga	agtgtaccag	780
gaagccaata	aggtgtttta	cggcggcgcg	gttaaaggct	ggtaa		825

<210> 93

<211> 931

<212> DNA

<213> Enterobacter cloacae

<400> 93

ttcccgacgc	ggatcttcca	gccccgtggt	caagaccccg	gtgcgtggag	tagcttcatt	60
gaagagcaat	cctgatggtg	cttcctgtct	tggcccgatg	gcagggtg	agaaacagcg	120
tgagcagtat	tcacacgccg	tccaggcatt	gtctgatccg	gatcgtaaga	ggctgggttt	180
agtggctcga	ctgcaaaaaat	caacgcttca	ggaagtcgcc	cgtactcatg	atgagcttgc	240

ggcgataggt	ctcaaaaatc	agtatctggt	catcaacggc	gtgttacctg	agacagaagc	300
agtcaacgat	actctggcgg	ctgcaatatg	gggcccggag	caggaggcgc	tggcaagtct	360
tcccgtggt	ctggacgctc	tccctactga	cacattatto	cttcaaccag	tgaatatggt	420
cgggtgtgtct	gctttaaggg	gacttctcac	ctcccaacct	gagacggctt	catttgctga	480
agtgtccgcc	ctgcaaaaac	cagcgatata	gtcgttgtct	gctctgggtg	atgagattgc	540
ccttaatgaa	cacggcctga	ttatgctgat	gggtaaagg	ggcgtgggta	aaacaaccat	600
ggctgcggcc	attgcagtca	gactggccga	aatgggattt	gatgtgcata	tcacgacgtc	660
agatcctgct	gcacacctga	gcacaaccct	caatggaagc	ctcaataacc	tgcaggtcag	720
cagaatcgac	cctcatgatg	aaacagaacg	ttatcgccag	catgtccttg	aaacgaaagg	780
acgtgacctg	gatgaagcag	ggaaacatct	gctggaagag	gatttacgct	ctccgtgtac	840
cgaagagatt	gctgtgttcc	aggccttctc	acgggtgatc	cgtgaagcgg	gtaaaacggtt	900
tgtcgtcatg	catacttctt	caccttcgta	g			931

<210> 94

<211> 183

<212> DNA

<213> Enterobacter cloacae

<400> 94

aacagaaaca	ccacctccgc	agagaaggta	gaaaacgttg	ttaagccgcc	gcagaaaaccg	60
gttgtaatca	gaaccttcca	catagggtcg	atgttggtca	tgcgattaaa	ccaggccagc	120
ccatcccaa	taataaacgc	cccgatcaga	tttgccgcc	gtgtcccat	cggaatggcc	180
tga						183

<210> 95

<211> 945

<212> DNA

<213> Enterobacter cloacae

<400> 95

tgcagagggt	taaaccgcat	gottaagagc	caccgcgcaa	cgctaccctg	gcctccacca	60
ataaaaaacg	ctataagtag	ttgtaaacact	gtcaataacct	gctatttgct	gtgtaagtgc	120
gtcgagtgtg	acgtgtttt	tgaccgggag	acaattatgt	atgttgagct	agggcagttc	180
gcggtgacgc	cggactggaa	tgaaaaacgc	gaaaaatgcg	tctccctgat	gcatgcggcg	240
aagcaaaaagg	gggcgtcggt	gctggtaact	cccgaggcgt	tactggcccg	tgatgatggc	300
gatccgggacc	tgtcggtaaa	gtctgcgcaa	acgctggaag	gggcgtttct	gaaacgactg	360
ctggccgaaa	gcgttggaac	caacgtcaac	accatattga	cggcccatat	tccgtcctcg	420
ccggggcgcg	cgggtgaacac	gctgggtggg	atagctgagg	gtgccattgt	cgcgagctac	480
gccaaaacttc	atctgtatga	tgcgttcagc	gttcaggagt	cgcgcctggg	cgatccgggg	540
agtgtaattc	cgcgcgtgat	tgagggtggg	ggttttaagg	ttggcctgat	gacctgctac	600
gatatccgtt	ttcccagagc	ggcgcgtgaac	ctggcattgc	agggggcgga	ggtgctgggt	660
ctgcccgcgc	cgtgggtcaa	aggaccgctt	aaggagcatc	actgggcgac	gctgctggca	720
gcacgcgcgc	tggataccac	ctgttaacgtg	gtagccgcgc	gtgaatgtgg	taacaaaaat	780
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cctgcgttat	tgtgacgga	gataatttca	gcccgaatag	cgtttgcgcg	gcagcaatta	900
cctgttctgc	gcaaccgcag	gtttgcgcga	ccgcaattaa	tgtga		945

<210> 96

<211> 396

<212> DNA

<213> Enterobacter cloacae

<400> 96

caggatttga	cagtgttaca	actacttata	gccgttttta	ttggtggagg	cacgggtagc	60
gttgccgcgt	ggctcttaag	catgcgggtt	aacctctctg	atcaggccat	tcgatgggg	120
acactggcgg	caaatctgat	cggggcgttt	attattggga	tggggctggc	ctggtttaat	180
cgcattgacca	acatcgaccc	tatgtggaag	gttctgatta	caaccgggtt	ctgcggcggc	240
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ggctgggcgc	tgacgaacat	tgccgttaac	atgcttggtc	cgtttgcgat	gactgcgata	360
gcattctggt	tattttcctc	cgccagcgga	cattaa			396

<210> 97
 <211> 456
 <212> DNA
 <213> Enterobacter cloacae

<400> 97
 ttacacatga atatattaat cacgaccact gcgtttacag ctttattttg tggggcagct 60
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 gtcagtcatg tgaattcctc gacgcatgaa aacttaccgg acagggttaa taaaaacaac 180
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 ggcagtgatg caaattcaaa gacctcgtct tcttctttta acgaactgaa tgccggagaa 360
 aaagccgctc tcgtgcatga gcaggtcaat aatgccgggt cggaagcaca tcagacgcag 420
 gcaagaaagc ttgcggggct gtattcgacc aggtaa 456

<210> 98
 <211> 839
 <212> DNA
 <213> Enterobacter cloacae

<400> 98
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 aaggacatac cggcgaaacg gtgcccggga caattgggtt cgcaaccgtt cgtgcaggcg 660
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 acaaagcgtc aagccgcagt acgtttgcga atggtgcagt tcgcgcgcgt ttgtggctta 780
 acgcgaagga aaagggtctt tttgatatgc gagatgtgct tgatctcaat aatttgtaa 839

<210> 99
 <211> 390
 <212> DNA
 <213> Enterobacter cloacae

<400> 99
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 ggggaagtgc ttttcaatac ttcaatgacc ggttatcaag aaatcctcac tgatccttcc 180
 tattctcgcc aaatcggttac tottacttat cctcatatcg gcaatgtcgg caccaatgcg 240
 gctgacgaag aatcctctca ggtacatgcg caaggcctgg tcatttcgca cctgccgctg 300
 attgccagca acttccgcaa caccgaagac ctctcttctt acctgaagcg ccataacatt 360
 gtggcgattg ccgacatcga tacccgtaag 390

<210> 100
 <211> 1269
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (1251)

<400> 100
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gacggctata	tcagcgccct	gctgcgccgt	ggcgaactgg	aaggcaaacc	agggcagacc	180
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<210> 101

<211> 2103

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (258)

<400> 101

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ttogtcagca	actacgccta	tgacgacctg	ccaacctcca	tcagtgaagt	gtggaacttt	360
ggtgataccg	ccgcgcgatac	cgcgatttat	gaccgcattg	aagtggttcg	cggcgccacc	420
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tga						2103

<210> 102

<211> 492

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (344)

<400> 102

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gcgcgggata	atggaattaa	tgacaatctg	ctgtttacct	ggcgccagcg	ttacagacat	180
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ctgcctgata	tggccctgtc	acaccatgct	gagccgcact	atgaaaccgc	cgctccagcc	300
tgccgcgagg	ccatgacatg	cgatgtgact	gtcggcggtg	gcancctgcg	tctgtccggg	360
ggatttatca	ccttgcaactt	cttgaaaacg	ctgatccgcg	cacctgaccg	gggagggagc	420
cgaatgattc	cccttaccgt	cggggcactc	cgtattctgg	ctgggttgcc	gggggtccccg	480
aaaaatgctt	aa					492

<210> 103

<211> 726

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (547)

<220>

<221> unsure

<222> (649)

<400> 103

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aacgcctga	cactcttcgc	tattgtggcg	tggattgcat	atgaagcatg	ggagagggtta	180
caagctccac	cagcgatact	ggcaggccca	atgctgatcg	ttgccattgt	aggattgttg	240
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ggcgctat	tacatgtgat	gggggatcta	ctgggttctg	ttggcgctat	tgctgcgcgt	360
attgtcattt	actatacggg	ctggacacca	attgatccaa	tactctccgt	tctcgtcgca	420
gcaactggtt	tacgtagtgc	ctggaagtta	ttagcaaaat	ctctgcacat	cctgttagaa	480
ggtgctccc	aaaatgcttc	cccagacaag	gtaaagcaga	gactaatcaa	ttctgttcaa	540
ggcttanctg	ccgtaagtca	tattcatgtc	tggcaataaa	cctcaggccg	aataatggca	600
acactggaag	taagagcaaa	ggaagatgtg	gacgtgaaag	acgtagtana	gcttggttaa	660
caagaacttt	atgagcattt	caaaaataga	acacgcaact	gtgggcatcg	actggaatta	720
cgatga						726

<210> 104

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 104
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 gaaattgggc tactttccga gattttccat ctactggggg accagtcaag actacgaatc 180
 ctgctttact gtatgcgtgg ttccggtctct gtaggtgaca ttgctgagtc gctccagtta 240
 tcacaatctc tggtcagtca tcatctgagg ttgttgccgg gtgcaagact cgttcgagga 300
 gagagaaagg gcaagtacat cttttatagc attatggatc agcatgtaag ccatgttctt 360
 caggatatgg catttcacat agcagaataa 390

<210> 105

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 105
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 gagcaccccc gcaaaaacaa agccgccatc atactcgaat acctgaaagc cagcatcagg 120
 gcaaagggtg agcaccggtt tagggttatt ataagtcagt ttggttttat caaagcacgc 180
 tacaaggggt tgatgaaaaa tgactcacag ttagcgatgc tattcacgct agcgaacctg 240
 tttaaagtgg atcagatgat acgacgacag actaaatccg cctaa 285

<210> 106

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 106
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 tttgtgcctt ttcaaagaac aggagtcaac atgcagaaga ttgtgatagt agccaacggt 120
 gcggcctacg gcagtgaatc cattagaaac agcttgccgc aggcaatcgc gcagcgagaa 180
 aaggagagag agcaggagca gcgccacaaa aagaagaccg acgccgtcac ggccgggggg 240
 tgcagaaggg gcaaaaaccc gcagagggca acaacaatca acaaaagcag gagatccaga 300
 ccgcgcaaaa cgaaccggac aaacagagca aaaccagaac cgacgggcga ggcaaaaccg 360
 ggacgcccga gaaagaagga gaggaaaaag gaacgcagga ggagcaggca gaaaggacgc 420
 aatccagccg gataa 435

<210> 107

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 107
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 tctcttgata tcgcccacaa ggtgagcgat cggaaggta tcgacctgat cctgctcggt 180
 ggaaagtggg atcagaaaca gcgcctggtt gccggaagcg ccaccctttc gctgctctct 240
 cgctaccggg cggatattgc cattcttggc gcatgcgcc a tccatgccga actcggattg 300
 agcgccagtc aggaggcgga tgccgaagtg aagcgtgcc a tgctggccgc aagccaggcg 360
 cactgggtag tcgccgacca tctaaaactc aatcagtgcg aaccgtatct ggtgtcaggg 420
 ttatccgaga ttcatcaact gtttttagat cgtccctggg cagagctcgg ggaccatagc 480
 gcggtgcagg ttaccgtttg cgcacattaa 510

<210> 108

<211> 1143

<212> DNA

<213> Enterobacter cloacae

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 aacgtggaga aggtcatgaa taaagtgaag acaatgaata ttgcgctgat cgggtatggg 120
 tttgtgggta agacgttcca tgccccgctg atccagtcgg ttgacggcct gaagctggcg 180

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gtgatctcat cccgggatga agagaaagtg aaacgcgacg tgccggacgt gctcgttgte 240
gccacgcgag aagaggccat tcagcaccgg gatatcgatc tgggtggttat cgcctcccct 300
aacgcgaccc atgcgccgct ggccaccctg gcgctcaatg ccggcaagca tgtggtagtg 360
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tcagaaacgg gtacaactca cgaactggac ttaacggcgc atgatcgcg cgaactgcaa 1140
taa 1143

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```

<210> 109
<211> 762
<212> DNA
<213> Enterobacter cloacae

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```

<400> 109
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gttattgacg taaacgatgc cgttatgctg cttatcgatc accagagcgg gctgttccag 180
accgttgagg acatgccaat gcttgagctg cgcgcccgct cagcagcgct ggcaaaaatc 240
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ccgcttatcc cggagatcca cgccaacgag ccgcacgcac agtatgtggc acgcaagggc 360
gagatcaaac cctgggataa cccggagctc gtggcgggcg tgaaagccac cgggcgcaaa 420
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gcgcaggaga tcaccctggc gcgcgtggtg caggcaggcg tgggtgccgag ggacacggca 600
gccgttgctt ccgaaattca gcgcacgtgg aaccgtgaag atgcggggtg atgggcagag 660
gtgtacacac acatcttccc tgtctaccag ctgctgatcg aaagctacag caaagcgcgag 720
gacgtggtga aaaatagcga agtgcctgat tcgcagcggt aa 762

```

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<210> 110
<211> 582
<212> DNA
<213> Enterobacter cloacae

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<400> 110
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tcgcagaaaag ccggtgaatt gaaaatgatg cagctgtggt tcaacctgcc cgccaaggac 120
aaatggggaa cgcctggata ccagagcatc actcaggcgg atatcccggt ggtaacctg 180
ccggataaca gcggaacatt gcgcgtgatt gctggccgct ttggagaggt aaccggcccg 240
gcgcatacct tctcaccgct gaacgtgtgg gatctcgcgc tgcatcaggg tagccacctg 300
acgtttaatc agcccgaagg ctggagcacg gcgctggttg tggttgaagg cagcgtgacg 360
gtgaacggca ccacgcctgc cggtaggcg caactggtcg tgctgagcca gagcgggtgac 420
aaactgcatc tcgaagccag cagcgatgcc aaagtgtgc tgatggccgg ggagccgctg 480
aatgaaccca tcgtgggcta tggcccgttt gtgatgaaca gtaaaaccga aatcgccgag 540
gctatttcgag atttcaactc cggccgcttt ggccaaatct aa 582

```

```

<210> 111
<211> 372
<212> DNA
<213> Enterobacter cloacae

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```

<400> 111

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ttccttgccg	acggcatgag	ctggaccccg	gctatcggcg	atgcggcgag	cgtaaatctg	180
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tgtttgetgg	cccaaccccg	cgtgaacatt	gccgggcgag	ttatgcagtt	aggtgatgcc	300
atcaaagtga	tgaacgacag	gctgaagcca	cagctgcgcg	ttgattcctt	cagcctcgaa	360
caggcggttt	aa					372

<210> 112

<211> 972

<212> DNA

<213> Enterobacter cloacae

<400> 112

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gatgcgccaa	cggaagtgtg	gggcaatcat	tttaccgcgc	gtatcgcgcc	ggataacatt	180
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gcgattggcg	gtgacggcac	gatcctgtgc	tgtagctgtg	tcccgaaaac	atccgtacag	960
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<210> 113

<211> 792

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (60)

<400> 113

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attctggttg	agaagtttgc	ctatggcatc	aaagatccga	tctaccagaa	aacgctgatc	180
gaaacgggtc	atccgaaaac	tggcgacatc	gtgggtgtta	aatatccgga	agatccacgg	240
ctggattata	ttaaaacgcg	ggtaggctcg	ccgggcgata	aagtgcacta	cgatccgggtg	300
gcgaaagagg	tgaccattca	gccaggctgt	agctctggaa	ctgcatgtga	aaatgcgctg	360
ccagtcaact	actccaacgt	tgagccaagt	gattttgtgc	agacctttgc	ccgccgtaac	420
ggcgggtgaag	cgaccagcgg	attcttccag	gtgccaaaag	gtgaaaccaa	agagaacggt	480
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tggattgtgc	caccggggaca	ctacttcatg	atgggtgaca	accgcgataa	ctctgcggac	660
agccgttact	ggggctttgt	gccggaagcg	aatctggtcg	gtaaaagcaac	cgctatctgg	720
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ggaattcatt	aa					792

<210> 114

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 114
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aatctgcttg ggcagaagat ttctatcacc tcgcgtaagg cgcagaccac gcgtcaccgc 180
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gacaatgtgc aggaaaaagc cgatctgctg ccgcacctgc aatggctggg cagccatctg 480
aacttctctg acatcgtctc gctgtctgcg gacacgggtc tgaacgttga t 531

<210> 115

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 115
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tggttttttc aggtcggttt cgtgtgctgc atttttgacg cattcattta ttggtatcgc 120
atgaaccccc tcgtaattaa tcggcttcaa ccgaagctgg gctacacttt tcatcatcag 180
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cagaccgcgc tggacgaaat cagcccgggc gataaacaaa aagatcctaa aacgcgtctg 600
caagaatatt tgcagggtcg tcattctgcc ctgccatcct atctggtggt gcagggtacgt 660
ggcgaagcgc acgatcagga atttaccatc cattgccagg tcagtggcct gagtgaaccg 720
gtggtcggca cgggttcaag ccgtcgtaag gctgaacagg ctgccgccga acaggcggtta 780
aaaatgctgg agctggaatg a 801

<210> 116

<211> 1307

<212> DNA

<213> Enterobacter cloacae

<400> 116
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gccatcgcca cagggtgtgt tatgggctcg ggcaaaacca tcagtcttgc cggcccgtcg 180
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<210> 117
 <211> 636
 <212> DNA
 <213> Enterobacter cloacae

<400> 117
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 gaagcgctgg tggcgggtat cgctgacgcg ctggaaggca agcagcccgc tgtgccggtt 180
 gacgttgtgc accgtgcgct gcgtgaaatc cacgaacgtg ctgacgccgt acgtcgcgcg 240
 cgtttcgaag agatggcggc agaaggcgtg aaatatctgg aagagaaccg tgagcgtgaa 300
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 ctggtgtttg aagtcgagct gctggaaatc ctgtaa 636

<210> 118
 <211> 1200
 <212> DNA
 <213> Enterobacter cloacae

<400> 118
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 ggaccagatg agaagttatt ttaccaaagc cgtcgactat atcgaaagtg ttgcaacatt 120
 tattacatcc aagtgagcat gatggtgaaa aaattcaaaa agttactttt agagttcatt 180
 gtagcagtta tgcctttcgt ttctataacc ggtatggcta tggcagcaga tgctggagtc 240
 cctgggggta tgtgtcagtc agctggagtg tggcagggtc tgattaagaa tatctgttgg 300
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 tcacgtccgg gttgctactg cacagatcag aacggcgtag cggaaatagg ttggcaattg 420
 agcttctttc agccggtgaa gattgtagaa gttgtaaaga gcccctggtg cagccccttt 480
 cttgaaggca cgatgcttca aaaatcgtag tttgatattg gtaaaagcaa cacaatcag 540
 ccaatgacag caactgaagc cggattttac gatgttcac tttgggagtt cccaatcatg 600
 acaatgctca aattactgat tattggcgag tgcactgctg aacctatat agatgccagc 660
 ctgacctata taagcggaagt ggacctatg tgggaaagtg atctgcttac actcgtcctg 720
 aatccagagg cagtagtttt tgcaaaccga attgctcaa tgggtgtgcgc tgctgactgt 780
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 aacctttatc cattaaccgg ccacatgtac gcaaatgatg acgctgtaag gacgagttca 900
 ctgataaccc atcgtcttct gactaaacta catcgccagg gaatgctgat gcgaacgatg 960
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 ctttcaatgc ttttccaac tcctgagggc aaaggggcgg attgctgtca tcgtcttggg 1080
 gattcggtag atgactggtc aaccttaaa ggtgggcgca aaaaaatagg caatgataat 1140
 tatgtctata tgttgtggcg ttacaatgac tgttgcgta gatataatcc aggcgcttga 1200

<210> 119
 <211> 879
 <212> DNA
 <213> Enterobacter cloacae

<400> 119
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 ccgtggggaa gcagcaataa tcaaggcggc aactctgggg gaaatggcaa caaagggtgg 120
 cgcgagcagg ggccgccgga tctggatgat atcttccgca aactgagcaa aaagcttggg 180
 ggccttggcg gaggaaaagg ttctggctcg gtgggcaatt ccactcagag tccgcgcccg 240
 ccaatgggtg gccgcgtggg gggcattgtc gccgctgcgg tagtaatcat ctgggcagcc 300
 agcgggttct acaccattaa agaagcagaa cgcggtgtgg tcaccggttt cggtaagtct 360
 agccatctgg ttgaaccggg cctgaactgg aagccgacct tcattgatga cgtgaccgcg 420
 gttaacgtgg agtccgttcg cgaactggcc gcctctggcg tgatgttgac ctctgacgag 480
 aacgtggtgc gcgttgagat gaacgtacag taccgcgtga ccgatccgga acgttatctg 540

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gatacccagc	gtgagctgga	agagaccatc	cgcccgtaga	acatgggtat	caccctgctg	720
gaagtcaact	tccaggtgc	acgtccgccc	gaagaggtga	aagccgcctt	tgacgatgcg	780
attgcgcgcg	gtgaaaacga	acagcagtac	atccgtgaag	cggaagcgta	caccaaggac	840
gttcgtcttc	acctcggaag	agcggatccg	cgtagagct			879

<210> 120

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 120

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cogattccgg	tctggctgta	tgctcaggcc	gggattgggt	tgccactgct	tttccaggct	120
ttgacagaac	gtctttccgg	tgaggtagct	cagcacacgc	tgcgactgcc	gccacaggaa	180
ggcaggctgc	gcagccggtt	ttatcagctt	caggcgatag	aaaaagagtg	gatggaggat	240
gacggcagcg	tggggatgca	ggtgcgtatg	ccgatcgttg	actggcgctc	cctctgtaaa	300
caagaacctg	cgctggcgga	ctatatcgtc	tga			333

<210> 121

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 121

ggacatcatc	accccgtttt	agggattgtg	ataaaatgcc	cgctctcttg	tgaaacccaa	60
caggaaagaa	tcatgatgag	cctggccggg	aaaaaaatcg	ttcttggcgt	cagcggcggt	120
attgctgcct	ataaaacgcc	agacctgggt	cgccgtttgc	gcgagcgcg	ggccgacgta	180
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tcgggatacc	cggtatccga	cagccttctc	gacccggcgg	ccgaagccgc	aatgggccac	300
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gcccgcctgg	caaccggtat	ggcgaacgat	ctggtaacga	ccatttgcct	cgccacgcct	420
gcgcccgtcg	cggttgtgcc	cgcaatgaac	cagcagatgt	accgcaacgc	cgctaccag	480
cacaatctgg	acacgctggc	ctcgcgcggc	ctgctgattt	ggggaacgga	cagcggcagc	540
caagcctgcg	gggaaattgg	gggcaggggt	tttctcctca	ccattaacga	ttgttga	597

<210> 122

<211> 204

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(153)

<220>

<221>unsure

<222>(155)

<400> 122

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aaccatttaa	cgattgttga	tatggccggc	gccattttct	cccctgtcaa	cgatctgcaa	120
catctcaaca	tcatgaatac	cgcgggcccc	ccnncnaaac	cgctgggatt	ccgtgcgtta	180
catcaacaac	caaagtttcg	ggaa				204

<210> 123

<211> 852

<212> DNA

<213> Enterobacter cloacae

<400> 123
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 gatgatgtcc ttaattcact ttgcgaggcg ttacgcaaga acgaaatgcc agcatcgaac 120
 cccgaatttg cctgtggcag cataatggca aacagaagga ggccaggcat ggaagagact 180
 gaactgctgc taccgctga aaaaatgctg cgtcatggcg tcacgttggt aaaggacgac 240
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 aaagaactga tagaccattt cggttcactg tatggattgc tgaccgctga gctggaggcg 360
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 agccatgttg aggtgcattc gcgtgaaatc gtgcgggaag cgataaaaagt gaatgcagcc 660
 ggcgtgatcc tcgcgcataa tcacccctct ggctgtgcag aaccaagcag agctgacaaa 720
 gcaattaccg aacgtattat caaatgctgt caattcatgg acattcgtgt gctggaccat 780
 ctgataattg gccgcggaga gtacatttgt cttaccaca gggggtcgaa ggagccgcgc 840
 tatgcgtgta ta 852

<210> 124
 <211> 336
 <212> DNA
 <213> Enterobacter cloacae

<400> 124
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 gagagcagcc agtggagcga agcgtctggcg gagaaaattg cggataacga aggaattacc 120
 ctctccccgg aacactggga agtgggtgcgc ttctgtgcgag aattttacct tgaattcaac 180
 acgtcgccag ctatccgcgt gctgggtcaaa gccatggcga ataaatttgg cgaagagaaa 240
 ggcaacagcc gttatctgta tcgctgttt ccgaaaggcc cggctaaaca ggcgacaaaa 300
 atcgccggcc tgccaaagcc ggtaaaatgc atttaa 336

<210> 125
 <211> 663
 <212> DNA
 <213> Enterobacter cloacae

<400> 125
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 gtgtgcgca atacctattt catgctcagc ctgacgctgg cgttttcggc gatcacgcga 120
 acggccagca ccgtactgat gctgccttct ccaggcctga tcctgacgct ggtgggtatg 180
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 accagcaaca tcattcacgg aggtgagacg aactatatcc gcgccaccgt gagcctgtat 600
 gtgtcgtgtg acaacatttt tgtcagcctg ctgagcatcc tgggcttcgg cagccgcgat 660
 taa 663

<210> 126
 <211> 282
 <212> DNA
 <213> Enterobacter cloacae

<400> 126
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 gatggcagcg tggaggttgt ggctgcggt gaggcgcat ggggtgagaa gctgggtggcg 180
 tggctgaaag cgggcgggcc gcgcagcgcg cgggttgata aggtgctaac ggaaccgcgt 240
 caaccggcc gggaatacgc tgacttcagt attcgtctatt aa 282

<210> 127
 <211> 1152
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(1)

<220>
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 <222>(16)

<220>
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 <222>(1109)

<220>
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 <222>(1113)

<220>
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 <222>(1151)

<400> 127
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 accgcaggga tctgtgctgc cagcacggca acctggcgcg ctaacgtgcc ggcaggaacc 180
 cagctggcag ataagcagga actggtcagg aacaacggca gtgaaccggc ctcgctcgac 240
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 gtcagcgtct ctccggcagg tgaaatccag ccgcgcctgg cggagaaatg ggaaaaataa 360
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 atcaccgcgg aagatattgt ctggagctgg cagcggctgg tcgaccggaa aaccgcctct 480
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 aacccccgat na 1152

<210> 128
 <211> 948
 <212> DNA
 <213> Enterobacter cloacae

<400> 128
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 gaccttaaca aggcctttcac cagctctgag aagggcttcg gacagttcaa tgcttctgta 180
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 gtggatagtg ctgaacaatt tgctatcggg gctgctgggtg tgttgggtgt gggttaagtct 420
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aatattagcg	ttaacatgga	ttctcaaaaag	attggaacat	tccagacaca	ggttcttact	900
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<210> 129

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 129

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cacgcctgct	gcatcatcaa	tttgtccggt	cttgcttgcc	cggatgagca	cggatgtcac	120
cgcatcggtg	cgcaggatcc	aggccagtgc	catttgcgac	agcttttgcc	tccgtttttc	180
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<210> 130

<211> 1047

<212> DNA

<213> Enterobacter cloacae

<400> 130

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gatgatgcag	caggcgtgct	tgaaaattgt	cggttcacgg	cagaagagct	caagacgata	1020
gatacgatcc	tgtccagttc	agattaa				1047

<210> 131

<211> 1392

<212> DNA

<213> Enterobacter cloacae

<400> 131

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aaagtacgta	ttgacggctt	ccgcaagggc	aaagtaccaa	tgaatgttgt	tgctcagcgt	180
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gcgatcatca	aagaaaaaat	caatccagcc	ggtgcgcga	actacgttcc	aggcgaatac	300
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gacggcatcg	tggataccct	gcgtaagcag	caggcgaact	ggaaagagaa	agaaggcgct	480
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gaaggcggta	aagcgtctga	tttcgtactg	gcgatgggcc	agggctcgat	gatcccaggc	600
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octgaagaat	accacgctga	aaacctgaaa	ggtaaagcag	cgaagttcgt	tatcaacctg	720
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gtggaagacg	gttctgttgc	gggcctgcgt	accgaagtgc	gtaaaaacat	ggagcgcgag	840
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gctgcacacg	gcttcgggtg	caaccagcag	caagcgatgg	aactgccacg	cgagctgttc	1020
gaagagcaag	cgaacgctcg	cgttgttgtt	ggcctgctgc	tgggcgaagt	gattcgtacc	1080
cacgagctga	aagctgacga	agagcgtgtg	aaaggcctga	tcgaagagat	ggcttctgca	1140
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atgcgcaacg	tcgcgttgga	agagcaggct	gtagaagcgg	tactggcgaa	agcgaaagtc	1260
accgaaaaag	agacctcttt	caccgaaactg	atgaaccacc	agggcgtaat	ttcgccccaa	1320
cgttttaaaag	ttttgaacaa	aaaacccggt	ggccctcccg	gcgacggggg	tttttttaat	1380
cacaagcttt	aa					1392

<210> 132

<211> 1092

<212> DNA

<213> Enterobacter cloacae

<400> 132

ggtctccacc	acgctgggga	tcccggttac	cgcctgcgt	attgtcttat	tgtgacctg	60
tgccattgtt	accgcaacgc	tggtagcgc	caccggcgca	gtgggggttg	tcgggctggt	120
cattcccat	gtgacgcgca	tgctatgcgg	gocgggcoat	cgctcgctcga	tcccgtgac	180
gtttcttatc	ggcgcccaact	ttatgatcct	cgcgatatac	gtctcacgca	cgctgattgt	240
gcaccaggtt	ctgcccatcg	gggtggtgac	tgcctggtg	ggcgcccccg	tctttgtggc	300
gttgctttat	caaaaccgaa	aggagcatcc	atgaatatta	ctgtggcccg	gttaaccgta	360
acccgacaag	cgcagacggt	gcttaagaat	atcgatctcg	acctgccatc	cgggcagatt	420
atcggcctgt	tagggccaaa	cggctcgggc	aagtcgacgc	tgtgcgctg	tctcgccggg	480
ctgtttccac	gactcagcga	acgcgtggcg	cttaatggca	caacgttcgg	catgatgccg	540
ctgaaaaaac	gcgcgcagca	catggcggtt	gtcccgcac	atgctgaggt	cgacggagaa	600
ctgaccgttg	aggacattgt	cagactgggg	cgtacgccct	accggaaaac	attccagaga	660
acctcgccg	acgatgaggc	tgcggttgag	caggcgattg	gcctgatgca	gttatgccgc	720
ttacgcgcag	ggcgatggca	ctctttgtct	ggcgagagac	gccagcgaag	ccagatagcc	780
cgcgcgctgg	cccagcagcc	gcaggtgctg	ttgctcgatg	aaccgacaaa	ccacctggac	840
attcagcacc	agctggagct	gatgcggctc	gtttcacagc	tgcgcgttac	ggtgggtggt	900
gcactgcacg	atctcaatct	tgcagccaat	tattgccagc	gtctgatcct	cctgaaggcc	960
gggcagatcg	ccgccacggg	cgcgccgcaa	gcggttctga	cgcgcgcaaa	cattgaggac	1020
acctggtgcg	taaaagctca	ggtctgcaaa	gccgacgccg	ggatcacgat	aagctacaac	1080
atggtggcat	ga					1092

<210> 133

<211> 558

<212> DNA

<213> Enterobacter cloacae

<400> 133

ctggetggca	ttgcggggcg	ccagctcttc	aacgccatga	ccgcgtacgt	cgctggcacg	60
tccgccaatg	ccgagcagtc	ccgtagcgtc	atgttctggc	tgtggaag	tctgagcggc	120
gtgcgtggcg	ctgacgcgct	gctggcgctg	gccgttacgc	tggcggtttt	actggtggta	180
ttgctctttt	cacgggcgct	ggacaccttc	accttcgggg	atgaggtctc	caccacgctg	240
gggatcccg	ttaccgcgct	gcgtattgtc	ttattgctga	cctgtgccat	tgttaccgca	300
acgctggtga	gcgccaccgg	cgcagtgggg	tttgtcgggc	tggtcattcc	ccatgtgacg	360
cgcattgctat	gcggggccgg	ccatcgctcg	tcgatcccg	tgacgtttct	tatcggcgc	420
cactttatga	tcctcgccga	tatcgtctca	cgcacgctga	ttgtgcacca	ggttctgccc	480

atcgggggtgg tgactgcgct ggtggggcgcc cccgtctttg tggcgttgct ttatcaaaac 540
cgaaaggagc atccatga 558

<210> 134
<211> 402
<212> DNA
<213> Enterobacter cloacae

<220>
<221> unsure
<222> (4)

<400> 134
aagnacctcg gcggtggaggc gaagctgcaa aatcaggagt ggaaaaccat gcttgatacc 60
atgcacaccc ataactttga cgcggtacgc tacgcctgga ttgccgatta cgacgatgcg 120
gcaaccttcc tgaacaactt ccgtaccggg gacagccaaa acaccactca gtacagcaat 180
cggactacg atcgggcact ggtgaacgcg gcgaaatcga aaacggcgga ggagcgcggt 240
aaattctacc agcaggcaga agatctgctg ggacgggatg taccggcgat ccctgtttat 300
cattacgtgc gcacgcacct ggtgaaacgc tgggtagggg gcttcacgcc agacaagctc 360
gggtactact acaccaaaga tatgtacatc aaaaagcact aa 402

<210> 135
<211> 576
<212> DNA
<213> Enterobacter cloacae

<220>
<221> unsure
<222> (123)

<220>
<221> unsure
<222> (201)

<220>
<221> unsure
<222> (212)

<220>
<221> unsure
<222> (215)

<400> 135
cttacttacg ataaaaataa tctaattgatt aaactttcca atatcaccaa agtgttccag 60
caggggaacc gaaccattca ggcgctgaac aacgtcagcc tgcattgttc tgcgtggtcag 120
atntatggcg tcattggcgc atcgggtgca ggtaaaagta cgctgatccg ttgtgttaac 180
ctgcttgagc gcccaaccca ngggcagcgt anaanttggc ggccaggagc tcaccgctct 240
ctcagaaaaa agaactcacc aaagcgcgct gccagattg gcatgatttt cctgcacttt 300
aacctgctgg cctcacgctc cgttttcggg aacgttgcgt tacccttgga gctggatttc 360
tcacctttag aagaaatttc gcgtcgcgct tcggaactgc tcgatctggg tggctctggg 420
gataaacatg acagctaccc ggctaatttg tccggcgggc tttatctgcg agtatctatc 480
gctcgcgcgc tggctaacaa cccaaaagtg ctgctgtgcg atgaatcctc cagcgcatta 540
tatccggcta ccacgcgctc tattctggaa ctgtaa 576

<210> 136
<211> 483
<212> DNA
<213> Enterobacter cloacae

<400> 136
aaagacatta accgtcgtct gggcctgact atctctctta ttacgcatga aatggatgta 60

gtgaaacgta	tctgcgactg	tgtagcagtc	atcagcaacg	gtgagctgat	tgagcaggac	120
acggtgagcg	aagtcttctc	gcaccgaaa	acgccgctgg	ctcagcagtt	cattcagtcc	180
acactgcatc	ttgatattcc	ggaagattat	ctggaacgac	tgaaaacaga	agccgttgca	240
gacagcgttc	caatgctgcg	catggagttt	acgggtcagt	ccgttgacgc	accgctgctg	300
tccgaaaccg	cgcgctcgct	taacgttaat	aacaacatta	ttagcgcgca	gatggattac	360
gccggtggcg	tgaagtccgg	cattatgctg	acggaaatgc	acggcacaca	ggaagaaacc	420
caggcggcaa	ttgcctggct	gcaagaacat	cacgtaaaag	tagagggtact	gggttatgtc	480
tga						483

<210> 137

<211> 614

<212> DNA

<213> Enterobacter cloacae

<400> 137

aggtagctggg	ttatgtctga	gccgatgatg	tggctactgg	ttcgcggcgt	ttgggaaacg	60
ctggcaatga	ccttcgtatc	gggcttcttt	ggttttgtga	ttgggctgcc	ggtcggcgctg	120
ttgctgtaog	tcacgcgccc	gggtcaaatt	attgaaaacg	cgaagctgta	tcgcacgctc	180
tctgcgctgg	tgaacatttt	cgggtctatt	ccgttcatta	ttctgctggg	gtggatgatt	240
ccgtttactc	gcgtgatcgt	cgggacgtcg	attggtttgc	aggcggcaat	tgtcccgcgtg	300
acagtagggc	cggcacccgtt	tatcgcccg	atgggtgaaa	acgccctgct	ggaaatccca	360
acaggcctga	ttgaagcttc	cgcgcgatg	ggtgcaacac	caatgcagat	cgttcgcaaa	420
gttctgctgc	cagaggcgct	gcctgggctg	gtgaacgcag	caaccatcac	gcttatcacg	480
ctggtcgggt	attccgcaat	gggcggcgcc	gtagggtgctg	gcggtttagg	ccaaattgga	540
tatcagtagc	gctatatattg	ctataacgct	accgtaatga	ataccgttct	ggtattgctg	600
gttgtgctgg	ttta					614

<210> 138

<211> 630

<212> DNA

<213> Enterobacter cloacae

<400> 138

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ccggtggcaa	aatctgtacc	cgcaattttt	ctcgatcgctg	acggcactat	taatgtggat	120
cacggttacg	tccatgagat	tgatgagctc	gaattttatcg	agggcgtaat	agatgccatg	180
cgccagttga	aagagatggg	ctatgcgctg	gtgggtggtaa	ctaaccagtc	cggtatcgcc	240
cggggtaaat	ttaccgaagc	gcagttcgag	acgctgacgg	aatggatgga	ctgggtctctg	300
gccgatcgcg	gcgtcgatct	tgatggcact	tattattgtc	cgcatacccc	gcagggaagt	360
gtagaggcgt	atcgtcagac	ctgcgattgc	cgtaagccac	acccgggcat	gtttatctct	420
gcacaggaat	tctgcacat	tgatatggcc	gcattcttata	tggtgggcga	taaactggaa	480
gatatgcagg	cagcaacggc	ggcaggtgta	ggtaccaaag	tattagtgcg	taccggtaaa	540
ccggtcacc	cagaagcaga	aaatgcagcc	gactgggtga	taactagtct	ggcagaactg	600
ccaaaagaga	ttaaaaagca	ccaaaaatag				630

<210> 139

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 139

cgacgctgga	aattcagtta	ttacccttta	tactgcccta	tcccattacc	gcgcgggcat	60
tacgggttaa	acacatcgat	gagtcagact	gaaactaccg	ccccaaagca	attctccctt	120
ctaccgggca	gcataccccc	tttctttctt	ctgttgatcg	ttgtgctggt	agtcacaatg	180
ggagtgatga	tccagagcgc	cgtaaaccac	tggcttaaag	ataaaaagcta	tcaaatcgct	240
gatatcacc	atgcggtgca	taagcgcat	gatacgtggc	gctatgcgac	ctggcaaatc	300
tacgacaata	tcgctgccgc	gcccggccac	tcatacggcg	aagggttgca	ggaaacgcgc	360
cttaagcagg	atgtgtatta	ccttgaaaaa	ccgcagcgta	agacggaagc	cctgattttc	420
ggctcgcacg	acagcgccac	gcttgagatt	taccaacgga	tctcctccta	tctggacacc	480
ctgtggggcc	ccgaaaacgt	aaccgtgggt	ccatgtatta	cctga		525

<210> 140
 <211> 429
 <212> DNA
 <213> Enterobacter cloacae

<400> 140
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 ctggctggta tactgggtatt agccccggtg ttttccgcaa tggcggtccc tcaggctgca 120
 accggttgcg aagccaaacg ccagaatatt gaacaacaga tagaacacgc cagaacccat 180
 aataacgata atcgtgtagc gggcctgcaa aaagcgcttt ctgaacttaa cgctaactgc 240
 acggaggaag gattacgtgc tgaacgtcaa gctgatgttc gcgaaaaaga gcgtaagggtt 300
 gaagagcgac gccaggagtt ggctgaggca caggctgacg gccgtactga taaaataagt 360
 aaaaaggaaa gaaaactgaa agacgctcag gctgagcttg atgaagccag aagtgtgttg 420
 aataaataa 429

<210> 141
 <211> 654
 <212> DNA
 <213> Enterobacter cloacae

<400> 141
 agaaccacgc ctatggctgg gtttttgctt ttctgtcccc gctacgcatt gaattttccc 60
 ttctgtcagg taatagtgat tttttttcct gacaatgaaa atgatatgac cttatctgct 120
 ttaaaagccg ggtcactgct cctgctgatg atcctgtttt ataccggcct gttcacgagc 180
 gatcgcgta cctgggttgat ggaggtgacg cccgtcatta tcatcatccc acttctgctt 240
 gccacacacc ggcgataccc tttgactccc cttctctata ctctggtttt cttccacgcc 300
 atcattctga tggttggtgg aatgtacacc tacgcaaagg ttccggttgg ttttgaggtt 360
 caggagatgc tcgggcttag ccgaaatccg tatgacaagg tcggtcactt cttccagggg 420
 ctggttcccg cactggcagc gcgagaaatt ctgctgcgcg gtgggtatgt tcgtggacat 480
 aagatgacgg ggtttctggt gtgctgtgtt gctctggcca ttagcgccac ctttaactca 540
 ttgagtgggt ggctgctttg gcgatgggac aggggtgcga tgattttctg gggacgcagg 600
 gcgatccatg ggataccag tctgatatgt tttgcgcgct gcttgggtgcg ttaa 654

<210> 142
 <211> 189
 <212> DNA
 <213> Enterobacter cloacae

<400> 142
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 cagggcgatc catgggatac ccagtctgat atgttttgcg cgctgcttgg tgcgttaacg 120
 acggtgctga tccttgggcg tttccatcag cggcaattgc gtcgtttgaa tgtggatagt 180
 gcgctctga 189

<210> 143
 <211> 369
 <212> DNA
 <213> Enterobacter cloacae

<400> 143
 atgtgtcctc cgcggctgtt gaaaacttgc ggggccgaaa tagccatctc catccctgcg 60
 catgtccgcc tgggtgatgg ggcagaagcg ccgcctgccc tgaacgagcc cctgattgag 120
 gatgtccttc gcagcctgaa ggtgacccac gatcaggatg tacagctggc gcccgaaagc 180
 gtgcgcatgc ttccctctga cagccgctgt aacagctggc gaatcggggc ggtggatgag 240
 ctacccttgc aaggaagcca gatcagttct ccagcgctgg acgaactgaa agccaacca 300
 aaagcgcgta gcgcgctatg gcaacaaatt tgcgaatatg aacacgattt cttccctcac 360
 gacggctga 369

<210> 144
 <211> 492
 <212> DNA

<213> Enterobacter cloacae

<400> 144

aagccaaccc	aaaagcgctg	agcgcgctat	ggcaacaaat	ttgcgaatat	gaacacgatt	60
tcttccctca	cgacggctga	cctgaccacc	gcgttcgcga	ttgaaacccg	cgcccatgcc	120
tttccgtgga	gcgaaaagac	gtttgccagc	aatcagggcg	aacgctattt	aaatctccgc	180
ctggacgttg	acgggtgcgat	ggctgcgttc	gccatcacgc	aggctgttct	ggacgaggcg	240
acactgttta	atatcgcggt	cgatcccgca	taccagcgcc	gcgggctggg	cagggaactg	300
cttgagcacc	tcattcatga	gctggaaacc	cgtgacgttt	tcacctgtg	gctggagggtg	360
cgcgcgccca	atgtcgccgc	catcgcgctc	tatgaaagct	taggcttcaa	cgaggcgact	420
atccgccgta	actactaccc	caccgcagag	ggacgtgaag	acgccattat	catggctctg	480
ccgattggat	aa					492

<210> 145

<211> 351

<212> DNA

<213> Enterobacter cloacae

<400> 145

gaagaattga	ttatgacgtt	gtctccttat	ctgcaagag	tggccaaaacg	ccgcactttt	60
gccattatct	cgcacccgga	tgccggtaaa	acgaccatca	ccgagaaggt	gttgctgttc	120
ggacaggcga	tccagaccgc	gggtaccgtt	aaaggccgtg	gctccagcca	gcatgctaaa	180
tccgactgga	tggagatgga	aaagcagcgt	ggtatttcga	ttaccacctc	cgtgatgcag	240
ttcccgatc	acgactgtct	ggtgaacctg	ctggacaccc	cggggcacga	agactttctc	300
gaagatacct	accgtaccct	gacggggccg	gaggtcttca	cttcggattg	a	351

<210> 146

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 146

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ccattatcat	ggctctgcgc	attggataac	gaaaataagg	ttgtaacgat	gaaatgggac	120
tggattttct	ttgatgcgga	cgaaacgctg	tttacgtttg	actcgttcgg	cggcctacag	180
cggatgtttc	tcgactatag	cgtgacgttc	accgcggaag	attttcagga	ctatcaggcg	240
gtgaacaaac	cgtctgtgggt	ggattaccag	aacggagcca	tcaccgcgtt	acagcttcag	300
catcagcgtt	ttgacgtgtg	ggctgaacgg	ttaaactgga	gtcctggggg	gctgaacgag	360
gccttcctga	atgcgatggc	ggatatctgc	gcgcgcgtgc	ccggcgccgt	ttctttgctg	420
gattcgctga	aagggaaggt	gaagcttggg	atcattacca	acggctttac	cgcgcttcag	480
cagattcgcc	ttgaacgcac	cggcctgcgc	gatcatttcg	acgcgctggg	gatctccgaa	540
gagggtggcg	taccgaagcc	ggatccgcgt	attttcgatt	atgcgttggc	gcaagcgggc	600
aatcctgacc	gcgatcgcg	gctgatgggt	ggggatacgg	cagaatctga	tattctggga	660
ggtatgagat	cgggcctgtc	gaccgtctgg	ctgaatgcgc	atggccgcat	gctgccggaa	720
ggcatcgagc	cgacctggac	cgttacgtca	ttgaacgaac	tggagcagct	cctgtgtaaa	780
caatga						786

<210> 147

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 147

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aacgaaacca	gtgaacttga	tttgctggat	caacgtccat	ttgatcagac	cgacttcgat	120
attctgaaat	cctacgaagc	ggtagtggac	gggttagcga	tgctcattgg	ttcccactgc	180
gaaatcgtat	tgcatccct	gcaagatctt	aagtgttcgc	ctatccgcat	tgcgaatggg	240
gagcacactg	gccgtaaaat	tggttcgcca	atcaccgacc	ttgcattggc	tatgttgcac	300
gacatgaccg	gcgcggacag	cagcgtctca	aaatgctatt	tcaccgcgc	caaaagcggc	360
gtgctgatga	aatcagaaac	gatcgcgatt	cgaaaaccgc	aacaccgggt	aatcggtttg	420
ctgtgcatca	acatgaacct	tgatgtgcc	ttctcgcaaa	tcatgagcac	cttcatcccg	480

ccagaaacgc	cggaactggg	ctcatcgggt	aactttgctt	cttcggttga	ggatctcgtg	540
acccagacgc	tggaattcac	cattgaagaa	gtgaatgccg	atcgcaacgt	atccaacaac	600
gccaagaatc	gtcagatcgt	cctgaacctc	tatgagaaag	ggattttgat	atccaagatg	660
ccatcaaccc	agtggcccg	tcgctgaat	atctcc			696

<210> 148
 <211> 684
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(28)

<400> 148						
cgaccagaaa	tcgctacgc	actggggngt	tttctgggtc	gttacatgga	aaactctctg	60
aaagaacaag	agaaactggg	catcaaactg	gacaaaaacc	agctgatcgc	aggggtccag	120
gatgcgttcg	cagacaagag	caaactgtct	gaccaggaaa	tcgagcagac	tctgcaagcg	180
tttgaagcgc	gcgtgaaagg	cgccgctcag	accaagatgg	aagcagatgc	taaagataac	240
gaagcgaaa	gcaaagccta	ccgcgacaag	ttcgctaaa	agaaaggcgt	taaaacgtct	300
tctactggcc	tgatctataa	ggttgagaaa	gaaggtaactg	gcgacgcgcc	taaagacagc	360
gacaccgttg	tggtgaacta	caaaggtagc	ctgatcgacg	gtaaagagtt	cgataactct	420
tatacccggtg	gtgagcctct	ctccttccgt	ctggatgggtg	tgatcccggg	ctggaccgaa	480
ggcctgaaga	acatcaagaa	aggcggtaaa	atcaagctgg	tcatcccacc	ggatctggct	540
tacggcaaaa	ccggcggttc	gggtatcccg	gctaactcca	cgctggtatt	tgatgtagaa	600
ctgctggaca	tcaaacgggc	gccgaaagcg	gatgcgaaaa	cagacgcacc	ggctgacgac	660
aaagccgcag	cagctaagaa	gtaa				684

<210> 149
 <211> 1331
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(12)

<400> 149						
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accgtttgaa	agctattctg	attcatggcg	tgaacgtgg	tacattgact	gaccagaagc	120
aatacacctc	cgaatcactg	aacagtccaa	tggaacttgat	aatgtctatc	ctgaccgctc	180
aaagagcgca	tgaagaaagt	cagtcaaaagt	ctaagaggat	gcgtgaagta	tgggctaaaa	240
aacgaacaga	ggcagaggaa	agcggaaaaga	ttatcactaa	gtcgtgtcct	cgtttggttaa	300
ccgtgaacag	tgaccgtaca	ggctttgaac	ctatacctga	acacgttgaa	tcaatccggc	360
ttatgttcga	aatgaggcta	tcagggaag	gctttgcagg	tatcgcacag	gctctaaacg	420
agtctggaag	attgaccctt	acaggacgct	ctaaagggtg	gaatcagtea	tctgtacagc	480
agcttttaag	taacaaggct	ctgatagggt	acaagatacc	atcccgtaaa	gctgtggtga	540
attacattga	gatacccgac	tatttccct	ctgtgattcc	tcttgaacag	tttcaacagg	600
ttcagttaat	cggtgcagat	aagcagggac	aaagggcagc	taatgaccgc	cctatgaatg	660
ttaacctgtt	caggggtgta	atgaagtgcg	ctgaatgtgg	tgcaactgtg	attgttagcg	720
gggtggatga	taaaagggtc	ggttattatt	cttgctcatt	cagacgggta	ggacgctgta	780
acacctctaa	accaatgaac	aggggaatgg	ttgacgaagc	actgataaag	gggcttctct	840
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caaagagggc	agacttaaca	gaacgctctc	agaagctgtt	agcagccctt	gaaatagctg	960
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agacacagat	taagacctgt	aaagaccttg	aacaggttca	cactgttcag	agtgttcagg	1080
gtatggattt	aaccgtcaaa	tctcaaagg	aagaggttca	gttactgggt	aagaaaacct	1140
tcagagaaat	caacttagac	ggcatcagaa	agacggttaa	cgtttatctt	cacaatgggc	1200
ttacattgct	taatgttccg	gtaaatcaga	ttgtggatgc	tggagagtgg	atagaactgt	1260
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accttgatta	a					1331

<210> 150
 <211> 669
 <212> DNA
 <213> Enterobacter cloacae

<400> 150
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 aaagtgggtct gcgtgggcag caactatgca aaacatattc aggagatggg cagcgccgtg 120
 ccggaagagc cggttctgtt tattaagcca gaaaccgcac tgtgcgatat tcgccagccg 180
 ctggttctgc cgcagggact gggctcgggt catcatgaag tggagctggc ggtgctgac 240
 ggcgcgacgc tgcgccaggc gaccgaagag catgtagaga aagcgattgc gggttacggt 300
 gtcgcgcttg acctgacgct gcgtgatgtt cagggcaaaa tgaagaaagc ggggcagccg 360
 tgggaaaaag cgaagggttt tgataattca tgcccgattt ccggtttcat tccggtgagt 420
 gaattttaccg acgatccgca gaacacgccg ctacgcctga aggtcaacgg cgagatccgc 480
 cagcagggaa cgaccgctga catgatccat aagatcgctt cgctgattgc ctacatgagc 540
 cgcttcttca ccctgaaacc tggcgacgtg atcctcaccg gcactccgga aggtgtgggg 600
 ccgctgctta gcggcgacga actggatgtc agttttaacg gcctgtcgct gaaaacccgc 660
 gtgctgtaa 669

<210> 151
 <211> 402
 <212> DNA
 <213> Enterobacter cloacae

<400> 151
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 tatcaggcat gttatagtca ggagtatatt gaggcaagca accaccggtt aattcagagt 120
 aaaaacatgt tttgtgtgat ctacagaagt accagccgag accagaccta ctttatgtc 180
 gaaaagaaag acgatTTTTT cgcgtgctt gaagaattaa tgaaaagctt tggccgaccg 240
 cagctggcga tgctgctgcc gctggacggc cgtaagaagc tgggtgaacgc cgatctggag 300
 aaagtcaaaa aggcgttaac cgagcagggc tattattttac agcttccgcc gccaccggag 360
 aattttattaa aacagcatct tgagggtgagc ggaaagaaat aa 402

<210> 152
 <211> 726
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (681)

<220>
 <221> unsure
 <222> (717)

<400> 152
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 atcgacttcg atatcggtct gcgtaacctg gacctgatca tgggttgcca gcgtcgcggtg 180
 gtgtatgact tcgtgaacgt cattcagggc gatgccaccc ttaaccaggc gctgattaaa 240
 gataagcgta ccgagaacct ctacattctt ccggcgctccc agacccgtga taaagacgcc 300
 ctgacccgcg aaggcgtgga aaagggtgct gacgatctga aaaagatgga gttcgacttt 360
 gtgggtctgcg actccccggc cggatcgaa accggcgcgc tgatggcgct ctacttcgag 420
 gatgaagcca tcatcaccac caaccggag gtctcgtcag tacgtgattc cgaccgtatt 480
 ctccgcatte tgacctcgaa atcccgctgc gcggaaaatg gccaggagcc aatcaaagag 540
 cacctgctgc tggacccgta caaccgggc cgggtgaaca aaggtgacat gctgagcatg 600
 gaagacgtgc tggagatcct gcgcatcaaa ctgggtggcg tgatcccgga agatcagtc 660
 gtgttgcgcg cctctaacca nggcgagccc ctgatcctgg atacacaggc agaagcnggt 720
 aaagcg 726

<210> 153
 <211> 807
 <212> DNA
 <213> Enterobacter cloacae

<400> 153
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 tcgcgcgcat gtgttgcggt taatagcaaa ttgagtaagg ccaggatgtc aaatacgccc 120
 atcgagctta aaggcagtag cttcacctta tcagtggttc atttgcataa tgcaaaaccc 180
 gaggttattc gtcaggcggt agaagacaaa atcgcgaggg ctcgccgttt tcttaagcat 240
 gctcctgtcg tcgtcaatgt aagcgacatt gaggggcccg ttaactggaa gcggtccag 300
 caggccgtca cctccacggg gttgcgcata gtgggcatta gcggtgcaa agacgcagag 360
 ttaaaagccg aaattgaacg cgcggggttg cccttggtta acgagggcaa agaaaaagcc 420
 ccacgtgcaa cgcctgcaac cgttcccgtc ccccgccctc cggcgcaaaa tgtagcccca 480
 gtcacaaaaa cgcgattgat tgatctgccc gttcgttccc gtcagcgcat ttatgcgcca 540
 aactgtgatc tgattgttac aagccacgtc agtgccggcg ctgaactgat tgcagatggc 600
 aatattcacg tttacggtat gatgcgtgga cgtgcgcttg cgggcgccag cggcgatcga 660
 gaagcacaaa tttttgtac tcacctgacg gcagaactgg tgtctatcgc aggtgaatat 720
 tggctgagcg ataaaaatcc agccgaattt tatggcaaa gggcccgctc gcaactggca 780
 gataacgctt tgaccgttca accgtga 807

<210> 154
 <211> 1848
 <212> DNA
 <213> Enterobacter cloacae

<400> 154
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 cagcgattaa tgaatagaaa aattttacaat aatgtaaaaa tttttatgat tgtcctggcg 120
 ttaagcctga ttacgatccc cttttcccggt tatactctccc cgcgcgctat cgtcaacgaa 180
 aatgatgttt atttagcggt gttgccttta agcgccatgc tcgccatcgt attgttattt 240
 ggacgtcggg caatcattcc tttactgatt ggatttagtg ttactaacat ttattacttt 300
 gatttagcat tactacaatc ttccgtgtta ttaatttgtc agacgtttgc cgtcttcgct 360
 gctgtggtcg tcatccgtct gatgctgggc aaacgctggc gacacagcat cccgaataag 420
 tacatcggga tacgtatttt ctggctcgga tttgtggttc ctgtaggcat caaattatcg 480
 atgtatctgg cgggatattt atttgatttt ccggtgacaa tctcctccta tttcggcgaa 540
 ggctctgcaa tttataacgt tatcgatatt caaagcctga tttgtgcgcg cctgattttc 600
 accatgatgt tctactaccc gtttaagaatg ataattaatc cccgggtatgc ccgaacattc 660
 tggcggcgaa gcgtgaagcc cctcttttgt cacaaaaaag tgttatttat cgttgtgtgg 720
 ctgatgctgt tggctctgat gatcgctatt ttgtgcgcgc ctttcgagtc acagtttatt 780
 gctggttatt tgatgccaat cgttttttatt ctttttacc cggggatttg tctctgagc 840
 tatgcgctca tctctttact ctgggcgggc tcggcgctca tgcgtttgac ctacaattat 900
 aattttctta atggcggtga atcgggccac tcgctctcct ttatcttgtc ggtactgatc 960
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 caggggtggc aggagagggc gcttaccgat ccgctcaccg gtctgcttaa cattcgtgcg 1080
 ctggaagtgt ttttacagca ccaccccgaa gccaaaatct gctgctgcg cctggataat 1140
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 accgctgcgc tgcaaccgtt attgcaaaaa gacgagaagc tctttcagtt gccaggcagt 1260
 gagctggttg tggctctgtt ggggcccggc acggtgaac gtctgcaata tatggttgat 1320
 catctgaaca gccgtaagat tgcctggaac aagactgagc tcgacattga gtttggegc 1380
 tcttggggcg aagtaccgga tggggaaaag ctgcaccaca cgttgggtca gctgagctgg 1440
 ctgtccgagc aatcctgttg cgggcataac gttctggcgt taaccaacag tctggatgat 1500
 gtctctggtc agacgacgga cagggtgcta atgctggccc gcataaaacg cgccttgat 1560
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 ccgatggctc aattcaacct gaacccccgg tttgactcga acttttggaa caaatgtgga 1740
 tgtcgattcg ccaccacccc tctcgaactg atcgaaagcc ctccccgtca aactgatgac 1800
 ctgaacctca agcaacataa aatgggggag aaattcttcg ccttttga 1848

<210> 155

<211> 1506
 <212> DNA
 <213> Enterobacter cloacae

<400> 155
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 ctgggtttta ccgtcgcgat tgaaagcggc gcgggcacac tggcgagttt cgatgacgag 120
 gcctttactc aggctggcgc ggacgtcgtg gacgggtgtg aggtctggca atcaccatc 180
 attctgaagg taaacgcacc ggaagagggg gaaattgaac tgctgaacgc gggcactacg 240
 ctggtgagct ttgtctggcc agcccaaaac ccggagttga tggagaagct ggcggcacgc 300
 ggtgtcaccg tgatggcgat ggactccgtg ccgcgtatct cgcgcgcgca gtctctggat 360
 gcgctgagct ccatggcgaa cattgccggc tatcgcgcca ttgtcgaagc tgcgcatgag 420
 tttggtcgct tctttaccgg tcagattacg gcggcaggta aagttccacc cgcgaagggtg 480
 atggtgattg gtgccgggtg ggcaggctct gctgctatcg gggccgcaaa cagcctgggc 540
 gctattgttc gcgcgtttga taccgggccc gaagtgaagg agcagggtgca gagtatgggc 600
 gccgaattcc ttgagctgga cttcaaggaa gaagcgggca gcggtgatgg ttacgcgaag 660
 gtcattgtct aagcctttat caaggcggaa atggcgctct ttgcggcgca ggcaaaagag 720
 gtagacatca ttgtcaccac cgcgcttatt ccgggtaaac cgcgcgcgaa gctgatcacc 780
 cgtgagatgg tggattccat gcagccgggc agcgttatag tcgatctggc ggcgcaaaac 840
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 cctgcaccgc cgattcaggt ttccgctcaa cctcaggctg cgcgaaaagc ggcaccagag 1140
 cccgcggagc cagcaaaaac tcgctcgccg tggcgcaaat acgccatcat ggcgctggtc 1200
 ataactctgt ttggctggct ggcggacgtc gcgcctaaag agttccttgg ccacttcacc 1260
 gtcttcgcgc tctcctgctt ggtgggttac tacgtcgtgt ggaacgtttc ccatgcgctg 1320
 cataccccgc tgatgtcggt caccaatgcc atctccggga ttatcgtggt cggggcattg 1380
 ctgcaaattg gtcattggcg ctggatcagc ttcttgagct tcattgcggt gctgatcgcc 1440
 agtatcaata ttttcgggtg tttcaccgtg actcagcgca tgctgaaaat gtttcgtaaa 1500
 ggctaa 1506

<210> 156
 <211> 579
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(39)

<220>
 <221>unsure
 <222>(172)

<220>
 <221>unsure
 <222>(195)

<220>
 <221>unsure
 <222>(247)

<400> 156
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 gaggttgccg acggtaaatg ggcgctgctg acttcgggtt ccaaaaagctt tcacattccg 120
 gcgctgacgg gcgcctgggg gcttttcgcc gatgacgcca gccgtaacgc cnatctgaat 180
 gcattaaaag gtcgngacgg actctcttcc ctttccgtgc tggcgctgac cgcgcatatt 240
 gctgctnacc gacagggcga accctggctg gacgcgctgc ggacctatct cgaagagaat 300
 ctgcgggtat ttgctcgcgga attaaacagt gcttttccgg cactcagctg gcaaccacct 360
 gaggtacact atcttgctg gatcgacctc agcccgctcg gtattgacga caatacgctg 420

caaaaggtgc	ttattgagca	gcaaaaagtg	gccatcatgc	cgggatatac	ctatggagcc	480
gaagggaaa	gctacgttcg	tctgaacgcg	ggttgcccc	gtagtaagct	tgaacagggc	540
gttcagcgcc	tcatcgcggg	catcaaacag	ctgctgtaa			579

<210> 157
 <211> 1011
 <212> DNA
 <213> Enterobacter cloacae

<400> 157						
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ctccctgccg	aaacgcttga	aaccctgata	cctcatgttc	aggtcacgtc	gaacgaaccg	180
gatctggtga	gctttctgag	caagctcgac	tggggcgtga	agatgctggc	ctcggtcgat	240
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gtcgaactgc	gtttctcccc	gggctatatg	gcgatgaccc	acaatctccc	cgtagcgggc	360
gtgggtgaag	cggtcattga	aggcgtgcgt	gaaggctgca	aaacctttga	cgttcaggcg	420
cgtttgatcg	gcattatgag	ccgtaccttc	ggtgaagcgg	cctgtcttca	ggagctggaa	480
gcattactgg	cgcatcgcca	ccagatcacc	gccatcgacc	tggccggtga	cgagctgggc	540
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ggtgcggaac	gtattggtca	cggcgtgaaa	gccattgaag	atcgcgcgct	gatggatttc	720
ctcgccgaac	aacgtattgg	aatcgaaatc	tgcctgacct	ccaatattca	gaccagtaca	780
gtggcatcgc	tggcgcaaca	cccgtgaaa	accttccttg	aacacggggg	gctggcttca	840
ctgaacaagg	acgatccggc	gggttcagggc	gtggatatta	ttcacgaata	caacatcgcc	900
gcgcgcgagg	ccgggctgag	ccgcgagcag	atccgtcagg	cgcaaataca	cgggctggag	960
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<210> 158
 <211> 399
 <212> DNA
 <213> Enterobacter cloacae

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<400> 158						
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ttcggccagg	ctgctggcct	cctcgcagtg	ggtgccatcg	tcgagccgca	acagctcggc	180
aatctcgtcc	agactgaacc	ccagccgctg	tgcgatttcc	acgaatttca	cccgaaccac	240
gtccgcctcc	ccatagcggc	ggatgctgcc	gtaaggettg	tcgggttccc	gcaacaggcc	300
cttgcgctga	tagaagcgga	ttgtctccac	gttgaccccg	gccgccttgg	caaaaacggc	360
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<210> 159
 <211> 297
 <212> DNA
 <213> Enterobacter cloacae

<400> 159						
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acattcccc	ttcgtgcatg	gcaggcgcac	acgagttcag	acagcacggg	ttccatgcgc	120
gccaaagtcg	ccatcttctc	gcgcagctcc	ttgagcttgg	gttcggccag	gctgctggcc	180
tcctcgcagt	gggtgccatc	gtcgagccgc	aacagctcgg	caatctcgtc	cagactgaac	240
cccagccgct	gtgccgattt	cacgaatttc	accogaacca	cgcccgcttc	cccatag	297

<210> 160
 <211> 339
 <212> DNA

<213> Enterobacter cloacae

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<400> 160							
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attcttgcat	cgacctgctg	cctggggggc	ctantannnn	nnnnnnnnnn	nnnnnnnnnn		240
nnnnnnnnnn	nnnnacaacg	ttttctgcct	ctgaagcctc	cttttattgg	tctcaaaatg		300
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<210> 161
 <211> 663
 <212> DNA
 <213> Enterobacter cloacae

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<222> (243)

<400> 161

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cgaagagcgc	accgcgcgct	tttggttggt	cagacatacg	ttggcccttt	tgaatttgga	180
ttggatagcg	taaccttact	tccgtactca	tgtacggagt	caagcgatat	ggaaaataat	240
ttngaaaacc	tgaccattgg	cgtttttgcc	aaggcgggcg	gggtcaacgt	ggagacaatc	300
cgtttctatc	agcgcaagg	cctgttgccg	gaaccggaca	agccttacgg	cagcatccgc	360
cgtatgggg	aggcgagct	ggttcgggtg	aaattcgtga	aatcggcaca	gcggctgggg	420
ttcagtcctg	acgagattgc	cgagctgttg	cggtcgcacg	atggcaccca	ctgcgaggag	480
gccagcagcc	tggccgaaca	caagctcaag	gacgtgcgcg	agaagatggc	cgacttggcg	540
cgcattgaaa	ccgtgctgtc	tgaactcgtg	tgcgcctgcc	atgcacgaaa	ggggaatgtt	600
tcctgcccg	tgatcgcgtc	actacagggc	gaagcaggcc	tggcaaggtc	agctatgcct	660
tag						663

<210> 162

<211> 960

<212> DNA

<213> Enterobacter cloacae

<400> 162

cgtaagcttg	ctcccgcgct	gatcacccggc	aacaccatcg	ttatcaaacc	gagcgaattt	60
accccaaaca	acgccattgc	gtttgccaaa	atcgctcgatg	agattggcct	gccgaaaggc	120
gtctttaacc	tggtgctggg	ccggggtgaa	accgtcggac	aggagctggc	cgggaatccg	180
aaagtggcga	tggtcagcat	gaccggcagc	gtcggggcag	gtgaaaagat	catggctgcg	240
gctgcgaaaa	acatcaccaa	agtggggctg	gagctgggcg	gtaaaagccc	ggccatcgtg	300
atgggcgatg	ccgatcttga	gctggccgtg	aaggccattg	tggattcacg	cgtcatcaat	360
accgggcagg	tgtgtaactg	cgcggaacgt	gtctatgtcc	agaaggggat	ctacgaccgc	420
tttgtgaatc	gtctgggcga	ggcaatgaaa	gccgtccagt	ttggcaatcc	ggctgagcga	480
acggatattg	ccatggggcc	gctgatcaac	gccgccgcgc	tggagcgcg	ggagcagaag	540
gtggcgcgcg	cgggtgcagga	gggggccaaa	gtggtccttg	gcggtaaagc	ggcagaaggt	600
aaaggggtatt	tttatcccc	aacgctgctg	ttggacgtgc	gtcaggatat	ggccatcatg	660

cacgaagaga	cctttggccc	ggtgctgccg	gtggtggcct	tcgacaccct	ggaagaggcc	720
ctgaacatgg	ccaacgacag	cgactacggt	ttaacctcgt	ctgtttatac	gcaggacctg	780
aacgtcgcca	tgaaagccat	taaggggctt	aagttcggcg	agacctacat	taaccgtgaa	840
aactttgaag	cgatgcaggg	cttccatgcg	ggctggcgga	aatccggaat	cggcggggca	900
gatggtaaac	acggtctgaa	tgagtatttg	cagacgcagg	tggtctattt	acagtcgtaa	960

<210> 163

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 163

tcaggagccc	cctccatgcg	aggggggttca	cattttcagg	aaagggtggt	atgttggcgc	60
gataatgggt	atztatcggg	aaacaacatg	cgcacaaaat	atacgggtct	gcaaatcagc	120
attcaactggc	tggtttttct	gttagttatt	atggcctatt	gcgccatgga	gttcatggga	180
tggttcccg	gaagcgatcg	tccgctcatt	aatatgatcc	acgtttcctg	cgggatcagc	240
atcctggtgc	tgatggtggc	gcgcctgctt	atccgcctca	aattcccggc	tccgcctatt	300
caaccgaaac	caaaagcgat	gatcaccggg	ctgtcccato	tggggcatct	ggttatctac	360
ctgctgttca	ttgccttgcc	gctgatctgc	atggtgatga	tgtataaccg	gggaaatgac	420
tggtttgcgt	tttgccctga	ctaa				444

<210> 164

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 164

tgtataaccg	gggaaatgac	tggtttgcgt	tttggcctga	ctaataccga	tgccgctgaa	60
gggaattttg	acctggtgga	taccctaaaa	acgtggcacg	tgaacctggc	gattctggga	120
aattccctta	ttggtttgca	cccccttgcc	ccgctgaatc	ctccctattt	ccttgaaaag	180
acaacacccc	tgctgcccc	ttaa				204

<210> 165

<211> 345

<212> DNA

<213> Enterobacter cloacae

<400> 165

atccacaatg	gccttcacgg	ccagctcaag	atcggcatcg	cccatcacga	tggccggggc	60
tttaccgccc	agctccagcc	ccactttggt	gatgtttttc	gcagccgcag	ccatgatctt	120
ttcacctgcc	ccgacgctgc	cggtcatgct	gaccatcgcc	actttcggat	ccccggccag	180
ctcctgtccg	acggtttcac	cccggcccag	caccaggtta	aagacgcctt	tcggcaggcc	240
aatctcatcg	acgatttttg	caaacgcaat	ggcgttggtt	ggggtaaatt	cgctcgggtt	300
gataacgatg	gtgttgccgg	tgatcagcgc	gggagcaagc	ttacg		345

<210> 166

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 166

acacgttccg	cgcagttaca	cacctgcccg	gtattgatga	cgcgtgaatc	cacaatggcc	60
ttcacggcca	gctcaagatc	ggcatcgccc	atcacgatgg	ccggggcctt	accgcccagc	120
tcagcccca	ctttggtgat	gtttttcgca	gcgcagcca	tgatcttttc	acctgccccg	180
acgttgccgg	tcatgctgac	catcgccact	ttcggattcc	cgccagctc	ctgtccgacg	240
gtttcacccc	ggcccagcac	caggttaaag	acgcctttcg	gcaggccaat	ctcatcgacg	300
attttggcaa	acgcaatggc	gttggttggg	gtaaaatcgc	tcggtttgat	aacgatggtg	360
ttgccgggtga	tcagcgcggg	agcaagctta				390

<210> 167

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 167

tgctgaactg	actcacctgg	ccatttcgcca	tggtttgtgc	aatgcggagt	cgtttaataag	60
tcagtgaagt	aagcggttcga	ttcaaaaagca	tttctgaaaa	ccgtcaccag	ccagccgggc	120
gtctaccgaa	tgtacgacgc	tggcggtagc	gttatctatg	tcggttaaggc	aaaagatctg	180
aaaaaacgcc	tttccagcta	tttccgcagc	aaccttgcct	cccgtaaaaac	cgaagcgctg	240
gtcgcactta	tacacaacat	tgatgtcacc	gtgacgcaca	cggaacggga	agcgctgctg	300
cttgagcaca	actatatcaa	gctgtatcag	ccgcgctaca	acgtcctgct	gcgcgatgat	360
aagtcctacc	cgtttatctt	cctgagcggg	gatacccatc	ctcgcctggc	gatgcacgtg	420
ggcgctaagg	atgcgaaggg	tgaatacttt	ggccctttcc	cgaacgggta	tgccgtacgc	480
gaaacgctgg	cgctgttgca	aaaaatcttc	cccgttcgcc	agtgtgaaaa	cagcgtctac	540
cgcaaccgtt	cccgcccggt	cctgcaatat	cagattggcc	gctgcctggg	gccgtgcggt	600
gaagggctgg	taagcgaaga	agagtacgcg	cagcaggtgg	aatatgtccg	cctgttttta	660
gccgggaaag	acgatcaggt	gctgacgcaa	ctgattactc	gtatggaaaa	agccagcgcg	720
gcgctgggaa	tttga					735

<210> 168

<211> 240

<212> DNA

<213> Enterobacter cloacae

<400> 168

caacagacag	ttaccgtcat	catgcgattt	aatatcccta	cgttgctcac	tctctttcgc	60
gttgtgctca	ttccgttctt	cgctcctggc	ttttacctgc	cggtcgtctg	ggcgcttttt	120
gcctgtgcgc	ttattttcct	gatecgtgcc	gtgacggact	ggtttgacgg	ttatctggcg	180
cgtcgctgga	accagagcac	ccgctttggc	gccttcgtct	tgccgcacag	gcctggctga	240

<210> 169

<211> 1203

<212> DNA

<213> Enterobacter cloacae

<400> 169

ttactcgtat	ggaaaaagcc	agcgcgggcg	tggaattttg	aagaggccgc	acgcacccgc	60
gaccagatcc	aggcggtgcg	cagggtgacc	gagaagcagt	ttgtttctaa	tacgggcgac	120
gacctcgatg	ttatcggcgt	agcctttgac	gcgggtctgg	cctgtgttca	cgtgctgttt	180
attcgtcagg	gcaaagtgct	cggcagccgc	agctacttcc	cgaagtgcc	ggcgggcact	240
gagctgggtg	aagtgggtgga	gacttttgtc	ggccagtttt	atttgcaggg	cagccagatg	300
cgtacgctgc	cctcggagat	ccttctggac	ttcacgctcg	acgataaaac	cctgctggca	360
gattcgtttt	cagagctggc	aggccgcggg	gtgaatgtcc	agacgaaacc	gcggggcgat	420
cgcgcgcggt	atctgaagct	ggcgcgaaac	aatgccgcga	cggcgctgac	caccaaactg	480
tcccagcagt	cgaccgtcag	tcagcgttta	accgcccttg	ctacgctgct	caagctgccg	540
gaagtgaaac	gcattggaatg	cttcgacatc	agccatacga	tgggtgagca	gaccgtggcg	600
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ggtaaaagca	ttgaagagag	caaaaatccc	gacgttatcc	ttatcgacgg	cgggaaaggg	780
cagttggggc	aggcgaaggc	ggtattcgaa	tcgctcgacg	tagagtggga	caagaacat	840
ccgctgctgc	taggggtagc	gaagggggca	gatcgtaagg	ctggcctgga	aacgctgttc	900
tttgagccgg	aaggcgaggg	cttttagcctg	ccgcgggatt	cccctgcgct	gcacgtgac	960
cagcatattc	gcgatgagtc	gcacgatcat	gccatcagcg	ggcaccgtaa	aaaacggggc	1020
aaagtgaaaa	ataccagtac	ccttgagacg	attgaaggcg	tcgggccaaa	acgtcgccag	1080
atgctgttga	agtatatggg	cggattgcaa	ggattactca	acgccagtat	ggaagaaatt	1140
gcaaaaagtgc	cgggtatttc	gcaagggtcg	gcagaaaaga	tctactactc	gttgaaacat	1200
tga						1203

<210> 170

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 170
 caaagactct gttatcaacg tgaacacagtt cggcggcgccg aacggcgccg cggtagacca 60
 gacagcgctc ggctcaacgg tgactgtgca ccaggttggc tttggcaaca acgcgaccgc 120
 acaccagtac tgattcattt ctgtaccaa aaacagggca tgcgccctgt tttttttcgg 180
 gaggatctca tgagcacctt cattctcctt gccgcgcttg ccagccagat aacgttcagc 240
 acctcacagc aggcaaatat gacaaccatt attcctcagg tcacgctggc agacgcctgc 300
 gaatgtcagg ttgaggtggt atctgtccga caggggcagg ggggacaaag tacatcgccg 360
 cagaaaaata ctctttttat acccgcta atcagcgatt atttaacgcg aatcagttta 420
 aatattcgct caggggatgc ggtaaaaata atcgtcaccg tttccgatgg aaaatcgctt 480
 catttatcac agcagtggaa cgcaccggta agtcgcgttt aa 522

<210> 171
 <211> 561
 <212> DNA
 <213> Enterobacter cloacae

<400> 171
 acatgtttcg gcagacatac tcttttccgt aacgcggcgt taacaaaacg aatcgcgta 60
 acggagcaag agatactttt ttatagccag gtccagggtg acagcatgaa aaacaaaacg 120
 ttgtttatga tgtttacatt actgggtgcg cctgggtttg taatcgagg tgattcagat 180
 ttaggcagtt ctgaatataa ttttgcgata aatgaattaa gttaaagctt atacaatcag 240
 gcagccatta ttggtcaaca ggggttcagga aataattctg atgtacgcca ggacggttct 300
 aaattgctgt ccgttatctt tcaggagggc ggggaataacc gcgcgaatgt tgatcagtca 360
 gggacgtata accttgctta tatcgatcag accggcaacg gcaacgatgc gagtattaag 420
 cagggcgctt ttggcaacac cgccatgatt atccagaaag gctcgggtaa cagggcggaat 480
 ataacgcagt atggtacgca gaaaacagca gttgtagtac agagacagtc gcaaatggct 540
 attcgcgta ttcaacgtta g 561

<210> 172
 <211> 477
 <212> DNA
 <213> Enterobacter cloacae

<400> 172
 tcaatccgat gggggtttac catgaaactt ttcaaagtgg cagttattgc agcaatcgta 60
 gtttctggca gtgctttcgc aggtgcggtt ccacaatttg gcggcgccca cgggtggtggc 120
 tggggtggcg gcaataacgg cctgactca accctgagca tttaccagta cggcgccggt 180
 aactccgcgc ttgcttttga acgggacgcc cgagattctg aattgacct taccagcat 240
 ggtggtggtt acggcgccga tgttggccag ggctctgatg acagttctat cgatctgctg 300
 caaaaaggct ttggtaacag cgccaccatc gaccaatgga atagcaaaga ctctgttatc 360
 aacgtgaaac agttcgccgg cgccaacggc gcggcggtag accagacagc gtccggctca 420
 acggtgactg tgcaccaggc tggcttttggc aacaacgcga ccgcacacca gtactga 477

<210> 173
 <211> 891
 <212> DNA
 <213> Enterobacter cloacae

<400> 173
 aagaatatta tgatgcgaat cgcgctcttc ctgctcacca acctggcggt gatggtggta 60
 ttccgggctgg tgctaagcct gacgggaatt cagtcgagca gcgttcaggg tctgttgatt 120
 atggcgctgc tgtttggtt cgggtgctct ttcatctcac tgctaattgc gaagtggatg 180
 gcactgaaat ccgtgggcgg tgaagtatt gagcaaccgc gtaacgatat ggagcagtgg 240
 ctgatgagca cggttgtca gcagtcaaag caggcaggca ttgccatgcc gcaggtagcc 300
 atctaccacg cgccggatat caacgcgtt gctaccgggt cgcgtcgtga cgcgtccctg 360
 gtggccgtca gcaccggtc gctgcaaaac atgagccgtg acgaagcgga agcgggtatt 420
 gctcacgaga tcagccacat cgctaattgc gatattgtca ccatgacct gatccagggc 480
 gtggtgaaca ccttcgttat ctttatttcc cgtattctgg cgcagattgc tgccgggttt 540
 atgggtggca accgtgatga ggggtgaagag agcaacggca acccgctgat ctattttgct 600
 gtttcaatgg tgctggagct ggtgttcggt atcctggcaa gcattattac catgtggttc 660

tcccgtcatt	gtgagttcca	tgcggatgcc	ggttccgcga	aactgggtggg	tcgtgaaaag	720
atgattgctg	cgctgcaacg	tcttaaaacc	agctacgagc	cgaggaagc	aaacagcatg	780
atggccttct	gcatcaacgg	caagtcaaag	tcgctgagcg	agctgtttat	gtctcaccgg	840
ccgctggata	aacgtattga	agcgcctgcg	agcggcgaat	atctgaagta	a	891

<210> 174

<211> 1608

<212> DNA

<213> Enterobacter cloacae

<400> 174

ttggaccgca	gcaaagctcc	atggccgaaa	gacgaggctg	aactgaatgt	gctgtgggat	60
ggaaaagtca	aatatgacga	actgagcctc	aagctcacag	gcaaagacga	gaaagagatc	120
cgtgagacgt	taaacgcagc	ctacaagttc	gatattcgcc	gtctggcgca	gaccaacagt	180
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accggaaaaga	gcatggtgga	cgtgattggc	tggcgtcttg	atgacgtagt	tgcgctgac	480
aaagggccga	agggcagcaa	agttcgccct	gagatcctgc	cagccggtaa	ggggaccaa	540
accogtatcg	ttactctgac	ccgtgagcgt	atccgtctgg	aagatcgcg	ggtgaaaatg	600
tcggtgaaaa	ccgtgggtaa	agagaaggtt	ggcgttctgg	atatcccagg	tttctacgtc	660
ggcctgaccg	atgatgtgaa	agtgcagctt	cagaagcttg	aaaagcagaa	tgtcagcagc	720
gtgatcattg	acctgcgcag	caacggcgcc	ggggcattga	ccgaggccgt	ctcgctttcc	780
gggctgttta	tcccgctctg	cccggtggta	cagggtgcgcg	ataacaacgg	taaagtgcgt	840
gaagatgcgg	ataccgatgg	tgtggtctac	tataaggggc	cgctggtggt	gcttgtcgat	900
cgcttcagcg	cctctgcatc	ggaaatcttc	gctgctgcc	tgcaggatta	cggccgggcg	960
ttaatcgctg	gcgaaccgac	gtttggcaag	ggcaccgttc	agcagtaccg	ctctctgaac	1020
cgtattttacg	accagatgct	gcgcctgaa	tggccggcgc	tgggctcagt	acagtacacc	1080
attcagaagt	tctacgcgt	caacggcgcc	agcacgcagc	gcaaaggcgt	gacgccggat	1140
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ctgccgtggg	atagcattga	tgcgcgcaca	ttcgtgaaat	cgggtgatat	gaaacagttc	1260
ggaccggaac	tgtgaaaaa	tcacaacgat	cgcacgggga	aggatccgga	attccagtag	1320
atcatgaaag	acatgcgcgc	tttcaacgcc	ctgaaagcaa	aacggaacat	tgtgtctctg	1380
aactacgctc	agcgtgagaa	agagaacaat	gaagatgaag	cgacacgtct	ggcgcgtatc	1440
aacgatcgct	tcaaacgtga	aggcaagcct	ctgctcaaaa	aactggacga	tctgcctaag	1500
gattaccagg	agccccgatc	gtatctggac	gagaccgtgc	atategcgct	tgatctcccg	1560
aagctggaaa	aaaataaacc	tgtgtttcaa	cctgctccca	caaaaataa		1608

<210> 175

<211> 926

<212> DNA

<213> Enterobacter cloacae

<400> 175

ctcaccttcg	ccgatagtga	attcagcaact	aagcgccgctc	agaccgcgaaa	agagatttttc	60
ctctcccgcg	tggagcagat	tctgccaatg	cagaatatga	ccgctgtcat	cgagccgttt	120
tatcccaagg	cgggcaatgg	ccgacggccc	tatccgctgg	agaccatgct	gcgtattcac	180
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atcatgaatt	tccgccacct	gctcgagcag	catcaactgg	cccgtaaat	gttcaagacc	360
atcaatcgct	ggctggccga	agcaggcgtc	atgatgacc	aaggcacttt	ggtggatgcc	420
accatcattg	aggcaccag	ctctagcaag	aacaaagagc	agcaacgcga	tcgggagatg	480
catcagacca	agaaaggcaa	tcagtggcac	tttggcatga	aggcccacat	tgggtgtcat	540
gccaagagtg	gcctgaccca	cagcctagtc	accaccgcgg	caaacgagca	tgacctcaat	600
cagctgggta	atctgcttca	tggagaggag	caatttgtct	cagccgatgc	cggctaccaa	660
ggagcgccac	agcgcgagga	gctggccgag	gtggatgtgg	actggctgat	cgcgcagcgt	720
cccggcaagg	taaaaacctt	gaagcagcat	ccgcgcaaga	acaaaacggc	catcaacatc	780
gaatacatga	aagccagcat	ccgtgccaa	gtggagcacc	cgtttcgcat	catcaagcgg	840
cagttcggct	tcgtgaaagc	cagatacaag	gggctgctgc	aacacgataa	ccttttcacc	900
agccgcggag	gatcagcatc	cggaaa				926

<210> 176

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 176

tctgtcttcat	ggagaggagc	aatttgtctc	agccgatgcc	ggctaccaag	gagcgccaca	60
gcgcgaggag	ctggccgagg	tggatgtgga	ctggctgac	gccgagcgtc	ccggcaaggt	120
aaaaaccttg	aagcagcatc	cgcgcaagaa	caaaacggcc	atcaacatcg	aatacatgaa	180
agccagcatc	cgtgccaaagg	tggagcacc	gtttcgcatc	atcaagcggc	agttcggctt	240
cgtgaaagcc	agatacaagg	ggctgctgca	acacgataa			279

<210> 177

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 177

gctgtgggtc	aggccactct	tggcatcgac	accaatgtgg	gccttcatgc	caaagtgcc	60
ctgattgcct	ttcttgggtc	gatgcattct	cggatcgctg	tgctgctctt	tgttcttgct	120
agagctgggt	gcctcaatga	tgggtggcatc	caccaaagtg	ccttgggtca	tcatgacgcc	180
tgttcgggcc	agccagcgat	tgatggtctt	gaacaattga	cgggccagtt	gatgctgctc	240
gagcaggtgg	cggaattcca	tgatggtggt	gcgatccggc	agggcgctat	ccagggataa	300

<210> 178

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 178

tccggcaaac	aggcgcatgg	aggcgatttc	gtacagggca	tcttccatgg	caccgtcgct	60
caggttgtag	caatgctgca	tgcagtgaat	acgcagcatg	gtctccagcg	gatagggccg	120
tccggccattg	cccgccttgg	gataaaacgg	ctcgatgaca	gcggtcata	tctgccatgg	180
cagaatctgc	tccatgcggg	agaggaaaat	ctcttttcgg	gtctgacggc	gcttagtgct	240
gaattcacta	tccggcaagg	tgagttaatg	gctcatgatg	tccctctggg	atgcgctccg	300
gatgaatatg	atgatctcat	atcaggaact	tgttcgcacc	ttccctag		348

<210> 179

<211> 1560

<212> DNA

<213> Enterobacter cloacae

<400> 179

gtccttccag	cgcctgtgg	tgaaaaacgat	tcccgtcggg	cagaaatgct	gcaacaggcc	60
aacgcgctgg	acgagcgca	aagtttctcg	tcattacgcc	gtcttgccctg	gcagaatggg	120
cactacttta	cgctgcgaac	cacctttaac	cagccggggc	atctggcgac	cgtgggtgcc	180
ttcgacctgc	cgattaacga	tctcatccca	cgggatatgc	cgctggacag	cttcggtctg	240
gagccagaca	acagcaccca	aaatatgcgc	tgcgcgtcgg	ataaagaagg	cgcggacagc	300
gtagccatct	catttaattg	ctcaaagatt	gagattgcct	catcgctcaa	ctcaaccggg	360
atgcgtctgg	tgtggcaggt	gccttttggc	accctgatgc	ttgatactct	gcaaaacatt	420
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ttccgtttcc	agtcggggccg	ccagagcgac	tgcacatcgg	tatcagccgg	gaccagcaac	540
gagctgcgca	ttcttcgtgc	cctgaatgaa	gagattatct	ccgtgctgcc	gcttgggggtg	600
ctcgttcacg	atcaggaggc	aaaccgcacg	gtaatgagca	ataaaattgc	cgatcacctt	660
ctgcccgcac	ttaacctgca	aaatattacg	gccatggcgg	accagcatca	gggcgtcatc	720
caggccacca	ttaataatga	actgtatgag	atccgtcagt	tccgcagtc	ggtcgcgtcg	780
cgcaacgaaa	tcttcatcat	tgcgatcag	gatcgcgaa	tgctggtgaa	taaaaagctc	840
aagcaggcgc	aaaggctgta	cgagaaaaac	cagcatggcc	gcgcgcggtt	tatgcaaaat	900
attggcgatg	cctttaaaca	gccgttgaag	tactcgcca	cgcagattgc	tgatctgagc	960
acgccagaaa	gccgacagct	aagcagccag	gccgattcac	tggttcgtct	ggtggacgaa	1020

atccagcttg	cgaacatgct	ggagaatgac	atctggaagg	gcacccctac	gctcttctcc	1080
atccaggacc	tgattgatga	ggtggtgccg	gaagtcctgc	cggatgatcaa	gcgcaaggga	1140
ctccagctgc	tgatcaacaa	ccattttaccg	gccaacgacg	aacgtcatgg	cgatcgcgat	1200
gccctgcgtc	gcctcctgat	gatgttgatt	cagtatgccg	tcaccacgac	gcagatcggc	1260
aagatcaccc	ttgaagtcag	caccgatgag	tcacccgacg	atcgtctgac	gttccgcac	1320
cttgatacgg	gtgaaggcgt	gaccgtgagc	gaaattgata	acctgcactt	cccgttctctg	1380
aacgataccc	agcgcgacca	ctacggtgtaag	gcgaatgccc	tcaccttctg	gctttgogat	1440
cagctggcgc	gtaagctggg	cggatcatctg	aacattaagg	cgcgcgaaac	cctcggcacc	1500
cgctactctt	tacacgttaa	aatggtgtct	tcaccacggg	gatggagcat	ccgcccttga	1560

<210> 180

<211> 414

<212> DNA

<213> Enterobacter cloacae

<400> 180

tccgtaagga	gcaattcgat	gcgtcattac	gaaatcgttt	ttatggtcca	ccctgaccag	60
agcgaacagg	ttccgggcat	gatcgagcgt	tactctgctg	ccatcactgg	tgcagaaggc	120
acgatccacc	gtctggaaga	ctggggcgcc	cgtcagctgg	cttaccgat	caacaaactg	180
cacaaagcac	actacgttct	gatgaacgtt	gaagctccgc	aggaagtgat	cgatgagctg	240
gaaactacct	tccgcttcaa	cgatgccgtt	atccgcagca	tggttatgog	taccaaacac	300
gcagtgaccg	aagcatctcc	gatggtttaa	gcgaaagacg	agcgccgtga	gcgtcgcgat	360
gatttcgcaa	acgaaaccgc	agatgattct	gatgctgggg	attctgaaga	gtaa	414

<210> 181

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 181

tttctgatga	ccaaccgtct	ggtgttgtcc	ggcaccgtgt	gcaggacccc	ccttcgaaag	60
gtcagcccat	caggaattcc	gcattgccag	ttcgtgcttg	agcatcgctc	tgtgcaagag	120
gaagccgggt	ttcaccggca	ggcgtgggtg	caaattgccc	taattattag	cggacacgaa	180
aaccaggcca	ttactcacag	ttttaacggt	cggtaa			216

<210> 182

<211> 399

<212> DNA

<213> Enterobacter cloacae

<400> 182

acaacatcat	cagaaatggt	cacccatccc	aaccggggtg	gcgattacac	tttaatcaga	60
aaccctgaac	agagaaggag	agcattcccc	cgtatcacag	cacgcagtcg	tggagcgc	120
atcatgaaaa	gaatcgcaat	cgccattttg	gctgcgcttt	tgtcagtg	aaacgcgatg	180
gcagccatca	gaatagacag	ccaacaggcc	agaaacatgg	atgatgtgca	gagcttaggc	240
gttatattaca	tcaatcataa	cttcgccact	gaaagtgaag	cagatcaggc	gcttaatgaa	300
gaaaccgatg	cgcatggcgc	aaaatactat	cacgtcatgc	tgacacgtga	gcccggcagc	360
aacggtaata	tgcacgccag	tgcagatatt	taccagtaa			399

<210> 183

<211> 564

<212> DNA

<213> Enterobacter cloacae

<400> 183

aatcgggcgt	ttgctgaatg	taaacacgac	ggaagatttg	cagatgatgc	aggagagaaa	60
atgatacccg	tattagcgat	ctcagcctgg	agtggcaccg	ggaaaacttc	gctgctaaaa	120
aaactgatac	ctgcactttg	cgccaaaaggc	attcgtccc	gattgattaa	gcatacgcac	180
cataacatgg	atgtcgataa	accgggggaaa	gatagctatg	agctgcgtaa	ggctggcgct	240
gcacaaacga	tgggtggcgag	taaccagcgc	tgggctgtta	tgacagaaac	accggatgaa	300
gcaccgctgg	atctcgctta	tottgtcagc	cggatggatc	actccacgct	ggatctggtg	360

ctgggtgagg	ggtttaagca	tgaggctggt	gcgaagatcc	tgctattcag	aagcgatgcc	420
ggacatgacg	taagtgagtt	aacgctggat	gaacatgtga	ttgccgtggc	cagtgcagtt	480
gcgttgacgc	tgaaagtacc	ggttctggat	ttgaataatg	tggaggggat	tgcagcgttt	540
atttcggcgt	ggtgtgcagt	ctga				564

<210> 184

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 184

tttattcgta	aaggccaggg	cgtaaccccc	accgcgtacg	ccaccattct	gcatgagtac	60
atcagccagg	gtctggaatc	gattctgggc	gcgctggatc	tcaccggcag	ttacgataag	120
caacgaacca	tcaccatagg	cacctctccc	tctgtgggcg	ttctggtcat	gcccgtattt	180
taccaggctg	ttaaacagca	tgcgccacag	ctgctgatcc	gcaacgtgcc	cgttaacgat	240
ccggaaactc	agctggcgca	attccagacg	gacctgatca	tcgacagcaa	cagcttcgcg	300
gccagagcat	tagggcataa	cgttctctat	accgactctc	tggcgctcgt	ttgtcgtcag	360
aatcatcctg	tattgagcgc	acctttgacg	cctgaaaatt	tgcgtcatta	cgaacatgca	420
acctttatgt	ccgaggggca	gggcccggat	ccgctgcgcc	agcgtattga	cgaactgttc	480
ccggaccgtc	tgatcagctt	cagcagttac	aatatgttta	ccctcgcggc	cctgattggc	540
agcagcgatt	tgctctgtat	tatgcctgtg	cgtctcttcg	ctttgcttca	aaaatgctgg	600
ccgctggaga	gcattccatt	gagtcacact	acgacggaat	ctggtgaaat	ctcactgcat	660
tacaacaagc	taagcctgcg	cgatccgggt	ctggaaaacg	tcattaacgt	gatccgccag	720
gctttctga						729

<210> 185

<211> 1011

<212> DNA

<213> Enterobacter cloacae

<400> 185

attgaaacgc	tttctctcga	tattcgcaac	tggaacacgc	acgctatgag	taaaccattt	60
gtgatggaac	gcggtgttaa	ataccgcgat	gccgataaaa	tggcccttat	cccgggttaa	120
aacgtggcta	cagagcgcca	ggcgctgtta	agaaaaccgg	aatggatgaa	aatcaaacct	180
ccggccgact	cttcgcgtat	ccagggggat	aaagcggcga	tgcgcaaaaa	tggctctcac	240
tctgtctgtg	aagaggcctc	gtgccctaac	cttgcctgaat	gtttcaatca	cggtaaccgc	300
acatttatga	ttctgggtgc	catctgcacc	cgccgctgtc	cgttctgtga	cgttgcccat	360
ggccgctccc	ttgcgccaga	cgctaacgaa	ccgcaaaaac	tggcgccagc	gattgccgat	420
atggcgctgc	gttatgttgt	tattacctcc	gttgaccgtg	acgatctgcg	cgatggcggt	480
gctcagcatt	ttgctgactg	tattaccgcc	atccgcgaaa	aaagcccgaa	cattaagatt	540
gagacgctgg	tgccggattt	ccgtggccgt	atggatcgcg	cgctcgatat	cctgaccgcg	600
acgccaccag	acgtgttcaa	ccacaacctg	gagaacgtac	cgcgatatcta	ccgtcaggta	660
cgteccgggt	cagactacaa	ctggctcgct	aagctgctgg	aacgctttaa	agaagcccat	720
ccgcataatc	caaccaagtc	tggctctgat	gtcggcctgg	gtgaaaccaa	cgtcgagatc	780
attgaagtga	tgcgcgatct	gcgcgccacc	ggcgtcacca	tgctgacgct	gggccagtac	840
ctccagccaa	gccgtcacca	cctgcctgta	cagcgttacg	taagcccgga	tgagttcgat	900
gaaatgaaag	ccgaagcgat	ggcgatgggc	tttaccatg	ccgcgtgcgg	tccgtttggt	960
cgtctctctt	atcacgccga	tatgcaggcg	aagggcgaag	aagtgaata	a	1011

<210> 186

<211> 561

<212> DNA

<213> Enterobacter cloacae

<400> 186

aggtgcatct	gcctagtaaa	aatattcttc	agtgccagtg	agaaaaatat	gagcgactac	60
atacctaaaa	agagagggtt	gcttatactg	gattgggtat	tcccccttaa	tattttattg	120
ctgattctcg	ttatgtgtgt	ctttttcacc	cgttatacat	ttggatacgg	tttattgaat	180
gggtgcctgc	ctgctgattt	ttatatgatt	gatcattcgg	ataaaaagtat	taaaactggg	240
gaactcatac	catttaacat	gccgaaatcg	gtacgtttta	tcccacaaaa	tgaacgagtc	300
ataaaaaattg	ttgccgggtg	gggcgggtgac	aaacttaaa	taacaatgga	tgggggttat	360

aacggggaca	aatTTTTtga	aactaatgca	cgTcgTatTT	cgaagaaata	caatattccg	420
tccattttga	ttgaaaaaga	attgataatt	cctgaaggcg	aagttttcct	aattgggcaa	480
accgatcact	catgggattc	ccgtttttgg	ggaacagtaa	agctgaattc	agtaattggg	540
aaaacatatg	cgatctttta	a				561

<210> 187

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 187

tgtgcagttt	taagtaatac	aaatgcaagc	actgaatatt	aacatgatgc	tgacctaatc	60
gctcagcaag	caaaggggct	tggggcacag	gctaaagggtg	cacagcagcc	agatggggct	120
cttagccttg	atgctacgct	aaaatcacca	gatgtgcaga	agtacatagc	gcaagctgaa	180
gcactccaaa	aaaaccagga	cctgagcaag	caaataaacc	gtggttacgt	ccccggtatg	240
aatgcggtata	gtgttcaagc	agttatagac	catacccagg	ctatcagggc	ccaaagtaat	300
aactctgaag	ctgtcaacga	tataattaga	agacgtgatg	aaattcaaga	aaacgccagc	360
cttaatgaag	cggctctgaa	agctgtggaa	aataagccgg	aagtcatgcg	aggacaagct	420
aaaaatatcg	aaaaattgtt	tggttcctcg	ggcatcacag	ctgctgactt	cgaaagaaaa	480
atggatagca	cacgtgaaga	agcactatca	actgaaaatg	gaataacgat	ctttgcttca	540
tttagcttgc	cggattatgt	actggaagac	cttctacgta	cggcctcaga	gcataaagct	600
cgtgtagttt	tcaatggctc	aaagaaaagg	actactcggc	taccagagac	acaggcagca	660
ataaaccaaa	tgattgtcaa	aggaaaattt	gaatctcctt	tgattacaat	tgatcctgat	720
agcttcagtc	aatatcaagt	aactcaagta	ccgacaatta	tttctaggga	gcaagctcgt	780
tttgccaaaa	tgggtaagct	ccttcaacgt	tga			813

<210> 188

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 188

atgaattttac	gaacaaaagg	atttctgtta	atcattaaag	atgaagggtga	caccaaaagaa	60
tttacaattg	aaaatcctgg	caaataataca	ttgatgggtt	ttttcaaaga	taaccgaaac	120
aatgaacagc	gtatcgaaaa	tacctttgtt	gtcgatgaac	aaacgccaat	gaacgttgag	180
atgacacca	agttctctaa	caaataatag	agagctccac	tcgatgtaac	cttaagggtca	240
aacatcaaga	tatctcattc	ggcggactcg	atagatacgg	tcacatacaa	ggtgaacggg	300
gaagtaatac	ccagcggcaa	aaattattgg	gctcaactga	tctcgggttt	aaaagaaaag	360
aaatacgaga	ttacaattga	tggtgttagt	aaacttggac	agagagggtc	agcatctggt	420
gagtttgatg	tcgttaaaaa	cgcagtgcc	aattgtacat	tgagctacac	ggaaaccaac	480
ctaagctgga	gctttaccaa	taaatgtgat	gatactgatg	gaaaaatgg	tagatatgaa	540
tgggttcata	acggcggaatt	aaggaaacgt	ttcggtagta	cggctacact	ttctaaaaac	600
cttaaccgtg	gtaagcagga	cataaaaagta	attgcttatg	atgatagtgg	agactttgca	660
acacagcacg	tgacagtttt	cggaccggct	gaagaggcaa	gtaagtctga	aaacactgta	720
tcaataccaa	gcagtgagta	g				741

<210> 189

<211> 417

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (153)

<400> 189

gtacttgacg	cgcaaatatc	agtttgtgog	tgctcgctgc	tgattcgctg	tattaatata	60
accccgcata	tgcgggggtt	ttttgttccc	gattccaggg	tatcgctgog	atgccgggtg	120
goggttgogc	attaccgggc	atacagaatt	cantatgctc	gaatcgaacc	ttggtcgaag	180
ctttttatcc	gtccccgc	gggagaacca	tggggcattg	tgcttttgga	tagtgctaaa	240
gaatccggaa	gtgatggtgg	tgggggaagg	attactcagc	gcttcgogct	tcgcccctcg	300

ggtcgttgca	tgcggcaacg	ctttctcgat	acgtctgaat	cgaaccttgg	tcgaagcttc	360
tcattcattcc	cgcactgaa	gaacccatggg	gcattgtgct	ttgagagagt	gctgtag	417

<210> 190
 <211> 336
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (110)

<400> 190						
ttcgtctgtat	taatacaacc	cgcctatgct	gggggtttttt	tggtcccgat	tccagggtat	60
cgtgcgggatg	cggggtggcg	gttgcgcatt	acccggcata	cagaattcan	tatgctcgaa	120
tcgaaccttg	gtcgaagctt	tttatccgtc	cccgcatggg	agaacctg	ggcattgtgc	180
ttttggatag	tgctaaagaa	tccggaagtg	atgggtgggg	gggaaggatt	actcagcgct	240
tcgcgcttcg	cccttcgggt	cgttgcatgc	ggcaacgctt	tctcgatacg	ctcgaatcga	300
accttggtcg	aagcttctca	tcattccccg	caactga			336

<210> 191
 <211> 519
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (490)

<400> 191						
ttcgaggaag	cgaagacca	cgcggggaac	tccacagagg	cgaaaaccat	ccgcgatgac	60
cgcaaataca	ccaagcgca	gcgcgaactg	ccagcgaatc	gtctcaaccg	aaagcgagcc	120
cgcagccagg	cgaagaagga	cggcaacgca	aaagagcagc	agcaggatca	gatcgaaacc	180
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cgcgagatca	aggaaggcca	tcaggggagaa	gagaacgacg	aagcgaagac	cacgcaggca	300
gagcaggaag	aaatcggcag	gaaggagcga	aagagacaga	aggaaacca	gcgcgcgaag	360
aaatccagg	agcgcaaggc	gcgtcagccg	ggcggacagc	aggagcaggc	gcgagagatc	420
aaacgcgaaa	tcgaatccca	gcagccgcac	aacgaatccc	tggtccagaa	ggtcaattac	480
ctgagctatn	ttaaccgccg	gggtcgaagg	acacgcgca			519

<210> 192
 <211> 810
 <212> DNA
 <213> Enterobacter cloacae

<400> 192						
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aagctttttc	ccgatccgcg	acgtatcgcc	ctgttaaaac	aaatagaaca	aactggctcg	120
attagccagg	gagcaaaaaa	cgcgcgcac	agctataaaa	gtgcctggga	tgcgattaac	180
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ggcggcgcgc	tggttgacgcg	ttacgggcaa	cgtctgatcc	agctctacga	tttactggcg	300
cagatccagc	aaaaagcatt	tgatgtgctg	agcgatgacg	acaacctgcc	gctggacagc	360
ctgctggggc	ccatctcccg	ttctctcttg	cagaccagcg	cccgtaacca	gtgggttggt	420
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ggcacgacgc	gcctgaaagc	cgccatcacc	gcgcaaagtg	gtcaacgcct	tggtgtgaac	540
gaaggtcagg	aggtgctggt	attactcaaa	gccccctgga	tcagcatcac	gcttaaccct	600
gagcaggccg	cagaggccga	caaccagctg	cggggacgca	tcagccacat	cgagcgcggc	660
gcagaacagt	gtgaagtgt	gatgacctg	ccggatggac	agttgctctg	cgccaccgtt	720
cgggtgaacg	acgcgaccga	attagacgaa	ggtgctgtgg	tgaccgcata	tttcaatgca	780
gacagggtaa	ttatcgccac	attgtgctaa				810

<210> 193
 <211> 1164
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(985)

<220>
 <221>unsure
 <222>(1131)

<400> 193
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 tcgctgccag agttaaccct tcgcgcggga gaaagctggg cgtttgtggg ctctaattggc 120
 agcggaaaat ccgcgctggc ccgcgctttg gctggcgaaa taaccctaact gaaggggtgaa 180
 cgtcgggtgca cctttaccocg gctgacgcgc ctttcottcg aacagctgca aaagctggtc 240
 agcgatgagt ggcagcgtaa caataccgat ttgctcagcc ccggcggaaga agataccggc 300
 cgcacgacgg cggaaattat ccaggatgag ataaaagatc ctgcccgtg tcagcagctg 360
 gcggagcaat ttggcattac cgccctgctt aaccgcgctt tcaaatatct ttctaccggc 420
 gagacgcgca aaacgctgct gtgccaggcg ctgatgagcg agccggaact cttgatcctg 480
 gatgaaccgt ttgacggact ggatgtgcag tccgcgcgc agctggcagc gttgctggcg 540
 tcgcttaacc agcagggata cacgcttgct ctgggttctta accgctttga tgagatcccg 600
 gatttcgtac attatgcagg cgtgctggcg gactgtagcc tgaccgaaat cggcgagaag 660
 gcgctcctgc tccgtcaggc gctcattgca cagctggccc acagcgagaa actggacggg 720
 attgccttgc cggagccgga tgcgccttcg gcgcgccacg ggctggagcc tgaccagccg 780
 cgcattgtgc tgcgcgatgg ggtggttgc taccgacatc gccctattct taatcacctc 840
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 tccacgctgc tgagcctgat caccggggat caaccgcagg gatacagcaa cgatctcacc 960
 ctgttcgccc gtgcgcgcgg gcaacnggat accatctggg atatcaaaaa gcaactcccg 1020
 tatgtcagca gcacctgca tctgggacta ccgggtgagc aacaccgttg caaaacgtta 1080
 tctctcttgg cttccttcga ctccattggg tatattatcaa ggcggttccc nacaaaccac 1140
 caccaacttg cgccaacatt gggt 1164

<210> 194
 <211> 792
 <212> DNA
 <213> Enterobacter cloacae

<400> 194
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 aactgcccta tttgcgacga tgagcgccag tatgtcccg tgacgggcca ggcattggacg 120
 gacttcgaca gccttacgac cagcacacac aacaaatggc aacagctgga gccgcagctg 180
 ttcagcatca aaaccgttcc cgcttttgcc atcaaccagc gcgcgcttct gctgcgtaag 240
 ccacagggca atgttctgtg ggactgcacg gccaatcttg acccggcgac cagagcgtta 300
 gttgacgcgc tcgggggcat cagcgcgacg gcgatttcgc acccgcatca ctacaccacc 360
 atgcaggagt gggccgcgcg gtttaacggc ccgatctacc tgcacgccag cgatcggcag 420
 tgggtgatgc gtgacagccc ggcgatacgc ttctgggagg aggacgccct ggagattatg 480
 cctttggtga ctctgctgcg gctgggcggg cattttgcag gcggcacggg gctgcactgg 540
 cagtcaggcg acggcgtgct gctggccggg gatattttgc aggttacacc cggaaaagac 600
 gccgtgtcgt ttatgtggag ttatccgaat atgctgcgcg tgccctgcccg caccgttgag 660
 tcgttgatcg gccgactgac cgggaaaacg taccagcgcc tgtacggggc ctttgaagga 720
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 tgtctccgct aa 792

<210> 195
 <211> 831
 <212> DNA
 <213> Enterobacter cloacae

<400> 195
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 acgccccttcg gcgcagacac ggtgttagct gatacccagt tcggttcgct gacgcgacct 120
 gtacaggatg aagcgatggc gaactggcag gaggagggtt ggaaggaagc gccgctgccg 180
 gtgtggaatc tgcttaacta cgcggtgctc caggaacggc gtaacgggat ggcgctgttt 240
 accgaagggg tacgcgaatt tgaagtgact ggcgagcgtc aaaaaacgtt tgccctgacg 300
 ttgcttcgog gcgtgggagt acttgggaag gaagatttac tgctgcgcc cggcagaccg 360
 tccgggatca aaatgccggg gcctgattcg cagatgcggg gccagttaac ctgtcgcttt 420
 agcctgttca gttttaatgg tacgcccgtc agtgctggtg ttgcgcagca ggcaagtcg 480
 tggtaaacgc cagtgcactg ttataacaaa attccgtggg atgcgatgaa gcttaaccgc 540
 gcctctttca ccaccccctg tagctatagt ctgctaacgc tggcgccctaa cggatgcgta 600
 ctcaagtgcg tgaaaaaagc ggaggatcgt gacgagatga ttcttcgtct gtacaaccct 660
 tcggagaccc gctcctgtga cgtggctttg tctgtgaacc gtgagatcca ggccctgctgc 720
 gaaacggaca tgaatgaggt gtacaaggcg caaggggaag agggctcagc cattacgggg 780
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<210> 196

<211> 204

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (51)

<400> 196
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 ccaaaaccgg aggatgtgga atttgatgcc aggagggacc tttttttttg ccatcattgg 180
 gccttccott tgcagtcggg ataa 204

<210> 197

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 197
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 ccggtggtgc aggttgacct gctggccagc cgtgagggtc gcattgcaac cgcaatctct 180
 gctggtaatg gcctatccca ggctgcaatc gtattcatac ccagctacgc cttcctcgcc 240
 ctttcaactgt cagagtccat ggccagtttc agcctcctcc ccttcgtcac caccatggcc 300
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 cctctcttca tacttgctga ggtgctcatg gccctcggac tcataaccgt cataggggca 480
 cccctcaggt acataatgct atctgaaact cccccgaac acagggcatc tggacaggcc 540
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 gtagcgtcca tgggtagtgg agtaatgggt tacaggttct cattcctctt ccttgttgca 660
 gttgcattca cactcttctt gctatcaacc ggtctcaagg gaagagacgt agagcttgag 720
 acaatgaaga gggacagctg c 741

<210> 198

<211> 750

<212> DNA

<213> Enterobacter cloacae

<400> 198
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 gatggcggct cgaacgacgg cagggcggag ttcttgaaa aactcaacgg tgagttcaac 180
 ttacgttaca tcagcgagaa agataaaggc atttacgatg ccatgaataa aggcattcaac 240

atggcgagc	ggcggtacgc	catcttctct	aattccggcg	atgtgttcca	tgaaaatgtg	300
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ctgcttgatt	tccgagaggg	gaaaaaagt	ctgcgcggtg	cgaaccagg	ctggtatatc	420
taccacagcc	tcccgccag	ccatcaggct	atcttcttcc	caatgagcgg	tctgaaaaaa	480
cagccttacg	atttgcgcta	taaagtgtca	tcagattatg	ccctggcgcg	cagtctttac	540
aaatctggct	acccgttccg	tgaattaaa	ggactggtat	ctgaattttc	aatgggcggc	600
gtgtcaacct	cgaataatct	ggaactgtgc	caggatgcca	aaaacgtgca	gcgtaaaata	660
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<210> 199

<211> 351

<212> DNA

<213> Enterobacter cloacae

<400> 199

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atactgtacc	gctggcgcgc	atctttactg	cgtctgtttg	gcgcaaaaat	aggaaaaaac	180
gtagtcatc	gaccttcggt	gaaaattact	tatccctgga	aattaacact	tggggattac	240
gcctgggttg	gggatgacgc	agtgttatat	acccttggtg	agattacgat	tggcgcaaat	300
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<210> 200

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 200

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aaaatgatga	ttaacgcgtt	tgggtgataac	cagaactttc	gcgtgcaact	ttatctgttc	120
acaccggtgt	cgttggtttt	taccgggtca	atattttagcc	cggaatatgc	attcttaatt	180
gtatgtccgt	ttattttgcg	caaggcgcgt	aatattacga	gcgtatga		228

<210> 201

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 201

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actctcaatc	gtggtgtcat	ggccccgaag	ctgcttatca	togatgaaat	aggttatctg	120
ccgttcagtc	aggaggaagc	caagctgttc	ttccagggtca	tgcgcaaatg	ttacgagaag	180
agcgcgatga	tcctgacctc	caacttgccg	ttcgggcagc	gggatcagac	gttcgcgggt	240
gatgcagcgc	tgacatcggc	gatgctggac	cggatcttac	atcactcaca	cgtcgtgcaa	300
ataaaagggg	aaagctatcg	actgaagcag	aaacgaaaag	ccgggggttat	agctgaagct	360
aatcctgagt	aa					372

<210> 202

<211> 2127

<212> DNA

<213> Enterobacter cloacae

<400> 202

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aaccataaaa	tccgtgaagt	tcatgacggc	gcagccacca	tggactggat	ggaacaggag	180
caggagcgtg	gtattactat	cacctccgca	gcgactactg	cattctggtc	aggatatggct	240
aagcagtacg	aaccgcacgc	cgtaaacatc	atcgacaccc	cagggcacgt	tgacttcacc	300
atcgaagtag	aacgttccat	gcgtgttctt	gacggcgccg	taatggttta	ttgcgcagtt	360
ggtggtgttc	agccacagtc	tgaaaccgta	tggcgtcagg	caaacaaata	taaagttcca	420

cgcatcgcg	tcggttaacaa	aatggaccgt	atgggtgcta	acttctgaa	agttgttggc	480
cagatcaaaa	cccgctctggg	cgcgaaacct	gttccgcttc	agctggcaat	tgggtgctgaa	540
gaaggcttca	ccggcggttat	cgacctggtg	aaaatgaaag	ccatcaactg	gaacgaaaca	600
gatgcgggcg	ttaccttcga	atacgaagat	atcccggcag	agatgcagga	cctggctgac	660
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atgaagggtg	aagtagaaac	tctgaagag	aacacccggtg	acgttatcgg	tgacttgagc	1920
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gaagtccgc	tgtctgaaat	gttcggatat	gcaactcagc	tgcgttctct	gaccaaagg	2040
cgtgcatcat	acactatgga	attcctgaag	tatgatgatg	cgccgaacaa	cgttgctcag	2100
gccgttatcg	aagcccgtgg	taagtaa				2127

<210> 203

<211> 378

<212> DNA

<213> Enterobacter cloacae

<400> 203

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atcggccacg	ttgaccatgg	taaaactacc	ctgactgctg	caatcactac	cgtactggct	180
caaacctacg	gcgggtgctgc	tcgtgctttc	gatcagatcg	ataacgcacc	agaagaaaaa	240
gctcgtggta	tcaccatcaa	cacctctcac	gttgagtatg	acaccccgac	tcgccactac	300
gcacacgtag	actgcccgag	ccacgcccag	tatgttagtc	ttcacccacg	ggcgctggac	360
ggatccacgc	ttaggttaa					378

<210> 204

<211> 705

<212> DNA

<213> Enterobacter cloacae

<400> 204

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aacttcagcg	tggatcttaa	cgccagttac	ttcggattcc	tgaccacgca	gcatacccg	120
acgacggctc	aagtcaccga	taacgtccac	gggtttctct	tcaggagttt	ctacttcaac	180
cttcatgac	ggctcaagca	gaactgggtt	tgctttctta	aagccttctt	taaaggcaat	240
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cagacgaaca	cccatgtcta	caaccgggta	accagccaga	ggaccagctt	tcagctgctc	360
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gttgatgaac	tcgtaacctt	tcgggttaga	gcccggtcc	agtgggtaca	tgatgatcac	480
aacgtgaccg	tactgaccgc	gaccaccaga	ctgcttagcg	tgtttacctt	caacgtcggt	540
aactttcgcg	cgaatcgctt	cgcggtaagc	aacctgaggt	ttacccacgt	tcgcttcaac	600
gttgaattca	cgttccatcc	ggtcaacgat	gatgtccagg	tgacgttcc	ccataccagc	660

gatgatgggtc tggttagatt cttcatcagt ccatacacgg aatga

705

<210> 205

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 205

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ttttggttca	actgcatgg	agattaccgg	ctcagggaa	tccatacgt	ccagaatgat	120
cgggtgatcc	ggatcacaca	gagtgtcacc	agtggtcacg	tctttcagac	cgatagcagc	180
agcatgtcg	cccgcacgaa	cttctttgat	ctcttcacgt	ttgttagcgt	gcattctgtac	240
gatacggcca	aaacgttcac	gcgcgccttt	cacggagttc	aggatggtgt	caccggagtt	300
aaccacacca	gagtaaacgc	ggaagaaggt	caggttaccc	acgaatgggt	cggtagcaat	360
tttgaacgcc	agtgcagaga	atggctcttc	atcacttgcg	tgacgtcag	ccggagtatc	420
tttaccgtcg	tccaggatgc	cgttgatcgc	aggaacgtca	atcggggatg	gcaggtagtc	480
aactaccgca	tccagcatcg	cctgaacacc	tttgttcttg	aacgcagaac	cacaggttac	540
caggatgatt	tctgtgttca	gaacgcgtcg	acgcagagca	gatttgatct	cttgctcaga	600
cagttcttca	ccaccaggt	atctttccat	cagctcttca	gaagcttctg	ctgcggattc	660
gatcaggttc	tgggtgccatt	cgtcagccag	gtcctgcac	tctgccggga	tatcttcgta	720
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gataacgcgc	gtgaagcctt	cttcagcacc	aattgccagc	tgaagcggaa	cagggttcgc	840
gcccagacgg	gttttgatct	ggccaacaac	tttcaggaag	ttagcaccga	tacgggtccat	900
tttgttaacg	aacgcgatgc	gtggaacctt	atatttggtt	gcctgacgcc	atacggtttc	960
agactgtggc	tgaacaccac	caactgcgca	ataaaccatt	accgcgcggt	caagaacacg	1020
catggaacgt	tctacttcga	tggatgaagc	aacgtgccct	ggggtgtcga	tgatgtttac	1080
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<210> 206

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 206

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ccaaaacggt	cacgcgcgc	tttcacggag	ttcaggatgg	tgtaaccgga	gttaaccaca	180
ccagagtaa						189

<210> 207

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 207

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gccgcattta	ttgtggctat	caggggaaacg	gtcacacaag	cagtattggt	aggtcttgcg	120
gcgacaattt	ctcatacctc	tattgtcttg	ctcattgcac	tgggcgggat	gtatatccgt	180
cagaaattta	cggcagaatc	agccgaaccc	tggttccagc	tgatttcagc	catcattatt	240
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gagcaggaag	atgagcatgg	ccacgttaat	caccctcatg	atgaaacccg	cgtcattgat	360
accggtcatg	gcagcgttga	actctcaatt	ttcgaagaag	gtcagccacc	ccactggcgt	420
ttacgctcgc	tcagtggcag	gaaatgggag	gccagcgata	ttactctggt	cactaaccgg	480
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catgtacacg	actatgatgt	ggagtccgc	gagcatgac	ataaccacga	tcactccgca	660
cttgagggac	ttgatgttag	ttactcgag	tatcaggacg	cgcacgaaaa	agcacatgct	720
aacgacatca	aaaaacgctt	tgctaatagc	agcgtaacaa	ccggacaaat	tatcctttct	780
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<210> 208

<211> 447
 <212> DNA
 <213> Enterobacter cloacae

<400> 208
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 gaaccagtc acatcacggc ccttcagctc atcccgtttc tctgcgccac gataaccgcg 240
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 ttcatagcg ggggtggcca ccagcgtatg agtaaggccg ctttcagcat cgactccaat 360
 atgagccttc atgccaaagt gccactgatt tccctttttg gtctgatgca tatcggggtc 420
 acgctgtttg tttttattct tggttga 447

<210> 209
 <211> 987
 <212> DNA
 <213> Enterobacter cloacae

<400> 209
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 cagcgtgacc ccgatatgca tcagaccaa aaaggaaatc agtggcactt tggcatgaag 540
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 aatgaacatg acctgaacca attgaataat cttctgcacg gtgacgaaga attgtctcc 660
 gccgatgcgg gttatcgtgg ccgagagaaa cgggatgagc tgaaggaccg tgatgtggac 720
 tggttcatcg ctgaacgtcc agggaaagtc aggatattga aaaagcacc cgcgaaaaac 780
 aaagcggcca tcaaacctga atacctgaaa gccagcatca gggcaaaggg ggagcaccgc 840
 tttaggggta ttaaacgtca gtttggtttt atcaaagcac gctacaaggg gctgatgaaa 900
 aatgactcac agttagcgat gctattcacg ctagcgaacc tgtttaaagt ggatcagatg 960
 atacgacgac agactaaatc cgcctaa 987

<210> 210
 <211> 1032
 <212> DNA
 <213> Enterobacter cloacae

<400> 210
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 gtactggctg tgcctcacac ctccatcttt gtggtgaaag agggcgagcg tgggatcaag 120
 ttccagtcca gcagcgtcgt gcgtgacggc gacaagcgtc cggtgattta tgagccgggt 180
 ctgcacttta agatcccgtt cattcagtcg gtgaaaacgc tcgatgcgcg tatccagacc 240
 atggataacc aggcgcgatc tttcgtgacc aaagagaaga aagacctgat cgttgattcc 300
 tatatcaaat ggcgcatcag cgatttcagc cgctacttcc tggcaaccgg ggggtggcgac 360
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 cgtgatgcga tgaactccgg ctctgcgggc accgagatg aagttgaaac cccggcgcca 540
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 gtgatcaacc cgaacagtat ggccggcgtg ggcacgaag tggttgatgt gcgcatcaag 660
 cagatcaacc tgccagcgga agtgccgag gcgatctaca accgtatgcg cgcgcagcgt 720
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 gacttctatg ctttcattcg tagcctgcgc gcttacgaga atagcttcaa gagcaaccag 960
 gatgtgatgg tgctcagccc ggacagcgat ttcttcggtt atatgaagac gccgaccaac 1020

gcaacgcgat aa

1032

<210> 211

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 211

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tataagacc	agaccatcct	ggaagcacag	ggtgaagtgg	ctcgcttcgc	gaagatcctg	180
ccggaatata	aagccgcgcc	ggaaattacc	cgtagcgctc	tctatatcga	gaccatggaa	240
aaagtgtctga	gccatacgcg	taaagtgtctg	gttaacgaca	acaaaggcgg	aaacctgatg	300
gtcctgccgc	tggatcagat	gctgaaaggc	ggttctgcac	cggcagcaaa	agacaacagc	360
ggtgcgaaca	acctgctgcg	tctgccaccg	gcctcctctg	gcagcgccag	tgogaacaca	420
acgccttctt	cgaacgatgg	tgacattatg	gaccaacgcc	gtgccaacgc	gcagcgtaac	480
gactaccagc	gtcaggggga	ataa				504

<210> 212

<211> 909

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (756)

<220>

<221> unsure

<222> (764)

<220>

<221> unsure

<222> (765)

<220>

<221> unsure

<222> (766)

<220>

<221> unsure

<222> (767)

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nnnnnnnnnn	nnnnnnnnnn	tactaacggg	cccaggcacc	aggtccatgc	caaaatgggc	840
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<210> 213

<211> 2229

<212> DNA

<213> Enterobacter cloacae

<400> 213

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aaaagatag						2229

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<211> 279

<212> DNA
<213> Enterobacter cloacae

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 ggttggtgccc gtactgtgac taaagtaatt cagaaccttg atccggatgc tagcatcgta 180
 actgatcctc caactogtaa agttgagata caaacgttgt tatcggttga tctgatttct 240
 gatgctttgc gtgaagcagg ttccctcccg anggaatag 279

<210> 215
<211> 1152
<212> DNA
<213> Enterobacter cloacae

<400> 215
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 gcgataacgg ccgagtattt ggtgacggcg gcgggttacc atttcgagga gaaccgctac 180
 gcgatcggtg agggggagac cattcacgcg accgatttca gcgtcattcc ggcgtcgggtg 240
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 attaacagct aa 1152

<210> 216
<211> 1092
<212> DNA
<213> Enterobacter cloacae

<400> 216
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 gctcgaaaagg gtgatacgtt atcctgctcg accgacggca gcgggtattat tgtggggggc 180
 tccgggtactg tcttcgttaa cgggtatgcc cttgcacgtc aaggagacaa gacgaagtgt 240
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tttaagccta	tactggattt	ctttgactat	ttgtatggcg	aagaggatga	gccagccgtc	1020
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ataggcgatt	aa					1092

<210> 217

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 217

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ggagagctat	gcgtatgtga	tctctgcacg	gcgctagagc	agtcgcagcc	taagatctcc	180
cgatcatctgg	cgatgctacg	tgaagcgga	ttgttgctgg	atcgcaagaa	tgggaaatgg	240
gttcaactacc	gcttatctcc	gcataatcct	tcatgggctg	ctcagggttat	tgagcaggcc	300
tgggttaagcc	aacaggacga	cgtacaggcc	atcgcccgtg	agctggcatc	agctaactgc	360
tctggtagcg	gcaaagctgt	ttgtatctaa				390

<210> 218

<211> 393

<212> DNA

<213> Enterobacter cloacae

<400> 218

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acctctattt	cctgtgccac	cgtatcagc	ctggcggaac	aaggcaagcg	ggttttgctt	180
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gccaggaat	atcgggccag	aatogttgat	cctatcaaag	gcattctgcc	ggagtcttca	360
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<210> 219

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 219

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acacggccaa	agttaatcga	atttttggcg	acatgccccg	ctacaaccat	cgcaatggaa	180
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ctgatatac	cacaatttgt	cgtccattc	gttaaaagta	acaaaaacga	gttcgtcgac	300
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<210> 220

<211> 954

<212> DNA

<213> Enterobacter cloacae

<400> 220

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tgtaaaagtc	ctcgcgaagt	tatggagtta	actaataatc	gagatgatct	gtctgcactg	180
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aaccagctc	gcatagttcc	tttagaagta	caggatgcgg	cccgggaaaa	tatgcagcag	900
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<210> 221

<211> 1770

<212> DNA

<213> Enterobacter cloacae

<400> 221

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atgttcagga	taacaaactg	cgtgtgcac	tgtatcacac	attcctttga	aaaattattt	1740
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<210> 222

<211> 1548

<212> DNA

<213> Enterobacter cloacae

<400> 222

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gttaatttaa	aagttcgtcc	tcactctatt	catgcattaa	tgggtgaaaa	cgggtcgggt	180
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ggtcgttatc	caaccaaagg	tgtctttgtc	gatcaggata	aaatgtatcg	cgacacccaaa	420
gccatttttg	atgagctgga	tattgatatc	gacccgcgcg	cccgcgtcgg	gacattatcc	480
gtttccocaga	tgcagatgat	cgaaattgcc	aaagcgttct	cctatgatgc	gaaaattgtg	540

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atccgtgaga	aagccgaagg	caccattacg	ctgcacggta	agaagatcaa	caaccacaac	1020
gccaacgaag	ccattaataa	tggttttgcg	ctggtgacgg	aagagcgctg	ttccaccggt	1080
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tccatgcgcg	tgaaaacgcc	gggccacgcg	acgcaaattg	gctcactttc	gggaggaac	1260
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gaacctacgc	gcggtatcga	cgtgggtgca	aaattcgaga	tttatcagct	tatcgagag	1380
ctggcgaaaa	aagataaagg	gatcattatt	atttcttccg	aaatgccgga	attgttaggg	1440
atcacagacc	gtattctggt	tatgagcaat	ggtctcgttg	ccggtattgt	tgaaaccaaa	1500
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<210> 223

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 223

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ggcggatatt	acgttggtt	tttagtctt	ctggcgatta	ttattttcca	ggaccctacg	120
ttcttaagtc	tgtgaaact	gagtaacatt	ctgaccacgt	cttccgtacg	tattattatc	180
gcgcttgccg	tgccggga	tatcgttacc	caggggactg	acctttcggc	agggcgccag	240
gtgggtctgg	cggcggtcat	tgcggcgacc	ctgttgacgt	cgatggaaaa	cgccaacaag	300
gtattcccg	agatggcgac	catgcgatt	ttcgtgggtga	tctgatcgt	gtgtgccatc	360
ggcgcggtaa	ttggcctgat	taacggcatc	atcattgctt	acctgaacgt	gacgccattc	420
atcactacgc	ttggcacgat	gatcactggt	tatggtatca	actccctgta	ctacgatttc	480
gtcggcgcg	ctccaatctc	tggcttcgac	agcggcttct	cgaccttcac	gcaggggttt	540
gttgcgctcg	gcagcttccg	tctctcctat	atcaccttct	atgcgctgat	tgcggtggca	600
ttcgtctgga	tctgtggaa	caaaacccgc	ttcggtaaaa	acatctttgc	tatcggcggt	660
aaaccggaag	cggcggaagg	ctccggggtc	aacgtggctc	tgaacctgct	gatgatttat	720
gcctgtccg	gggtcttcta	cgccttcggc	gggatgctgg	aagcaggccg	tatcggtctc	780
gcaaccaaca	acctgggctt	tatgtaacga	ctggatgcga	ttgcggcctg	cgtgggtggc	840
ggcgtctcct	tcagcggcgg	cgtgggtacc	gtgctggcg	tggtgaccgg	tgtgatcatc	900
ttcaccggtta	tcaactacgg	cctgacctac	atcgggtgta	acctgtactg	gcagtacatt	960
atcaaggggtg	cgatcatcat	cttcgcgggt	gccttggtat	cactgaagta	cgcgcgtaag	1020
aaataa						1026

<210> 224

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 224

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toatggatc	taagtacctt	tcgggagtg	ggtagctggc	tgaacgaaga	gatcgagcag	120
gaacagggtt	ctcctggcac	atttgcgatg	tggtggctgg	gctgcaccgg	gatctggctg	180
aaatcagaag	ggcgcgccaa	catttgtggt	gatttctggt	gcggcaccgg	caaacagagc	240
cacggcaatc	cactgatgaa	aaaaggccac	cagatgcagc	gtatggccgg	cgttgaagaa	300
ctccagccga	acctgcgcac	cacgcctttc	gtgcttgatc	cttttgccat	tcgccagatc	360
gacgcggttc	tctctaccca	cgatcacaa	gatcatatcg	acgtgaacgt	ggcggcagcg	420
gtaatgcaaa	actgcgcgga	cgacgtaccg	tttatcgggc	cgcagacctg	cgtggatttg	480
tggattggct	ggggcggtgc	aaaagagcgc	tgcactgtga	tgaagccggg	cgacgtgggt	540
aaaatcaaag	acattgagat	tcacgcgctg	gatgcctttg	accgcaccgc	gctgatcacc	600
ctgcctgcg	atcagaaagc	cgcaggcgta	ctgccagacg	ggatggacga	gcgcgcagtg	660
aactatctgt	tcaaaacgcc	tggcggttcc	ctgtatcaca	gcggtgactc	ccactactcc	720

aactactacg	cgaagcacgg	taacgagcac	cagattgacg	tggcgcttgg	ctcttacggt	780
gaaaacccgc	gcgggatcac	cgacaaaatg	accagcgcg	atatgctgcg	tatggccgaa	840
gcgctgaaaa	cccaaattgt	gaatcccgtc	caacaa			876

<210> 225

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 225

caccaaccac	acagggattg	ccccttgtgt	tctcattttc	tggagagagt	tatggagatc	60
ctctacaacg	tcttttacgt	tttctttaat	caggtaatga	ccaacgcccc	gctgttgctg	120
ggtatcgtga	cgtgcctggg	gtacatcctg	ctgcgcaaaa	gcgtcagcgt	gattatcaaa	180
ggcaccatca	aaaccatcat	tggttttatg	ctgttgcagg	cggggctctg	cattctgacc	240
agcaggttta	agccggttgt	tgccaaaatg	tcagaggtgt	acggcattaa	cggcgccatc	300
tctgacactt	acggtccat	gatggccacc	atcgatcgca	tgggagatgc	atacagctgg	360
gttgggtatg	cggtaactgt	cgcgctggcg	ctgaacatca	tttacgtgct	cctgcgccgt	420
atcacccgta	ttcgcaccat	catgtccacc	gggcacatca	tgttccagca	ggcgggtctg	480
attgcggttt	ctctctatat	cttcggctac	ccaatgtgga	ccacggtcat	ctgcacggca	540
gtgctggctc	cactttactg	gggcacaccc	tccaacatga	tgtataagcc	aacgcaggac	600
gttacggacg	gctgcgggtt	ctccatcggt	caccagcagc	agttcgccct	ctggattgct	660
tacaaagtgc	cgcggtacct	gggcaaaaaa	gaggagagtg	ttgaagatct	caaattgcct	720
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ttcggcgcca	tgtcttcaca	cacg				804

<210> 226

<211> 388

<212> DNA

<213> Enterobacter cloacae

<400> 226

accgcgcgt	ccagcctgcc	gcgaggccat	gacatgcgag	gtgactgtcg	gcggtgccag	60
cctgcgtctg	tcgggggatt	tatcacctgc	acttctgaaa	acgctgatcc	gcgagctgac	120
cgggaggagc	cgatgatacc	cttacccgtc	ggcactcgta	tctggctggg	tgccggggtc	180
accgatatgc	gtaagtcctt	caatggtctg	ggcgaactgg	tccagcatgt	tcttgatgac	240
aatccgttct	ccggccacct	gtttatcttc	cgtggctcgt	aaggtagacac	cgtgaggatc	300
ctctgggctg	atgctgacgg	tctgtgtctg	tttaccagac	ctctggaaga	gggactgtct	360
acacgcgcgg	atggaagaga	gaaagtgg				388

<210> 227

<211> 420

<212> DNA

<213> Enterobacter cloacae

<400> 227

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gcgcgggata	atggaattaa	tgacaatctg	ctgtttacct	ggcgccagcg	ttacagacat	180
cttctgcccg	atgaaataca	acggtcaatc	agagagcaag	actctgttat	ccccgttgtc	240
ctgcttgata	tggccctgtc	acaccatgct	gagccgcact	atgaacccgc	cgtccagcc	300
tgcgcgaggg	ccatgacatg	cgaggtgact	gtcggcggtg	ccagcctgcg	tctgtccggg	360
gatttatcac	ctgcacttct	gaaaacgctg	atccgcgagc	tgaccgggag	gagccgatga	420

<210> 228

<211> 633

<212> DNA

<213> Enterobacter cloacae

<400> 228

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aacaataaag	gtggctctgg	taagaccagt	tcggctacca	atctggctgt	tcactatgcc	120

agatcagggg	agcggacgct	gttgattgac	tccgaccagc	aggccaatac	gacagaagtc	180
accgcaaagt	gtaaaaagta	ctattccatg	tatgggtccaa	ctatttgcca	tctctacagc	240
aattctcgat	ttgatatccg	cgatgtcatc	atccccgcga	tggccgggtga	tgctcctatc	300
cctaacctgg	atctgattcc	gtctgacccg	acgttcgaaa	aaattattga	acagaccctt	360
accgcgagtc	accgcgaaaa	aatcctgggc	cgatcatctcg	agaaagtctg	caactgaatat	420
gattacatca	ttattgactg	tgcacctggg	ctcaatatcg	caaccggcaa	tgcaattttt	480
atcgccgagc	atgttctggg	acctgtcgat	ggcgggagtt	tttctctgag	tggtcttgaa	540
atcatgctgg	actatatgga	tgagatctct	gaggaagatt	atgcacgctt	cagtgtcttc	600
accacagagc	gcgacggatc	cgcgctagaa	tat			633

<210> 229

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (82)

<400> 229

acctgttca	tattgggagc	aaatatggac	cgcgtctctc	atthttgtcct	ggcacttggt	60
gtcgttactg	cacttgcaatt	gntgggtcagc	acagaccgca	aaaaaattcg	tatgcgctat	120
gttggtccagc	tgctgggtcat	tgaagtttta	cttgcggtggt	tcttctctgaa	ctccaacgta	180
ggcctcggtc	tcgtgaaagg	cttctccgaa	atgttcgaaa	aactgctcgg	atttgccaac	240
gaagggacca	acttcgtctt	tggcagcatg	aacgatcagg	gcctggcctt	cttcttctctg	300
aaggtactct	gccctatcgt	cttcattctct	gcctgatcgt	gtatccttca	gcacatccgc	360
gttctgcggg	tggttatccg	tgcgatccgg	ttcctgttat	cgaaagttaa	cggcatgggt	420
aaactggaat	cttttaacgc	agtcagctca	ctgatcctcg	gtcagtcctga	gaacttcatt	480
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gcaatgtcta	cgttttccat	gtctatcgtg	ggcgcgata	tgactatgct	ggaacctaaa	600
tacgtgggtg	cgggccctggt	tctgaatatg	ttcagcacct	ttatcgttct	ttcgctgatt	660
aaccggtacc	gcgtggatgc	cagcgaagag	aacattcaga	tgtctaacct	gcacgagggg	720
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cgtgcggaag	ggactcctgtc	cgtcttctctg	gtctccttcg	cgaacttctc	ttccatcggt	1080
atcatcgctg	gcgcgattaa	aggcctgaac	gaagagcagg	gtaacgtggt	ttctcgcttt	1140
ggcctgaagc	tggtttacgg	ttcaacgctg	gtgagcgctc	tgtctgcctc	tattgcagca	1200
ctggttctgt	aa					1212

<210> 230

<211> 651

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (249)

<400> 230

aattttgaaa	tcctatttcc	aggtttgaaa	agcgattggc	gagatcatcc	acctctgacg	60
gtttttatttc	cgggtgattgg	tcattttaaac	ttgagcaacc	ggttgaaactt	gaagttgttg	120
gaaaaattgt	tgatctggat	gcgcagcaat	cgggtccggac	gtgcaggaaac	gcgtttctcc	180
gtcaaatctg	tgcgcgtgac	gctgatgcaa	aatgagattg	cggctgagat	cattgccttt	240
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ttctcagact	cgggaagcag	catcaaaaaat	attcagcagc	tgcgtgatta	cggcttccgc	360
attgccatag	acgaactttg	taccggctat	gccaaactttg	agcgcttgaa	gcggctggag	420
gccgatataca	ttaagatcga	tggttgcttc	gtgaaagata	tctgcaccga	cagcatggat	480
gcgatgatcg	tgcagtcctat	ttgcaacatg	gcaaaaacga	aatcgctgtg	tgtggtggct	540

gaatatgtgg	aaacggctga	acaacgcgag	atgttggttc	gatttggcgt	agattatttg	600
cagggtatt	tgattggtaa	accccagcct	ctgacggcgc	tggaagcata	a	651

<210> 231

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 231

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cagccattgt	cactggataa	tgtggcggca	aaagcaggct	attccaagtg	gcattctgcaa	120
aggatgttca	aggatgtcac	cggatcatgt	atcgggtgct	atattcgcgc	acgtcgttta	180
tcaaagtctg	ctgttgcggt	gcgcctgacc	gcgcgaccaa	tccttgatat	tgccctgcaa	240
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ctgggcgagt	ttgcgatgcc	aaaatatgaa	atcatcaccc	tgccagaaac	gcacctggtc	420
ggcaccacgc	agagctactc	ctgttccctt	gagcagatct	ccgagttccg	ccatcagatg	480
cgcgttcagt	tctggcgoga	atttttaagc	catgctccgg	cgatcccgcc	gattctgtat	540
ggtttgaacg	aaacgcaccc	aagccaggaa	aaagatgacg	agcaggaggt	gttctatacc	600
acggcgctga	cgcctgatat	ggcgaacggg	tacattcatg	gctcgaagcc	tgctcgtgctg	660
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atcctgaccg	tttaacgggac	ctgcatgccg	atgctgaatc	tgaatcgccg	taaaggctcag	780
gacattgagc	gctactatcc	ggcgcaagat	gctaaaccgg	aagaaggccc	tatcaatctg	840
cgtatggaat	tcctgattcc	ggtacgtcgt	ttaa			873

<210> 232

<211> 201

<212> DNA

<213> Enterobacter cloacae

<400> 232

ctcatggaga	gcgaagcgcg	cgccttcac	gcgctggtag	atgagtttta	cgagcgccac	60
gttaagctgg	tggtcagcgc	cgaggtgctt	ttatatgaga	tctatcaggg	cgagcgcttg	120
aagtctgagt	tccagcgctg	cctgtcgcgc	ctgcaagaga	tgcaagagca	agagtacctc	180
aagcgtgagc	atatgccgta	a				201

<210> 233

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 233

ggctccgcta	ccaggccggg	taagagacca	aagttggacg	aagatgagat	tggaacagcg	60
ttgctgagca	ttccctgcgt	cgaacactg	acagcgagta	ctatttcaac	tgagattggc	120
gacgggaagc	agtacgccag	cagtcgtgac	tttgccggcg	caacagggct	agtgcctcga	180
cagtacagca	cgggaggtcg	gacgacattg	ctgggaatta	gtaagcgagg	taacaaaaag	240
atccgaactt	tggttggttc	atgtgccagg	gtattcatal	aaaaactgga	acaccagtct	300
ggcaaatggg	cagattgggt	cagggatcta	ctgtgtagga	aaagcaactt	tgctcgtcact	360
tgtgctctgg	caaacaagct	ggccagaatt	gcctgggccc	taacggcacg	acagcaaaact	420
tatgtagcat	aa					432

<210> 234

<211> 882

<212> DNA

<213> Enterobacter cloacae

<400> 234

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ctaacaaaaa	tttgcgatac	tttcagttag	attcacggca	cagaacgatt	tcctgttaat	120
gttgagggaat	tgtctctgga	ggcggcagag	ttgttcaaat	gggctgaccc	tatagtaaaa	180
atagaaccgc	ttgacatcaa	aggatttgat	ggtgcattaa	tgccaatga	atctcgacgc	240

cgttggatgc	tactttacaa	taacgggttta	acatcccctg	gtagaattcg	attcactcag	300
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gaaatgaaaa	tacattcaga	acagtatgaa	tatgtcatca	cccttcta	cccttcccga	840
aaaacaactg	tatggcctcc	ttttcatggg	gaagatgagt	aa		882

<210> 235

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 235

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atcagtatcc	tccgcgaagc	cgaagctggg	gtaccgcgcc	gtgaactctg	ccgcaagcat	120
gccatttccg	atgccacgtt	ttacatctgg	cgtaagaagt	atggcgggtat	ggaggtgcct	180
gaagttaagc	gcctgaagtc	gcttgaggaa	gagaacgcca	gactcaagaa	gctgcttgcc	240
gaagccatgc	tggataaaga	ggcgcttcag	gtggctcttg	ggcgaaagta	ctga	294

<210> 236

<211> 185

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (171)

<400> 236

agaggcgctt	caggtggctc	ttggggcga	gtactgacga	cagaccaaaa	gcgggaaacc	60
gtgatgttga	tgtgtgatgc	gaacggctct	tcgcaacgct	gtgcctgcag	gcttacaggt	120
tttatcctgt	cgacctgcgc	ctatgaggct	caacgtccgg	ctgctgatgc	ncatttatca	180
gggcg						185

<210> 237

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 237

aacctcaatt	tttgccacat	cagcctaact	gtcctatctg	caatgaacat	aactgagtta	60
gtttttatag	atgatgatta	caatcatgtc	gtcatcatga	gtgatgttgt	gcagcggtta	120
cattttatata	gtcaattaca	ttatgccagt	accgaggcag	gaggaaccct	tattggagaa	180
cgtcgaggga	aacatattgt	catcactcac	atatcagaac	ctggatcagg	tgatgtaaga	240
tcgcgaacac	gaatagaaag	aaaaggagaa	catcatcagc	aaaaagtgg	tgacttattt	300
cagcaatcag	atggttctct	agtctatttg	ggcgaatggc	atacgcaccc	cgaagatttc	360
ccacagccat	caagtactga	tatgaggtct	tggcgaaccg	gactgaaagc	gaccgagcca	420
atggttttgc	ttattatggg	taggaaacaa	gcatggtgtg	gtaaaaagca	tgggaatgtc	480
ataaaaaaat	tagaagaaaa	aaacaatcat	tga			513

<210> 238

<211> 1122

<212> DNA

<213> Enterobacter cloacae

<400> 238

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cttcacagta	aagactcagt	aatcaatcat	tatgccgac	gttatcaatg	ttatatgcca	120
attgatgtcc	gtaatggatt	aagaagcaat	agtatagatg	cgtcgaattc	atctctccca	180
tgggatgtaa	cattaccttt	agtcacgact	gaagatgttt	cacgtgataa	agcgcttggg	240
gcggttggtg	gattggctgt	tggggacgcc	gtcggcacca	ctcttgagtt	taagaaaaga	300
gacagtgaac	atgtagcaga	tatgattggt	gggggacctt	ttcaattaaa	acctggtgaa	360
tggacagatg	atacgtccat	ggcattatgt	ctggcagaga	cttatctttc	agaaaacaga	420
atgcacaccg	atgtgcttag	aaaatatctc	ctgaaatggt	atcttgacgg	agagaatagc	480
agtaatggtc	ggtgcttcga	tatcggcaat	acgacgcggt	tcgcgcttga	acagtatatg	540
cgtgtcggac	cttcctggta	tggtaataca	gagaaacaca	ctgctggtaa	tgctgggggt	600
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tcacaggctc	agagtgcgag	aacgcacggc	gcggtagaat	caattaacgc	atgccaaatt	720
ctcggattgg	tattgcacta	tttaatcaac	ggttatcaaa	aagaaggagc	tttttcgcct	780
catgttttcc	caactgtgcg	gcgtgtaatg	atcataaacg	cgggtgagta	taagcaaaaa	840
actcgcgacc	agattcgttc	aagtgggttat	gttatcgata	cgcttgaggc	tgcatgtgtg	900
tcogtatgga	atacggataa	tttcctgat	gccattctgc	tggcagccaa	ccttgccgat	960
gatgctgaca	gcgttgccgc	gacggcgggg	caaatacgcg	ggcgcttgta	tggttattcc	1020
gctatccgcg	aggactggaa	agataaactc	gtacaacacg	aacgtattgc	cacaatggcg	1080
ggtaaaactat	tcgatagagc	acctgaggat	aattttttat	ag		1122

<210> 239

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 239

tttgatacga	gccagggtgag	gatgagaacg	atgaaaaaat	gggcagtaat	tatctcagca	60
gtcgggttag	cggttgccgt	atcgggttgc	agcagcgact	atgtcatgtc	aacgaaagat	120
ggtcgtatga	tcttgaccga	tggcaaaccc	gaagtcgacg	acgataccgg	tctggtgagt	180
taccgcgacg	gcgaaggcaa	tcaaatgcag	attaatcgcg	acgaagtctc	ccagatcatc	240
gagcgctaa						249

<210> 240

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 240

aaaaggaaac	cggtatgca	ttatcatcgt	atccccaca	gcgctctgga	gatcagccaa	60
ctgggggttg	gcaccatgac	atttggtgaa	caaacacgcg	aagccgatgc	ccatgcacaa	120
ctcgattacg	cgctcagcca	gggcattaac	ctgattgacg	tggcggagat	gtaccccggt	180
cctccccgcc	cggaacaca	aggtcttact	gaaacgtatg	tcggcaactg	gctggcgaaa	240
cgcggaatc	gcgaaaagct	ggtcatcgcc	tccaaagtca	gcggaccttc	ccgtaataac	300
gatgcgggga	tccgccttaa	tcagatcctc	gatcgcaaga	atatccgtgc	ggcgctggat	360
gcaagcctca	agcgccctga	aaccgactat	ctcgatcttt	atcatgtgca	ctggccgcag	420
cgtccgacga	actgcttcgg	taagcttggc	tacacctga			459

<210> 241

<211> 324

<212> DNA

<213> Enterobacter cloacae

<400> 241

aacgaaagtg	ctcggccgt	taccctgctg	gaaacgctgg	aaacgctcac	ggagtgccag	60
cgggcgggta	agatccgcta	catcgccgtt	tccaacgaga	cggcggttgg	cgtgatgcgc	120
tatctgcata	tggccgataa	acacgatctg	ccgcgcacgc	tgaccattca	gaaccogtac	180
agcctgttga	aacgcagtta	tgaagtgggt	ctggcgagg	tgacgcagta	cgaagagggtg	240
gagctgctcc	cccaactcct	gtctgggctt	cggtagcctg	acgggcaaatt	acctgaacgg	300
cgcgaaaccg	gctggcgcgc	gtaa				324

<210> 242

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 242

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tccctcccg	tcagtgaagc	ccagttgctc	cagcaggcgc	aacgtctggc	aggctattca	120
ctgggcgagc	tggccgtgat	ggcggggttg	acgataccca	acgatctgaa	gcgtgataaa	180
ggctggatcg	gcgtgttgct	ggaacgctgg	ctggggcgaa	gcgcgggcag	taaaccgcag	240
caagattttg	cggcgctggg	ggtggaactg	aagacgatcc	ccatcgatag	ccaggggcgg	300
ccgttgaaaa	ccacctttgt	ctgcgttgcg	ccgtcacagg	gtaacagcgg	agtgacctgg	360
gaaaccagcc	acgtcaggca	taagctgaag	cgggtgttgt	gggtaccctt	tgagggcgac	420
aggcagatcc	cgtcggcaga	gcgtcgcgtt	ggcgccccgc	tgcctcggag	tccgaatgat	480
gaagaggaga	gactgctttc	ccaggactgg	gaagagctga	tggacatgat	tgtgctggga	540
caggttgagc	ggatcacccg	ccggcatggc	gaaatgctgc	aacttcgtcc	taaagccgcc	600
aatagcaaag	cgtcactcga	agcggtatgc	gcacagggcg	aaccgatcct	gacgtgccg	660
cgcggtttct	atcttaaaaa	gaatttcacc	ggggcactgc	tggcacgcca	cttcctgttg	720
aaaacatag						729

<210> 243

<211> 375

<212> DNA

<213> Enterobacter cloacae

<400> 243

cgcagtacga	agaggtggag	ctgctccccc	aactcctgtc	tgggcttcgg	taccctgacg	60
ggcaaatacc	tgaacggcgc	gaaaccggcg	ggcgcgcgta	acacgctttt	cagccgcttc	120
acccgctata	gcggcgagca	gacgcaaaaa	gccgttgccg	cctacgtgga	tatcgcgaaa	180
cgccacggag	tcgatccggc	gcagatggcg	ctggccttcg	tgcgtcgtca	gccatttgtg	240
gcgagtaccc	tgctcggcgc	aacgacgatg	gatcagttga	aaaccaatat	tgagagtttc	300
aatctgaacc	tgagtgaaga	ggtattagcg	gagatagaag	cgggtgcatca	ggtttatacc	360
tacccggcac	cgtaa					375

<210> 244

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 244

accgtcgcgc	gctgcatgcc	tgcgggggac	gtgattggcg	tgcgcgttct	gttctttctcc	60
ctgcaacatg	ccctattgcc	tgcctatgcc	ctgctgttgc	tgatcggcat	gttagggcgt	120
ttctttgttg	tgcgcgtaaa	cgcgctgttg	caggagcgcg	gcaagcagac	cgttggggcg	180
ggtaacgcca	ttgcgggtga	aaaccttggt	gaaaacatgg	cgatgttgct	gatgctgggg	240
atttactcgc	tggcggtaaa	agcagggtgc	ccggtcgtgg	caatcggggg	aggattcggc	300
gcgctgttcg	cgtcggcgat	tagcgggctg	tgggtctggc	agcgtcgtcg	ttga	354

<210> 245

<211> 915

<212> DNA

<213> Enterobacter cloacae

<400> 245

agtcggggtg	gaggaatgat	gcgaatgaag	agaaatttga	aggccatacc	tgttctggtc	60
gccggtttgt	ttacctcaca	gctttctatt	gcggcgggct	ccgtctctgc	agatccccac	120
gccgggcacg	acatgtctgc	catgcagatg	ccagcagatg	agaatttcac	tgagatgacg	180
tcaatggagc	ccattgtaac	tgagagcaga	acgccaattc	cgctgttac	cgatgccgac	240
cggaaaggctg	cattcggcaa	tttacagggg	catgcgattc	acgacagtgc	gattaattat	300
ctggttctgc	tggatcaact	ggaatggcaa	cggtcggata	acaccaacaa	tttcagctgg	360
agtgttaaca	gctggattgg	aggcgacaca	gatcggattt	ggctaaagag	tgaaggtgaa	420
cgaagcaatg	gggaaacgga	ggcggctgaa	gcgcagttac	tctggggaca	tgcggttggc	480
ccatggtggg	atttggttgc	gggtgtcagg	caggatttca	gacctgcttc	tgcccggacc	540

tgggctgctg	tcggttttca	ggggctggca	ctctataatt	ttgagtctga	aattacgggt	600
tttgtcagta	atggcgga	agcagccctt	cgtctgggag	gagaatacga	cgttttactg	660
actaaccggc	tcatactcca	gccatcctat	gaggtgaatt	tctacagtca	ggatgatgaa	720
tcgcggggtc	gcggcagggg	actgactgac	acagagctgg	ggctccggct	gcgctatgaa	780
atacgccgtg	agtttgcacc	ctatataggg	gtttcctgga	atcaacttta	cgggaaaaca	840
tccgatatgg	cgaaaagaga	aggtgagaaa	gaccatcagg	tagtattcct	ggcgggagcc	900
agaatctggt	tttaa					915

<210> 246

<211> 420

<212> DNA

<213> Enterobacter cloacae

<400> 246

cgactgata	taaaacactc	aactaaacag	gtaaataaaa	tgtcgatttt	aaataaagcc	60
attcttacag	gtggcctcgt	tatgggcgtt	gctttctctg	ctatggccca	tccggaatta	120
aaaagctctg	tgccacaggc	tgattcagcc	gtagcggccc	cggaaaagat	tcagcttaat	180
ttctcgga	atctgaccgt	gaaattctca	ggtgcaaaat	taacgatgac	gggtatgaaa	240
ggcatgtcat	cacattctcc	gatgcgggtc	gcggcaaaag	tggcgccagg	cgctgaccct	300
aaatcgatgg	tcattattcc	gcgagagcct	ttaccgcgtg	gcacttatcg	tgttgactgg	360
cgcgcggttt	cttcagatac	gcaccctatt	accggtaatt	acacctttac	agtgaagtaa	420

<210> 247

<211> 1473

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (2)

<400> 247

anacatttta	tgggcgtaca	gcctgatgat	acctacgttt	acacctttta	ggttaagcag	60
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gccattatca	tcgatgccgg	ggagccagaa	ccgtttactt	acgatcgtga	gcattgtggtc	180
atgtttgtctg	actggaccga	tgaaaatcct	cacagcctgc	tgaaaaaatt	aaaaaaacag	240
tcggattact	acaatttcaa	taaaccaacc	gttggctctt	ttttccgcga	cgtgaatacc	300
agggggctgt	cagccaccat	tgcgatccgg	aaaatgtggg	ctgaaatgaa	aatgaatccg	360
actgacctcg	cggatgtcag	tggctacacc	tacacctatc	tcatgaacgg	gcaggccccg	420
ctgaaaaact	ggaccggact	gttcctgccc	ggtgaaaaga	tacgcttacg	gtttatcaac	480
ggctcgca	tgacctattt	cgatatccgt	atccccgggc	tgaaaatgac	ggtcgtggct	540
gcagatggcc	agtatgtaaa	cccggttacc	gttgacgaat	tcaggattgc	cgttgccgaa	600
acctatgatg	tcattgtgga	gcctcagggt	gaggcctata	ccatcttcgc	acaatccatg	660
gacaggaccg	gttacgctcg	agggacactg	gccacgagag	aggggttaag	tgctgccgtt	720
ccccccctcg	atccccgtcc	tctgttgacc	atggaagata	tgggtatggg	gggaatggga	780
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atgtctatgg	acggtgctga	ccttcgggat	agcgggacat	cctccgcgcc	catggatcac	900
agcagcatgg	cgggtatgga	tcattcccgg	atggccggaa	tgccgggtat	gcaaaagtcac	960
cctgcgtcag	aaacggataa	cccactggtt	gatatgcagg	cgatgagcgt	ctctccgaaa	1020
ttaaatgatc	cgggtattgg	tcttcgaaat	aacggaagaa	aggttctcac	gtacgcggat	1080
ttgaaaagcc	gctttgagga	tcctgacgga	cgtgaacctg	gccgtaccat	agaactgcat	1140
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gcaccgggtgc	tgctgaaata	cgggtgagcg	ctcaggatca	cgctgatcaa	cgataccatg	1260
atgactcacc	ccattcacct	gcattggtatg	tggagcgatc	tggaaagatga	aaacggtaat	1320
ttcatggttc	gtaaacacac	aatagatggt	ccccctggta	caaaacgcag	ttacagagtg	1380
acagcagatg	cgcttgcccg	ctgggcgtat	cactgccatt	tgctctatca	catggaaatg	1440
ggaatgtttc	gtgaagtcgg	ggtggaggaa	tga			1473

<210> 248

<211> 273

<212> DNA

<213> *Enterobacter cloacae*

<400> 248

agtaatat	tgaacgacct	gattatgatt	gttatcggtt	ttcttcttta	tctggatttg	60
atggtaatat	ttggattgcc	atTTTTTcag	atatatggaa	taagcggtgt	cagacatgaa	120
acctataacc	tgactaattt	caggTcgTtt	ataactTTTtg	ctgTtgTtac	aggcatcatt	180
cttactggca	ttaatatgct	cctggTatct	aatgccatga	gtggagtaac	tgacctcaga	240
gaattatcca	tccatgttat	cgagatggTg	ata			273

<210> 249

<211> 1362

<212> DNA

<213> *Enterobacter cloacae*

<400> 249

acaaactcaa	acagctcgca	ggTtaatttt	tactatatac	agggcagTca	tgctgccctg	60
tcaggaggtt	ttatgttact	ggcaggagca	atTTTcatcc	tgaccatcgt	gttggTtatac	120
tggcagccga	aggggttagg	gattggctgg	agcgccatat	ttggcgcaat	actggcactc	180
atatctggTg	tagtacacat	taccgacatt	ctggTggTat	ggaatatcgt	ctggaacgcc	240
acagcaacct	ttattgccgt	gattatcatc	agTTTgctgc	tggatgagTc	tggctTTTTt	300
gaatggggcag	cattgcattg	ttcccgctgg	ggaaatggcc	ggggTcgccT	gctgTttact	360
tatatcgTtc	tgtcggTgc	tgcggtagca	gcgctattTg	ccaatgatgg	tgcagctctc	420
atcctgacgc	cgatcgTtat	tgccatgTtg	ctggctctgg	gattcagtaa	aagcgctacg	480
ctggcattTg	taatggctgc	agggTttatt	gccgataccg	ccagcctgcc	gctgattgtg	540
tcgaacctgg	tcaatattgt	ttctgctgac	ttcttccatc	tgggattcac	ggaatatgcc	600
tccgtgatgg	tgcctgtgga	tattgccggc	attattgcca	cgctggTgat	gctgcattctg	660
TTTTTccgca	aagatatccc	accgacctat	gatcTgaacc	gactgaaaga	accggctctt	720
gctatcaaaag	acccggcgac	gttcagaact	ggctggattg	tattaatcct	tctgctggTa	780
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gctatcctct	TTTTTgtggc	taaaaaaggT	catgccatta	acaccggtaa	agtccTgcgt	900
ggTgcaccgt	ggcagattgt	gattttctca	ctgggaatgt	atctggTtgT	ttatgggtTg	960
cgtaatgccg	ggctgacaga	atacctctct	ggcgTattga	atttattTgc	agacaaagga	1020
ctttgggctg	ccacattTgg	cacgggattc	ctgacagcat	tcctgtcatc	catcatgaac	1080
aacatgccta	ctgtattgat	tggcgcatTg	tcgatcgatg	gcagcaccgc	atcggtgtgc	1140
atcaaagaag	caatgattTa	tgccaatgtc	atcggtTgcg	atctgggacc	taaaattacg	1200
cctattggTa	gcctggcaac	gctactctgg	ctgcactgac	tttcacagaa	gaacatgaca	1260
atcacctggg	gatactattt	ccgcaccggg	attatcatga	ctctgcctgt	gctgTttgTa	1320
acgtggccg	cgctggcgct	acgtctctct	ttcattTtgT	aa		1362

<210> 250

<211> 279

<212> DNA

<213> *Enterobacter cloacae*

<400> 250

gatactgata	tgagcaacat	taccattttat	cacaaccag	cctgcggcac	ctctcgcaac	60
acgcttgaga	tgatccgtaa	cagcggtaca	gagccgaccg	ttattcatta	tcttgagaca	120
ccaccatcac	gcgatgaact	ggTtaaactt	attgcggata	tggggatcac	agtacgagcg	180
ctgctgcgTa	agaatgtcga	acctTTTgaa	gcgttagggc	tggcggaaga	ccgttttact	240
gatgatcagt	taatcgactt	tatggTaaagc	gtTaaagtga			279

<210> 251

<211> 336

<212> DNA

<213> *Enterobacter cloacae*

<400> 251

aaacagaaaag	gccatgtctc	tacgccaatg	atgcagcttc	aggatccgga	aagaacaaaa	60
gtattactgg	tactctgcc	ggaaacgacc	ccgTtctTg	aggctgcaaa	tttacaagcc	120
gatcttgaac	gtgcgggat	tcatccatgg	ggctggatta	tcaataacag	tctttccatc	180
gctgaaaccc	gttcccgct	gcttcgtcag	cgctcgcagc	aggaactgcc	tcaaatcgag	240

gctgtaaaaga	accagcatgc	taccocgtgtt	gcaactgggttc	ctgtttcttgc	ggcagagcca	300
accggtatag	acaaactcaa	acagctcgca	ggttaa			336

<210> 252

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 252

gatagcattg	cgtggatgcc	tcgccccgct	gtggtgaaaa	cgttggttcag	cgcagagcgt	60
gaaggtggcc	cgttgacaga	agcggcatgc	tgggctcatg	cgcggcgcaa	aatccatgac	120
gtctatatca	gcacccggac	ggccacagca	gaggaggctc	tgaagcgcat	cagttagtta	180
tacgcgatag	aagaggaaat	acgcggcctt	cggcatctc	agcggctggc	cgcagacgg	240
tcccgaagta	aacogttgct	gatatccctg	catgactggt	tggtagagaa	aagagccact	300
ctgtcgaaaa	aatcccggtt	aggcgaggcg	ttcgcttatg	caactgaacca	gtgggatgcc	360
ctgtgttact	actgcgatga	tgggtctggca	gagccggata	ataacgctgc	tgagcgcgcg	420
ctacgagcgg	tctgtctggg	caagaaaaac	tacatcttct	tcggcagtga	tcatggtggt	480
gaacgtggtg	ccctgctgta	tgggtctgac	ggaacgtgca	ggctgaacgg	tatcgatcca	540
gagggttacc	ttcgccatat	cctgagcgta	ttgcgggagt	ggcccatcaa	caaagtggcc	600
gaactgctgc	catggaacgt	agatctcacc	aataaatag			639

<210> 253

<211> 426

<212> DNA

<213> Enterobacter cloacae

<400> 253

agacagccgc	agcctgggttc	acagccgatg	cagacgcagc	tggtcacacc	gtctaacgat	60
ccgggccag	ttgcgcgggt	tgaacctgaa	ccggttcagg	aagatcagga	gcaggccgcc	120
accccttcag	agccacaggc	gcaacagccc	accggcattg	agcagcagtg	gcgttcgat	180
cgcgtagagc	ctgggaaaaac	tcttgcccag	ctgttccgcg	accacaattt	gccagcaacg	240
gatgtgtatg	ccatggcgca	agtgcagggg	gcaggcaagc	cgctcagcaa	cctgcaaaat	300
ggtcagatgg	tgcagatccg	tcagaacgcc	agcggcggtg	tgaccggggt	aacgatcgat	360
accggcaacg	ggcagcaggt	actgtttacc	cgccagccgg	acggcagttt	catcagagca	420
cgttaa						426

<210> 254

<211> 462

<212> DNA

<213> Enterobacter cloacae

<400> 254

gaggataaag	taatgcaagt	tattctgctt	gataaagtag	caaacctggg	cagcctgggt	60
gatcaggtaa	acgttaaagc	gggttacgct	cgtaacttcc	tggttccaca	gggtaaagct	120
gttcagctga	ctaagaaaaa	cgtagagttt	ttcgaagcac	gtcgtgctga	actggaagcc	180
aaactggctg	acgtttctggc	ggctgctaac	gctcgcgctg	aagcaatcaa	cgcactgggc	240
accgttacca	tcgcgtccaa	agctggcgac	gaaggtaaac	tggttcgggtc	catcggtacc	300
cgcgatatcg	ctgatgcagt	tactgcggca	ggcgttaaaag	tggctaagag	cgaagtctgt	360
ctgccgaacg	gcgtttctgcg	taccactggt	gagcacgaag	ttgacttcca	ggttcacagc	420
gaagtgttcg	ctaaactggt	tgttaacgta	gtagctgagt	aa		462

<210> 255

<211> 246

<212> DNA

<213> Enterobacter cloacae

<400> 255

attctggaga	ctagccatat	ggcacgttat	ttccgtcgtc	gcaagttctg	ccgtttcacc	60
gcggaaggcg	ttcaagagat	cgactataaa	gatatcgcaa	cgctgaaaaa	ctacatcacc	120
gaaagcggta	agattgtccc	aagccgtatc	accggtactc	gtgcaaaata	tcagcgtcag	180
ctggctcgcg	ctatcaaacg	cgctcgctac	ctgtctctgc	tgccgtacac	tgatcgctcat	240

cagtaa

246

<210> 256

<211> 957

<212> DNA

<213> Enterobacter cloacae

<400> 256

aacgcaat	ttt	tatgag	attt	gtcatg	gata	ctgctc	tgccc	acgcc	cgtct	tttgcc	60
cg	tcgaa	atg	tg	gcctatgc	ctgc	gccacg	ctct	gctgctc	tgct	tttggg	120
ccggcc	atta	aaagt	ggcta	cgaact	cttt	cagat	cgcga	ccgat	gatat	ccctcc	180
gtcgt	ctttg	ccggata	ccg	tttct	gttt	gccgg	cgcgt	tgct	gctgct	ttttgc	240
gcccag	cga	aacog	attgg	caggct	cacg	cccac	gcag	ttgg	ccagct	cacgat	300
ggact	gaccc	agacct	ccct	ccagta	cacc	ttct	ttttata	tcgg	cctggc	ctacac	360
ggggt	gaacg	gc	ccatcat	gaat	gccacc	gggac	cttct	tcag	cgtgct	gctgg	420
tttat	ctacc	acaac	gacaa	actc	agctat	aacaaa	acgc	tg	gggtgtgt	tctgg	480
gc	gggggtga	tgt	gggtga	cttcc	acagc	gggtta	agt	gtccag	tt	tgtgtg	540
ggt	gacggat	ttgt	gggtgct	ggcgc	ccttt	attct	ctctg	cggcc	acgct	ttacg	600
cgc	atttccc	agacc	gttga	cccga	cggta	atga	cggg	gat	agcg	ggg	660
gcggc	actgg	ttg	cgggagg	ctat	gccacg	ggcgg	gacgc	tg	gaggtg	ca	720
gc	gtgcgcg	tgt	ggggta	tctg	acgctg	ctct	catccg	tg	gcgttcgc	cctgtg	780
gc	gtgtctga	aagta	aaccg	cgtg	agtatg	attg	ccccgt	tca	actttgt	cata	840
gc	aggga	cgg	tgtct	ccgc	catt	tttctc	ggc	gata	aca	ttatg	900
attg	cgtctg	tg	ttgggtctg	ctc	ggggatc	tggt	gggtga	ata	aacggcg	tg	957

<210> 257

<211> 287

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (61)

<400> 257

cgga	acggct	gcaat	ggctg	gccg	caactgc	tgct	ggatgc	gctc	aaaatc	cagc	agggg	60
ntac	gcttct	gact	cacct	gagg	tgtgg	cg	ttgg	gtc	cacact	tg	cgctgt	120
cagg	gcagtc	gctg	ca	gcgt	atcct	tc	atg	ctgcca	gag	tcgtga	caact	180
cggt	aa	ccgg	gggtctc	aat	cgcg	agc	ttt	tactgac	gc	accag	tt	240
aac	actac	ct	gca	acgggt	gtc	ata	ccgc	cgttt	ccca	cct	ctga	287

<210> 258

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 258

ccg	accag	tt	actg	cgtatc	gaac	actacc	tgca	accggg	tgtc	ataccg	ccggt	ttccc	60	
acct	ctgaga	gagac	attat	gttt	tttag	tc	gact	cacact	gccat	ctcga	tg	gcctgg	120	
tat	caatccc	tg	cata	aaaa	tgt	ggacgac	gtg	ctggcga	aag	ccgcgc	gcg	cgatgtg	180	
aaat	tttggc	tg	gc	cgtggc	gacc	acgttg	ccgg	gttacc	gctcc	atgcg	tga	actgg	240	
ggc	gagcgcg	ataat	gtcgt	cttct	cctgc	gg	tgtgc	atc	cgtg	aatca	gg	atga	300	
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tc	attctcgcg	gg	attgtcac	gtt	ccgcaat	gct	gag	caac	tg	cgtgatgc	gg	cgcgctat	660	
gt	tc	cgctgg	atcgt	attct	ggt	ggaa	acc	gatt	ccccgt	ac	ctggc	cacc	720	
cg	cg	gca	aag	aga	atcagcc	ag	c	gatgacc	cg	gatgtcg	ct	gagtatat	780	
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873

<210> 259

<211> 1467

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(726)

<220>

<221>unsure

<222>(1401)

<400> 259

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<210> 260

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 260

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tcaaaaatgt	actccactga	cacgttcaaa	aactacaatg	agcctcatcg	taatctccgt	420
tctgcactcg	gcattgtgat	gagcctgtct	tcaaatattg	agagccttac	cggtagcact	480
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<210> 261

<211> 738

<212> DNA

<213> *Enterobacter cloacae*

<400> 261

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agccactggc	ggaaatggac	tcagtcocga	accctcaagt	tgcagaaccc	gtttaagcaa	360
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tatacggacc	ttactcatat	tcataacata	acgacaaagt	acaaagcccc	gatgaaattc	660
gagcaacgag	taacatacat	tctgtctaac	tttatccatt	atctgtgggc	aagtctgttc	720
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<210> 262

<211> 825

<212> DNA

<213> *Enterobacter cloacae*

<400> 262

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gaggcttttg	acgaaaaagc	cttagtagaa	gaggaaccca	gtgataacga	tttggctgaa	180
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ggggaaattg	gttactcccc	actgctaacg	gccgaagaag	aagtctatct	cgcacgtcgt	300
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cgcgagttgt	cccataaaact	ggaccacgag	ccaagtgcgg	aagagatcgc	agagcaactc	660
gacaaaccgg	ttgatgacgt	aagccgtatg	ctgcgtctca	acgagcgcgt	tacctcggtt	720
gacaccccg	tgggtggcga	ctccgaaaaa	gcgctgctgg	acatcctggc	cgatgaaaaa	780
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<210> 263

<211> 1095

<212> DNA

<213> *Enterobacter cloacae*

<400> 263

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tctacacgct	tgcattttga	aattcgttac	aaggggaaat	ccgtaaacco	gctgcaatat	1080
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<210> 264

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 264

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ggtaattatg	gaagagaaca	aacagaagaa	gaaccaccga	aaggcacagc	accagaaaag	180
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gaaaagctca	tctcagaaca	aaacaggagt	cccaatgaaa	aaagaaatat	cagcgagag	300
aaaaaacgcg	aatccgctca	actggctcta	gatcagaatc	acaccgttgc	agctgtctta	360
caccgacggg	gcaggaagga	aacgcgattc				390

<210> 265

<211> 1815

<212> DNA

<213> Enterobacter cloacae

<400> 265

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<210> 266

<211> 1029

<212> DNA

<213> Enterobacter cloacae

<400> 266

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<210> 267

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 267

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gactgcggcg	cctgcgcagg	cgagcggcag	ctacgtgggt	caggttggcg	ctgtcagcga	480
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<210> 268

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 268

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<210> 269

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 269

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cagtttggcg	tgcaggcccg	cgttgagcaa	aacggtgcgg	tatggcgtat	ccagatgggt	180
ccgtttgcc	gtaaatcgca	ggcagcatcc	ctgcaacagc	gtttgcagag	cgaggcgcag	240
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<210> 270
 <211> 1305
 <212> DNA
 <213> Enterobacter cloacae

<400> 270
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<210> 271
 <211> 687
 <212> DNA
 <213> Enterobacter cloacae

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<210> 272
 <211> 1161
 <212> DNA
 <213> Enterobacter cloacae

<400> 272
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<210> 273

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 273

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<210> 274

<211> 1197

<212> DNA

<213> Enterobacter cloacae

<400> 274

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 <211> 345
 <212> DNA
 <213> Enterobacter cloacae

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 aagtctcgtc tacagtgcga tgatgatgaa gggattatga ttgaacggttg tatagcgcgt 180
 ttacgcaaat ttaagtccga tgaatatgaa ctgttaatcg ctcatTTTTgt tattgggtatc 240
 tctctgagaa caattgcaaa gaaaaagaaa tgctcggatg gtactgtaag aaaagatctg 300
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<210> 276
 <211> 636
 <212> DNA
 <213> Enterobacter cloacae

<400> 276
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<210> 277
 <211> 651
 <212> DNA
 <213> Enterobacter cloacae

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<210> 278
 <211> 2436
 <212> DNA
 <213> Enterobacter cloacae

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<210> 279

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 279

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<210> 280

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 280

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<210> 281

<211> 1149

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (980)

<400> 281

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<210> 282

<211> 213

<212> DNA

<213> Enterobacter cloacae

<400> 282

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<210> 283

<211> 690

<212> DNA

<213> Enterobacter cloacae

<400> 283

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<210> 284

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 284

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<210> 285

<211> 492

<212> DNA

<213> Enterobacter cloacae

<400> 285

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goccttgctg	ctgcgcgcga	caacggtgaa	cccggccaaa	ttgccaaaac	gctgtcacta	180
aaaattaaaa	atgacgtgat	tctggtggtt	gcaaaaggcg	atgcgcgtct	ggataacaaa	240
aagcttaaaag	agacattcgg	cgcaaaagcc	cgcatgctca	gcagcgatga	ggtagtacc	300
ctgacaggtc	atcctgtttg	cggcgtctgc	cctttcggac	tggaaaacc	gctttctgtt	360
tactgtgaca	tcacattaaa	acaatacgcg	gaagtgttac	ccgcagcggg	cgccatccac	420
agtgcggtgc	gtatatcgcc	cgacagaatg	gcggaactga	ccgcagcaaa	atgggtagat	480
gtgtgcattt	ga					492

<210> 286

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 286

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acattattgt	taagcgtcat	tttaactata	ctggttacta	tcgcctgttc	tgtgccaatc	180
atcgttgcg	gaataattaa	gctcctgttg	cctgtccctc	cggtatggcg	cgcggtgtct	240
gcttttttga	attttatgat	gtactgctgg	tgtgaaggcc	tggcgatcct	gctgcattctg	300

aacccctggc	tgaagtggga	cgttcagggt	ctggagaagc	tgaacaaaaa	gaactggtat	360
ctgctgatct	gcaatcacca	cagctgggcc	gacattgttg	tattgtgcgt	actgtttcgc	420
aaacacattc	cgatgaataa	atactttctg	aaacagcagc	tggcctgggt	gcctttcatt	480
ggtctggcct	gctgggcgct	ggatatgccg	tttatgaaac	gctattcacg	cagctatttg	540
attcgctatc	cggaacgccg	cggtaaggac	gtggaaacca	cgcgcggttc	ttgcgagaag	600
tttcgcgcgc	atcccaccac	cattgttaac	ttcgtcgaag	gatcgcgctt	taccgaagag	660
aagcgccaac	aaactcgctc	tccttatcag	aacctgtttg	cgccaaaggc	tgcgggcctc	720
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aaaaacttca	aacgtcgttt	ccagcttttg	cttaatacac	tctggaaaga	gaaagacgag	960
cagatagcga	agattaaatc	ttcatacaaa	aacgcgggtc	agtga		1005

<210> 287

<211> 555

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (408)

<400> 287

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atgggtggaa	aggataaggg	acttcagctc	ctgaacaaca	caccattatg	gcagcatgtt	180
gctgatacgc	ttgcagatca	ggtgtcatcg	atggcgatca	gcgctaaccg	acatgttgat	240
atctatcagc	gcagcgggta	tccggtttat	caggataacc	tggcgggacta	ccccgggtccg	300
ctggcgggaa	tgctttctgt	tatgcagcag	tcgtacggag	agtggtttct	cttttgtcca	360
tgtgatacgc	ccttcatccc	gtcctgtctg	gttgaacgtc	tgggtgcancg	gcgcggtggt	420
gctcccgtcg	tctgggtaca	cgacggtgaa	cgcgaacatc	caacgatcgc	attgattaat	480
cgctcgttaa	tatccgcgct	gggagctatta	ctggccgcag	gagatcgacg	cgttctggta	540
tttatgcccc	cattc					555

<210> 288

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 288

cgtgtctctc	taaatgaaag	gagcactacc	atgaaatgta	aacgtcttaa	tgaagtcatc	60
gaactttctc	agccggcctg	gcaaaaagag	ccagagctga	atctgatgca	attttttacag	120
aaactggcga	aagagtcagg	ttttgatggt	gaactggcgg	acctttctga	cgacatcctg	180
atctaccacc	tgaaaatgcg	tgactcggtc	aaagatgctg	ttattccggg	cattcagaaa	240
gattatgaag	aggattttta	aaccgcatta	ctgcgcgccc	gaggcgtaat	taaagagtaa	300

<210> 289

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 289

tttcgggatg	atcggatgaa	cgaccaggct	tttactttcc	agacactaca	cccggatacc	60
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agctatgaaa	accgtgtcta	ccaatttcag	gacgaagagc	gccagcgctt	tgctgtaaag	180
ttttaccgtc	cacagcgctg	gtccgcagaa	caaattcagg	aagaacatca	gtttgcccac	240
gatctactgg	atgacgatgt	tcccgtttgc	gcaccgatta	aattcaataa	ccaaacgctg	300
ctgaaccatc	agggttttta	ctacgcggta	tttccgagcc	tgggcggaag	acagtttgag	360
gcagataata	tcgatcagat	ggaatgggtt	gcccgtatc	tggggcgcat	tcacagacg	420
ggacgtaaaa	aaccgtttgt	tgcccgtccg	acgattgggt	ttaaggaata	tcttattgag	480
ccgcgacagg	tattcgaaac	atcggcgctg	atcccgaatg	cactaaagga	taatttctct	540

```

acggcgaccg ataagcttat tgatgctgta aaagccagct ggcggggatga tattactact 600
ctgcgcctgc acggtgactg ccacgcgggg aatattctct ggcgcgatgg tccgctattt 660
gtcgatcttg atgacgcacg tatgggaccc gcggtgcagg atctgtggat gctactcaac 720
ggtgataaag ccgagcagcg catgcagctt gagaccataa ttgaagctta tgaagaattt 780
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tattatctcg cgtgggtaat caggcgttgg gaagaccggg cttttcccg aaatttcccc 900
tggcttaccg gggaggatta ctggcgcaac cagatatcca catttaccga gcagggttaag 960
gttctacagg aacccccctt gcaattaacg ccgatgtatt aa 1002

```

<210> 290

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 290

```

ttggacacac ccaggagaga gttgatcatg aaaaaaatTT ggctggcgct ggctgggatg 60
attctggctt ttagcgcaac tgctgcgcag tttaccgacg gcaagcagta cattacgctg 120
gacaagcctg ttgctggcga gcctcagggt ctggagttct tctccttcta ctgcccgcac 180
tgctacgagt ttgagcaggt acctcatggt tctgacaacg tgaagaaaaa gctgccggaa 240
ggcaccaaaa tgacgaaata ccacgttgag ttccttgggc cactgggcaa agatctgact 300
caggcatggg cggtcgcgat tgcgctgggt gtggaagata agatcacccg gcctatgttt 360
gaagctgtac agaaaaccca gacgtacaa actacggcag atatccgtaa agtgttcgta 420
gatgcggtg tgaaagggtg agaactacgac gctgcctgga acagttttgt ggtgaaatct 480
ctcgtggcac agcaggaaaa agctgccgct gacttccagt tgcaggggcg gccggcgatg 540
tatgttaacg gcaaatacca ggtcaatatg cgtgggtatg acacgaccag catggatatc 600
ttcgtacaac agtacgctga taccgtgaaa tacctggttg agaaaaagta a 651

```

<210> 291

<211> 264

<212> DNA

<213> Enterobacter cloacae

<400> 291

```

gatgctcagc ctgcaaacct acctcacccg gggcgtaaaa gaagtgcgtg gaccatccct 60
gaggggtgca ctgcgcctca ggcgccgat aaaatccaca ccgatttcgt gaaaggcttt 120
attcgtaacac agactatcgt gtttgaagac tttatcacct acaagggaga gcaaggcgcg 180
aaagaaacag gcaagatgag tgcggaagga aaagattaca tcattaaaga tggcgatgtg 240
atgaacttct tgtttaacct ttga 264

```

<210> 292

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 292

```

tgccagcgaa tgacgttcag ctgcgtcaga cggttgtgag tgaccttctc agcagagtct 60
tcaagcggta aaggttctgt agaggtagcg gtttacgcgc cggttgaatc cgatatcgct 120
gaaatcatcg acggcgacca taaagagttc atggccgagc gggggctgaa ccgcgtgatc 180
cgcgcggggt atgagctgct cagcctgcaa acctacttca ccgcgggcgt gaaagaagtg 240
aacgcgtga 249

```

<210> 293

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 293

```

cgccagcgaa tgccgttcag ctgcgtcagg cggttgtgag tgactttctc agcagactct 60
tcaagcgata aaggttctgt agtggttagcg ttttgaacg cggttgaatc cgatatcgct 120
gaaatgaacg acgcgcatcg tgaagatttc atggccgagc agggctctgaa ccgcgtgatc 180
cgcgcggggc atgagatgct cagcctgcaa acctacttca ccgcgggcgt aaaagaagtg 240

```

cgtggaccat ccctgagggg ggcactgcgc ctcaggcggc cgataaaaatc cacaccgatt 300
tcgtga 306

<210> 294

<211> 1332

<212> DNA

<213> Enterobacter cloacae

<400> 294

```
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atgaaatctt cacgatcggc gtcgttcatt tcagcagatc cggattcaac cgcgttccaa 120
aacgctacca ctacagaacc tttatcgctt gaagagtctg ctgagaaagt cacgcacaac 180
cgctgacgc agctgaacgg cattcgctgg cgctatgaca tccacggccg caccgttgag 240
aaggataacg gccagaccgg ctggcactac cgctacgaag gtgagcaccg cctgacggag 300
gtgatcagcc agccgcggga ccgcaacagg ccgcagacgc tggtcagctt ccgctacgat 360
ccgctcgggc gacgcacag caaaacgcgc cgcagatgc tgggcggcca gccaacgggt 420
aagccagtc aacgcgggtt tgtctgggaa ggggtccggc tgttgaggga agtgcacggg 480
gatgtgccac tgacctacgt ctacagcgat caggacagct acgacccgct ggcgcgatc 540
gacggcggtt atgccagga aatcttctgg ttccactgtc agccgaacgg cacgccggaa 600
cggatgacgg atagcgaagg acaggtgcgc tgggaagggg taaacagcgc ctggggcaag 660
ctgttgccgg aaagcgagac gcaggtatca ggatatttcc agaacctgcg gatgcagggg 720
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ggtcgagggc ctggatatga gcttttcacc agtcgatatc ctgagtatgg taaagggtgg 1260
gcattacagt tgctaccaat cgaacgtaat taccctgtta tttttgaacg tgttactata 1320
attccggagt aa 1332
```

<210> 295

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 295

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acacaaaaga tctcgttgtc totaaaagaa ttgttaaaag tgggaggagt tgtggttgag 60
gtgaaaatat attataaagg aagtgttgat tttattgcag gtgaagggac tattctcaat 120
gagttcatag gagaagtagc cacgcgacaa ataaatatta tagatggaaa ttattatgct 180
tcttcctctt tgctagataa aaaagaaaaa gttggcttcc tgctgtatga tggtaagaaa 240
agcgacctga acttaagtga cgcgaagaa atttcaaagt aggaatttga agttttctgg 300
caaacatcaa cgggttcatt gcaagaaaaa aagcgaataa aatacttgtc tggagatgct 360
gtggaacctt tgaaaaaate cacagttatt gctcatattg tgaataataa aggggaagtgg 420
ggtaaagggt ttgttctgtc cctttcaaat aaatatcctg cggcaaaaaa aagctatctt 480
agttgcttca aagaaaataa cttcccagaa ttaggggtgg ttgattttgt tatggttgat 540
gctcaggaga agatatttat tgcgaatatg tatgcgagg atggtataaa gaaaaatctc 600
aacgacaaaa aacaatacgt atgttatgac tctctgaaag tttgtcttga aaaattatct 660
gactttgctt tagttaatcg cctttctata caaatgccaa ggataggagc tggcctcggt 720
ggtggtgatt ggaatggtat agagtcctta atactaaaaa atatttgcta taaaatgatt 780
gattgcaatg taataacttt ataa 804
```

<210> 296

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 296

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tctttcaagg agcaaagaat gctgattctg actcgtcgag ttggtgagac cctcatgatt 60
```


ggggatgagg	tcaccgtgac	agtttttaggg	gtaaagggtg	accaggtacg	tattggtggt	120
aacgctccta	aagaagtatc	tgtccaccgt	gaagagatct	accagcgat	ccaggctgaa	180
aatcccagc	agtccagtta	ctga				204

<210> 297

<211> 267

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(48)

<220>

<221>unsure

<222>(119)

<400> 297

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accccgcccc	ttgcggtacg	tgccaccgag	atttttctac	gatcatggcg	accacattnt	120
ggggcgcccc	tcccggaag	cgcggaagaa	gatggcgatc	gctatattga	gatctggaac	180
attgtcttca	tgcagttcaa	ccgtcaggcg	gacggcacca	tggagccggt	gccccaaaacc	240
gtccgtagat	accggtatgg	gccttga				267

<210> 298

<211> 2121

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(70)

<400> 298

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gaccacattn	tggggcgcc	ctcccgga	gcgggaaga	agatggcgat	cgctatattg	120
agatctggaa	cattgtcttc	atgcagttca	accgtcaggc	ggacggcacc	atggagccgt	180
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tcctgtgcgt	tcctgattgc	tgaaggcggt	atcccgctca	atgaaaaccg	tggctatgtg	420
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gtaaccgcgc	tgtttggtga	cggtaaagcc	gtagacagca	ttagcgccgg	tcaggacgcg	960
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gacgaccgcg	ttcgcggtgt	gagcatgggc	gacttctcta	ccgaaactgtg	tggcggtact	1500
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aaagaacagg	ctgcggcgca	ggagagcgca	aacctctcca	gcaaagcgg	agacattaag	1800
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tgggtaagcg	cgaaactgta	a				2121

<210> 299

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 299

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tactggcaca	accgcatgga	cggatgaatg	ttgtacaaga	cgcggaaga	catcaaaaaa	180
gagaccggcc	tgagccgaga	cgagcaggaa	acagcacgca	aaagactcgt	tgccctgggc	240
gttctgcagg	aagacctgcg	cgggtgtgcca	gcgactgtgc	attaccggat	taataccgag	300
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ccaaccagac	ggcggaacc	ccgccaacaa	gatggcgcca	acgcacccaa	caagatggtg	420
gaaaccccg	caacaagaag	ggtggaaccc	acccaacaag	ttggttgggt	tcccgcacac	480
tttctacag	gagattacac	agagattaca	caggagagta	cgaggagat	cactcaaaag	540
gcgggtgaga	aaaattctgt	ggataacttt	tccgagatct	accccgaggc	ggaaatcttc	600
gatgctgaga	aaaaaacgtg	gggcaccgcc	gaggatctgg	aatttgcgca	gtggtttttt	660
gcccgcacg	tcgagctaca	cgaaaaagcc	gccgagtacg	acggtatgct	atcgcgcca	720
aaggaacctg	actggaccgg	ctgggcccgc	gaagttcgac	agctgcggga	ggggcaacgt	780
tgtgatcacc	aggcagatgc	gaaacctgg	cgagcgtatt	cagcgcgacc	cgtgggtggt	840
gcccgaagat	tcagactgcc	gaagtgtctg	acgccaaatg	gccagaactg	gtccttaa	897

<210> 300

<211> 657

<212> DNA

<213> Enterobacter cloacae

<400> 300

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gggttggtg	attatgcaga	cggcggtctg	ttcctcggt	ccgcggcaaa	gcaaaagcca	180
aagcgtatcc	gacccaacaa	ggaatcggag	ctggttggcc	ggatccttgc	cgtgatgcag	240
gggcagggtg	ctataagcgc	ggagaaaatc	gcaaaactgc	tcggtaaaa	ctcccgggct	300
ctaaatgcct	cgttggtg	cttgggcaag	gaagggcgag	tggtacgcca	tgtggatggg	360
aaaaacatta	cctggagctt	gaaaaacgac	gatgcgccag	caccggcaac	cgagccccg	420
atcgctaacc	ccaggcaggc	ggaatccg	ctggcagaga	aaagcacggc	ccaaattatt	480
gaagaaatcc	cggcattcac	agcgcgacgc	aatgacctgg	caatcccatc	gtcccgtttc	540
atctcaagtg	aaattcgccg	cacaaaagcg	aagctggcca	gcctgcaaaa	actgcagtgc	600
gccgcgcgc	agctgcgcgc	ccataaacat	ctgctggtgg	ggctggacaa	tgaatga	657

<210> 301

<211> 417

<212> DNA

<213> Enterobacter cloacae

<400> 301

ttaatgaaa	tcaaacacga	acacatccag	tgctgtctgc	tgccctgggc	ggcggaagta	60
gggcaggcgc	atgcgcggga	ggcgatccac	gcagaatata	cccgcagg	cgcgccgag	120
ctgccgtgg	tggttgga	cacctggaac	aaccagcaga	acatcttcca	ccgctggctg	180
gatggcagca	cgcgcgagc	ccgcgcaaaa	atccgcgagc	tgctgcctgc	cattctggcc	240
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ctgctggctg cccaggacgc gctgggcgcg gctattgatg cccatgatga cgcgggtggaa 360
gcgctatttc agaaagtcac gcagcacgcc gctgctgatt caccgaagtt tcaactaa 417

<210> 302

<211> 378

<212> DNA

<213> Enterobacter cloacae

<400> 302

gttcacagag gtgatgtcgt gagcgtgaag tgttgtggct gccaggaact gctggaggaa 60
gatgaagttt ttaagccttc cgattcatgc ggtgtcgata ttgctgatcg ttgcgcgagc 120
agggtggtgc atagctataa cgagtggcac ggcggtttca gctacgcacc tgtaaagcag 180
aaaaatccaa ggaaaagcat ttcagccgca gtgaagttga agatatttca gcgggatggt 240
tttcgttgca agcactgcgg gaccagttag gcattaacca tcgatcacat ccaaccggtt 300
tcaaaagggtg gcagcaacca agatgaaaac ttgcagacct tgtgtgcctc atgcaatagc 360
aggaaggggg ttaagtga 378

<210> 303

<211> 615

<212> DNA

<213> Enterobacter cloacae

<400> 303

agaaagaacg gactagctta tatcaatgca gtttaccctt ttaattttat tattcccttc 60
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cagtcgaggc caatatcaag aacagcaatc ttattatcta taagagccaa aaaagcatta 180
gttgccggata tcagcctaga aaaatatoga gctaagcgtg atgtaactta cgagcggcac 240
gttgccggag ctgagaaaga gatacaagac atgcgtgaag agattgtgaa ttctaaggaa 300
agagttggcg aaatgaatgc tgcattgctt gaattaaacc aaaaaaatga tgaaattaac 360
gcattactgc aagactccaa cattagaaat aaaaaactct ctgatgaaat agaacgccat 420
aaaatagcag aaacaagatt ttttggagag attgaagatt taaataaaga acttgatcga 480
ttatattctt tactaaaaat ggagccactc cgaggtgttg gcttaggcac aagaaagatc 540
accactataa atggtgaaga aaattcagat acggatgaca cccaatatcg cccaggttcc 600
aatgaagata aatag 615

<210> 304

<211> 726

<212> DNA

<213> Enterobacter cloacae

<400> 304

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acgttaaaga gcatttttga agcagaaggc tacgatgtct ttgaagcgac cgatggcgca 120
gagatgcatac agatcctttc tgaaaatgat atcaacctgg tgattatgga tatcaacctg 180
ccgggcaaaa acgggcttct tctggcgcgc gaactgcgtg aacaggcgaa cgtcgcgttg 240
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gatgactaca tcaccaagcc gttcaacctc gcgagtttaa ccattcgtgc acgcaacctg 360
ctgtcccgcga ccatgaatct gggtacggtc agtgaagagc gtcgtagcgt cgacagctac 420
aaattcaacg gctgggaact tgatatcaac agcgttctgc tgattagccc gaacggtgag 480
cagtacaaac tgcgcgcgag tgaattccgc gcgatgctgc acttctgcga gaacccgggc 540
aagattcagt ctgctgcaga actgctgaag aaaatgaccg gtcgtgagtt gaagccacac 600
gatcgtaccg ttgacgtaac catccgtcgt attcgtaaac atttcgaatc tacgcctgat 660
acgccggaaa tcategccac gatccatggt gaaggctatc gtttctgcgg tgacctccag 720
gagtaa 726

<210> 305

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 305

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cgtgccatga	agactatggg	ttttaccgat	ttgcgtattg	tggacagcac	ggcgcacatg	120
gagcctgctg	cgcgctgggt	ggcgacggg	tgggtgata	ttctcgataa	tataaccact	180
tacgctacgc	tgcgcgacgc	actccacgat	atttcattta	cgtcgcgac	gaccgcgcgc	240
agccgggcca	agtttacta	ttacgccacg	cctgctgaac	tggtgccgat	gctggaagag	300
aaaagccagt	ggctggagaa	agccgcgctg	gtgtttgggc	gagaagattc	cgggctgact	360
aacgaagagc	tggcgtggc	tgacgtgctg	acgggcgcgc	cgatggtggc	ggattaccgc	420
tcactcaatc	tggggcaggc	ggtgatggtc	tattgctatc	aattagcatc	cttaatacaa	480
atttctcagc	caccgggtgac	agtttcggat	gaaaaccagc	tggcggcact	gcgtgttcgt	540
gcagataagc	ttcttgcgca	gttgggcgtc	gctgacgata	aaaaaatggt	ggactggtta	600
cagcagcgcc	tggggcgctc	tgaacagcgt	gacacggtaa	tgttgccaccg	attgcttcat	660
gatattgaaa	aaaaattagc	ggagtaa				687

<210> 306

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 306

ggtacaata	tgaatacaa	ggttttagtc	tttgcagcac	tggcactgat	ggcagggcgc	60
gtggcgagc	cggagcaaat	tggctccgtg	gataccgtgt	ttaaaatggt	tgggccggac	120
cacaaaattg	tgggtggaggc	gtttgaogat	cgggacgtta	aaaacgtcac	ctgctatgtc	180
agccgggcaa	agaccggcgg	gattaaaggc	ggcctggggc	tggctgaaga	cacgtctgac	240
gcggccatct	cctgccagca	ggttggaccg	gtggaattga	gtgacaaaat	taaaaacggc	300
aaagcgcagg	gcgacgttgt	attccagaaa	cggacctcgc	tgggtgttcaa	aaagctacag	360
gtggtccgtt	tttatgatgc	gaagcgtaac	accctggctt	atctggccta	ctcggacaaa	420
gtcgtggaag	gtccaccgaa	aaacgcgatt	agcgcgggtg	cgattatgcc	gtggcattga	480

<210> 307

<211> 864

<212> DNA

<213> Enterobacter cloacae

<400> 307

aagaagtgtt	tgtcggcctt	gcgccagata	ttggaaaaga	gcacgaggct	gattatgtcc	60
gggtcttccc	aagatgaact	cacggcgcg	gatatgttcc	gccggttacg	tgacatcata	120
aagcgcggtg	tgttcaaaga	agtaacagatg	cagccccgcg	gcgtccgggt	gactttcggc	180
ggagagcatc	agtccggctg	gctgcaatgg	tttacccttg	caacatcaga	acgcgtcgac	240
tggagcgcgc	cgaaagtggg	tgaccgggta	ccccccaatt	ccacagcggc	agaacggggc	300
ctggaagccg	ttctgtcaca	cgtcggcgac	cttcctggcg	atatccggat	catcaaaaac	360
cccgatattt	gccccgtcga	tttgcctccc	tggcttgcat	gggagtatgc	agtcacatac	420
tggaaactcg	gctggagcga	gcagcaaaaa	cggcaggtca	tcaaagcggc	agcgtggcaa	480
aacaagcacc	gcggtacgcg	cgggtgctgta	gaacgtgcgt	tgttgacggg	cggctatgaa	540
agccagttgc	aggaatggtt	tgaaaaagtg	ccgaaggggc	acccctacac	atttggcatc	600
aaaattttacc	tgttaaagca	aatgggggatg	gatttagacc	tgctcaacac	ttttattgcg	660
cagatattcg	atgcgaaaaa	ctgccgctcg	ttgctcgaat	ctatcaattt	tgaagcagaa	720
atcgacgggtg	aatttttatat	cgcggggacc	acggctgcgc	acgtcgtggg	agaaatcccg	780
gcagaggatg	agggggggagt	aaaagtaaac	ggctccctgt	ttatttcggg	tgtaccgaca	840
gctcatatca	cagtggaaat	atag				864

<210> 308

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 308

ggggggagta	aaagtaaaccg	gctccctgtt	tatttcgggt	gtaccgacag	ctcatatcac	60
agtggaaata	tagaaatggt	acaaaagaga	acagcgctta	aaagcgccac	atctactcca	120
gacgataaga	tatacgcaat	cctgactgac	cggggcgcg	agctggaagc	cgcagcgctc	180
gctaccggcg	tgccggttaa	attaacaaag	tttgttattg	gggacgcgaa	cgggcaggaa	240
gaagtcacac	ctgaccgggc	cagaactgcc	cttatccatg	aggtttatcg	cgtgatatc	300

aacggtgctg	aaagcaaggg	caaccaggta	acgtttactc	togatgtccc	cccgagagacg	360
ggcggttata	cgatccgtga	agttgggatt	ttaacagaag	caggggaatt	atattccggt	420
gcacgtttct	ctgataatct	aaaacccacg	gaaagtaacg	gggcagtaat	ttcaataacg	480
tttaaataata	ttcttgctgt	gtcgagcaca	tgcacggtaa	cagtagttgt	ttataatgat	540
tatttaaccc	cggatgctgc	tgatgcccg	tatttaaaag	ttaatgcgaa	tctaaaagaa	600
atcgagata	acggtgcatc	aagccagcaa	ttagcaagaa	aaaatattgg	cattgatggg	660
gatatagcgt	acagagataa	agaaaatata	ttcactaaaa	agaatacgtt	tggtgaaata	720
ctatatgtca	ataaatcaat	agttttatcg	ggagattggg	ccgtatcatg	gtcactagct	780
ggcgcttata	ttgaggccta	tctgggtcac	tcgaaactgc	cggaccggct	attctccaca	840

<210> 309

<211> 357

<212> DNA

<213> Enterobacter cloacae

<400> 309

cggtgtcgag	ccgcggttact	acaggcgatt	ctggatggcg	tggcgcagca	tggtcccttac	60
tttgtgattg	cgccaggcct	ggcgatgccg	catggccgcc	cggaagaggg	cgtcaagaaa	120
accggcttcg	cgctgggtgac	gctgaaaacc	ccgctggtgt	tcaaccacga	agataacgac	180
ccggtcgaca	tccttatcac	tatggcggtc	gtcgatgcc	ataccaccca	ggaggtgggc	240
atcatgcaga	tcgtcaatct	gtttgatgat	gaagctaatt	ttgaccgttt	acgcgcctgc	300
cgtaccgcgc	aggacgtgct	ggatttaatt	gataacgcc	ctgcggcggc	cgtttaa	357

<210> 310

<211> 663

<212> DNA

<213> Enterobacter cloacae

<400> 310

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cacgcttacg	aaaccacccg	tctgattgcg	gaagaagtgg	acatcatcga	agtcggcacc	120
attctgtgcg	tgggcggaagg	cgttcgtgcg	gttcgtgacc	tgaaggcgct	ctatccgcat	180
aaaatcgtgc	tggtcggtgc	caaaatcgcc	gatgcgggca	aaattctctc	tcgcatgtgc	240
tttgaagcca	acgccgactg	ggtcaccgtg	atctgctgtg	cggatatcaa	cactgcgaaa	300
ggcgcgctgg	acgtggcgaa	ggagtccaat	ggcgacgtgc	agattgaact	gaccggtttc	360
tggtacctgg	agcaggcgca	ggagtggcgc	gaagcaggta	tccagcaggt	ggtttatcac	420
cgcagccgtg	atgcgcaggg	cgcaggcggtg	gcgtgggggtg	aagccgatat	cagcgcgac	480
aaacgtctgg	ccgatatggg	cttcaaagtg	accgtaaccg	gtggcctggc	gctggaagat	540
ctgcgcgtgt	tcaaggggat	tccaattcac	gtctttattg	ccggtcgtag	cattcgcgat	600
gcggaatctc	cggtggaagc	tgcgcgtcag	tttaaacgct	caatcgctca	gctttgggggt	660
taa						663

<210> 311

<211> 870

<212> DNA

<213> Enterobacter cloacae

<400> 311

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ggggagtgtc	ggctggagcg	gttacagctg	gcgaagcagc	tggttttcga	ttttgtcgaa	120
atgtcgctgg	atgagacgga	cgagcgtctt	gctcgccctg	actggagccg	cgaccagcgt	180
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gtcatcgtc	gttttccgct	tggcagcgaa	gatgatgccg	tacgcgccga	agggctggag	300
atcatgcgt	aagctattcg	cttcgcacag	gatgtcggca	tccgcgtgat	ccaactggcg	360
ggttatgatg	tttactatca	ggaagccaat	gatgaaacgc	gccgtcgttt	ccgtgacggc	420
ctgaaagaga	gcgttgagat	ggcaagccgt	gcgcaggtga	cgctggcgat	ggagatcatg	480
gattatccgt	tgatgaactc	catcagcaag	gcgtgggct	acgcgcacta	tctgaataac	540
ccgtggttcc	agcttttatcc	ggatatcggc	aacctgtcgg	catgggataa	cgacgtacag	600
atggagcttc	agggcgggcat	cgggcatatc	gtggcggtgc	acgttaaaga	taccggtccc	660
ggcgtgttta	aaaacgtacc	gttcggcacc	gggggtggtg	atttcgaacg	gtgcttccag	720
acgtcctaac	agacagggtta	ttgcgggcct	tacctgattg	agatgtggag	cgaaaccgcg	780

gacgatccgg cggcagaagt ggcgaaagcc cgggactggg tgtgcgagcg catggcgcg 840
gcaggactga tggaggcgga acatgcttaa 870

<210> 312

<211> 654

<212> DNA

<213> Enterobacter cloacae

<400> 312

acgtggtgcc aggcggatgg cggggtaaaa cccaattgg cegtgttata tccatgcaaa 60
cccggtttat cccttagccg gtggccatit gtcacattc accccagggg cgtgcgtatg 120
ttcgtcgccg aactgtcgga agcgtttaat ggcacatccc agcgcctgat ccctggcgcg 180
gtgctggcga ttgactgtgc ggcatcttat agctttgcgc caaacgccgt tgtctggggc 240
tttatgtggg gcaccatcgg ccagctgatt gcggtcggca ttctggtggg ctgtggctcc 300
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atggcggact ggtcaattct ggcgcgcgcg atgatgcagg gctttgcgtc cgtcgggctg 540
gtctttatgg ccgtcatcat cctgattgcc ctggcttata tgttcttcgc tggcggttcg 600
ctgcgggctg aagaagatgc ggaaaaacaa acagcagaag tgtctgctca ttaa 654

<210> 313

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 313

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atgatcatga agatgaaagt ggaccagttt ttaaccaggt caaacattga ccacacgggtg 120
aacagctgcg cagtgggtga atacaaaagt gaactgaacg gcgcggacat catcatcgcc 180
tcaacgcaca ttgcggcgga gattagcgtg tcgggcaaca aatacgtggt aggcgtacgc 240
aacatgctgt cgctgcggga tttcggacca aagctgctgg aagtgatcaa agaacacttc 300
ccacaagacg tgaagtaa 318

<210> 314

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 314

ggatgccaca tgaaactacg tgattcgtg gcagagaata actccatcct tttacaggcc 60
gaagcaagca cctggcagga agcgggtgaag ctgagcgtgg atctgctggg taaggctgac 120
gttgctgagc cgcgttacta caggcgatcc tggatggcgt ggcgcagcat ggcccttact 180
ttgtga 186

<210> 315

<211> 570

<212> DNA

<213> Enterobacter cloacae

<400> 315

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cgctatggac tggtagcgtt tacgtggggc aacgtaagcg ccacgatcgc cgagcagggg 120
ctggtggtga ttaagccgag cggcgtggcc tatgacgcca tgaaagcgga cgatatggtg 180
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ggcgagtacg aacttaacac cggcaggggc attatcgaaa cgctgggtga gacggaacca 480
ctgcatacgc cgggtattgt ggtgtaccag catggtccat tctccggggc taatcttcac 540
ctcggacctg gcggaccgga gcttaggtaa 570

<210> 316
 <211> 708
 <212> DNA
 <213> Enterobacter cloacae

<400> 316
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 tgtttactca gcgaaaggag aatgccaatg caaaataaaa aaacaattca cgtggccggt 120
 gttgacagct gcgaattcac gatgattggc ctgcaatcac ttggaaagcg tgagcctgat 180
 gaaaaacacg acgttatttt ccattgggtt acccatatcg aagaacttgc tatgagtga 240
 caactctttg atatcatcat ttatgatccg ttgaatacgc gtcatttccg ggtgacgaca 300
 aatgacgaca ttctctgcat taaacagaaa caagtgcagg cgaagatcta tatctattcg 360
 ttatccgcgc gctatttgaa atttaaacat gttgatgggg taatcagtaa aagagtctcc 420
 ctgggggata tcaaagcgct gtggcaata ctgatgagcc agacgccgca agagtctggc 480
 cgttacaatg taggcagac gaccgcctta cgcaccccg cgaggctgtc cagcgaggag 540
 gccagcgctat tgcgcggcta ttctgtaat ctcaaaacca agcaaatcgc ccgtcagctg 600
 ggggtgtaacg tcaggctggg ttacttttat aagaacaacg ccattgaacaa gcttaaagcc 660
 gtgcgtggcc cctcgtttta ccagagcatt cgctggatcc tgaattaa 708

<210> 317
 <211> 762
 <212> DNA
 <213> Enterobacter cloacae

<400> 317
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 tcattttctg aaggctgttc catgtatacc gttcttccct ctcccctgtt gcaacgtatc 120
 tcagggtcgc gcttccagcc gcttgctgat ctctattcgg gccaggtgtt cgcgcataga 180
 gtgcttgttg agatccgtaa cgtcaatctt gaggctgtgt ttgcctcgct gccctcgcgc 240
 agcgcgctgc aaatcttctt ctggcaggcc aacactctct tacagatacc cgcccgggac 300
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 cggtcgagcg aggetgagca acgtcatctt catgccacgc ttgttcggtt aaaagaggcg 480
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 gcgctaccgc tggatggggg aaaaattgac cgttcagcac tgcgcgagcg cgcgcgctt 600
 gccccgtttg tgcaggaggt caggacaggt atcgcgcaat caattcttat cgaaggcatc 660
 gaaaactcgc gggatctggc gcgcgcgcgc acgtccggcg cacagtctgg ccagggtttt 720
 ctgtggcccg aaagccgaac cgatgccgcg gtaacgcttt ga 762

<210> 318
 <211> 186
 <212> DNA
 <213> Enterobacter cloacae

<400> 318
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 gcggaagtcg ccaaaaagggt ggcaaaggag aaatacggtc tggatgttga gctggtgggc 120
 tttagcggct cgctgctgcc caacgatgcc accaaccagg gcgaactgga cgccaacgtc 180
 ttctag 186

<210> 319
 <211> 555
 <212> DNA
 <213> Enterobacter cloacae

<400> 319
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 aataccttct tcttcccgat ggcgggttac tcccgaaga ttaaactcgt ctctgagctg 120
 aaggacggcg caaccattgc gattccaaac gatccacca acctggccg cgcgctgttg 180
 ctgctgcaaa aagagaagct gattaccctt aaaccggatg ttggcctgct gccaacggcg 240

ctggatatta	ccgcgaaccc	gaaaaactta	cagattatgg	agctggaagg	ggcgcagctg	300
ccgcgcgtgc	tggacgatcc	gaaagtggat	gtggccatca	tcagtaccac	ctatctccag	360
caaacggggc	tgtctccggt	acacgacagc	gtctttattg	aagacaaaaa	ctcaccctat	420
gtgaatattg	tggtcacgcg	tgaagacaac	aaagacgctg	aaaacgtgaa	ggaattttatc	480
cagtcctatc	agtcgccgga	agtggcgaaa	gcggcagaga	cccttttttaa	cggaggcgcg	540
gtgccgggct	ggtaa					555

<210> 320

<211> 240

<212> DNA

<213> Enterobacter cloacae

<400> 320

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tggtcgactg	ggttcatcgc	agtaaccgga	acggtaggac	gaacaccacg	ccagcgtgca	120
gcaccagctt	taccocagaac	gcgcagcata	tgctcagcat	tgccaacttc	gccagagta	180
gcgcggcagc	ctgcttcgac	tttacgcatt	tcaccagaac	gcagacgcag	ggtgacataa	240

<210> 321

<211> 237

<212> DNA

<213> Enterobacter cloacae

<400> 321

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gaagatgtgc	tgatcatcac	cgggtgagctg	gacgagaacc	tgctcctggc	cgcgcgtaac	120
ctgcacaagg	ttgacgtacg	cgacgcgact	ggtatcgacc	cggttagcct	gatcgccctc	180
gacaaagtgc	taatgactgc	tgatgctgtt	aagcaagttg	aggagatgct	ggcatga	237

<210> 322

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 322

aggcccaagc	atgaagcgca	ttatgccgcg	tgcgaaaggt	cgtgcagatc	gcctcctgaa	60
gcgcaccagc	cacattactg	tggtttgtgc	cgatcgctga	gactctggag	actagcaatg	120
ggtcagaaaag	tacatcctaa	tggatttcgc	ctgggtattg	taaaaccatg	gaactctacc	180
tggttttgcga	acaccaaaga	attcgcgtgac	aacctggaca	gcgattttta	agtacgtcag	240
tacctgacta	aggaactggc	taaagcgtct	gtatctcgta	tcgttatcga	gcgtccagct	300
aagagcatcc	gtgtgactat	tcacactgct	cgccttgcca	tcgttatcgg	taagaaaggc	360
gaagacgtag	aaaaactgcg	caaggctgta	gcgcatatcg	ctggcggttc	tgacagatc	420
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atcgacgta	ccgaatggta	ccgcgaaggt	cgcgtaccgc	tgacactct	gcgtgctgac	660
atcgactaca	acacctctga	agcgcacacc	acttacgggtg	taatcggcgt	taaggatatg	720
atcttcaaag	gtgagatcct	gggtgggtatg	gctgctgttg	aacaaccgga	aaaaccggct	780
gctcaacctta	aaaagcagca	gcgtaaaggc	cgtaaataa			819

<210> 323

<211> 423

<212> DNA

<213> Enterobacter cloacae

<400> 323

ggagcgtcgc	tgatgttaca	accaaagcgt	acaaaattcc	gtaaagtgca	caaaggccgc	60
aaccgtgggc	tggcgcaggg	tacggatgtt	agcttcggca	ctttcggtct	gaaagctggt	120
ggcgtgggc	gtctgactgc	acgtcagatc	gaagcagcac	gtcgtgcaat	gaccctgca	180
gttaagcgtc	aaggtaagat	ctggatccgt	gtattcccg	acaaaccgat	caccgagaag	240
ccactggaag	ttcgtatggg	taaaggtaaa	ggtaacgtgg	agtactgggt	tgcccttgatc	300

caaccgggca	aagtccttta	tgaaatggac	ggtgttccgg	aagagctggc	ccgtgaagcc	360
ttcggcctgg	cagcagcgaa	actgcctatc	aaaaccacct	ttgtaactaa	gacgggtgatg	420
ttaa						423

<210> 324

<211> 843

<212> DNA

<213> Enterobacter cloacae

<400> 324

gtaagtcgga	ggagtaatac	aatggcagtt	gttaaattga	aaccgacatc	tccgggtcgt	60
cgccacgtag	ttaaagtggg	taaccctgag	ctgcacaagg	gcaaaccctt	tgctccgttg	120
ctggaaaaaa	acagcaaata	cgggtggcgt	aacaacaatg	gccgtatcac	cactcgtcac	180
atcgggtggg	gccacaagca	ggcattatcg	attgttgact	tcaaacgcaa	caaagacggt	240
atcccagcag	ttgttgagcg	tcttgagtac	gatccgaacc	gttccgcgaa	catcgcgctg	300
gttctgtaca	aagatggcga	acgcgcgtac	atcctggccc	ctaaaggcct	gaaagctggc	360
gaccagattc	agtctggcgt	tgatgctgca	atcaaagcag	gcaacaccct	gccgatgcgc	420
aatatcccgg	ttggttctac	cgttcataac	gtagaaatga	aaccaggtaa	aggcggtcag	480
ctggcgcgtt	ccgcgggtac	ttacgttcag	atcgttgccg	gtgacgggtg	ttatgtcacc	540
ctgcgtctgc	gttctgggtg	aatgcgtaaa	gtcgaagcag	actgccgcgc	tactctgggc	600
gaagttggca	atgctgagca	tatgctgcgc	gttctgggta	aagctgggtg	tgacgctggg	660
cgtgggtgtt	gtcctaccgt	tgcgggtact	gcgatgaacc	cagtcgacca	cccacatggt	720
ggtgggtgaag	gtcgtaactt	tggttaagca	ccggttaact	cgtggggcgt	tcagacccaa	780
ggtaagaaga	cccgcagcaa	caagcgtact	gataaattta	tcgtacgtcg	ccgtagcaaa	840
ttaa						843

<210> 325

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 325

gaggaagaga	tggaaacttt	agctcaacat	cgccatgctc	gttcttctgc	acagaaggtt	60
cgcttctgtg	ctgacctgat	tgcgggtaag	aaagtgtcgc	aggccctgga	catcctgacc	120
tataccaaca	agaaagctgc	ggtattgggc	aagaaagtac	tggaaatctgc	cattgctaac	180
gctgaacaca	acgatggcgc	tgacatcgac	gatctgaaag	tgcgaaaaat	tttcgtagat	240
gaaggcccaa	gcatgaagcg	cattatgccg	cgtgcgaaag	gtcgtgcaga	tcgcctcctg	300
aagcgcacca	gccacattac	tgtggttgtg	tccgatcgct	ga		342

<210> 326

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 326

gactttactg	actcagaagg	cgggtgcgta	atgaccgata	aaatccgtac	tctgcaaggt	60
cgtgttggtt	gcgataaaat	ggagaaatcc	attgttgtag	ctatcgaacg	ttttgtgaaa	120
caccgatctc	acggtaaat	catcaagcgt	acgaccaaac	tgacgtaca	tgacgagaac	180
aacgaatgtg	gtatcggcga	caaggttgaa	atccgtgatg	ctgtccaggt	cgacgactac	240
tcctggacgc	tggttcgcgtg	taaaaaaaaa				270

<210> 327

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 327

ggagatgctg	gcatgattcg	tgaagaacgt	ctgctgaagg	tgctgcgcgc	accgcacgtt	60
tctgaaaaag	cgtctactgc	gatggaaaaa	acaaacacca	tcgttctcaa	agttgctaaa	120
gacgcgacca	aagcagagat	caaagctgct	gtgcagaaac	tggttgaaat	cgaagtcgaa	180
gtcgtaaca	ccctggtagt	taaaggga	gttaaactgc	acggacagcg	tatcggtcgt	240

cgtagcgact ggaaaaaagc ttacgtcacc ctgaaagaag gccagaacct ggacttcggt 300
ggcggcgctg agtaa 315

<210> 328

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 328

gccatgccac gttctctcaa gaaaggtoct tttattgacc tgcacttgct gaagaaggta 60
gagaaagcgg tggaaagcgg agacaagaag cccctgogca cttgggtcccg tcgttcaacg 120
atctttccta acatgatcgg tttgaccatc gctgtccata atggtcgtca gcacgttcca 180
gtctttgtta ccgacgaaat gggtgggcac aaactgggtg aattcgcacc gactcgtact 240
tatcgcggcc acgctgctga taaaaaagcg aagaagaaat aa 282

<210> 329

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 329

gacggtgatg taatgaaagc aaaagagctg cgtgaaaaaa gcgttgaaga gctgaacgct 60
gagctgctga acctgctgcg tgagcagttc aacctgcgta tgcaggctgc aagtggccag 120
ctgcaacaga ctcacctgct gaagcaagtg cgtcgcaatg ttgcgcgcgt taagacttta 180
ctgactcaga aggcgggtgc gtaa 204

<210> 330

<211> 1308

<212> DNA

<213> Enterobacter cloacae

<400> 330

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cttaacgtgt tattaactaa gcttgaaaaa gcggcgacta atattacgga aaagcgtaag 120
tcaggctggg atgaaaaaga cgttgtgtcg attacctatg ccgatcagtt ctccacaaaa 180
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tcccatgtcc atctgttacc tttttatccg tgggtcttcgg atgatggatt ttccgttatt 300
gattatcacg aggttgctcc tgaaacagga acctggcgag atgtcgcgga attaaaacat 360
tcagccagct taatgtttga cttcgtttgc aatcatatgt cagcgaaaag cgaatggttt 420
gctaattatc ttgcgcagaa gccgggctac gaagatttct ttatttctgt cgaccccgaa 480
accgatttat ccgcggtgac ggtgccgcgc gcattaccgc tgcctgacgc gttcacgctt 540
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ggggcgcggt atatecgtct ggatgcggtc gggtttatgt ggaagatccc gggaaccacc 720
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attgcgcggg tcatcctgtc gcatgctgtg ttgttaagtt ttccctggcg accggctgta 1260
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<210> 331

<211> 375

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(96)

<400> 331

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gaactcaata	ataagaagag	tatacgttat	caaantntatt	ctcgtttgag	tgagtttatt	120
gctattcgtc	gcggcgagag	tgcgttccat	ccggatagcc	aggctatfff	tgacgcaatc	180
ggcgaacata	tccttaaaat	tgttcgtgtt	gctgaaaatg	gcgagcgaat	gacagcatta	240
tttaatttta	gcaataaaat	gcagaccatt	tatggacaaa	cgctccttgg	tagggaatta	300
ctatcaggac	acgatattag	cgggtacggaa	ctgaacctca	atccatggca	ggtaatgtgg	360
attaaagaaa	actaa					375

<210> 332

<211> 1326

<212> DNA

<213> Enterobacter cloacae

<400> 332

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tcagcactgg	tttctgtgcgc	cctgttatca	ggctgtaagg	acgataaagc	atctcaggtc	120
accattgagt	ttatgcactc	gtcggtagaa	caggagcgtc	aggcagttat	tacgaaaactg	180
atcgaaaaat	tcgagaaaga	gaaccgcact	attacggtga	aacagggtacc	cgttgaggaa	240
gatgcctata	acaccaagggt	cattacggtg	gcccgtaccg	gcgcgctgcc	ggaagtgatt	300
gaagtcagcc	atgactacgc	caaagtcattg	gataaagagc	aactgctgga	ccgtgacgcg	360
atcgccaacg	cgattaaagc	cgtcggtgaa	gatacctfff	atgacggcat	tttacgcgtt	420
gttcgcactg	aagacggcaa	ggcatggacg	gggggtgccg	ttagcgcctg	gctgtccggc	480
gtctggtatc	acaaagatgc	gctcgcggca	gcaggaatcg	aagagccgca	caactgggag	540
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gagagctgga	aaaacaacga	cgtgatcaaa	gcctttgggtc	aactgcctta	cgagctgatt	1140
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ggagatgtta	ccgggtccgg	cattatcagt	tccatggtgc	ataacgtaac	ggtgggacaa	1260
aaagatctca	atgcgacggt	aagcaacagc	cagaagaaac	tgactgacct	gatctcacia	1320
cgatag						1326

<210> 333

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 333

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gccatgctgc	tggttgcccc	cagcctgatt	ttgctggggg	gcctgggtggc	ctggccaatg	120
atttccaaaca	ttgaaatcag	ttttttacgt	ttaccgctga	acccgcgtat	tgatgcggtg	180
ttcgtcggcc	tggataacta	cattcgcatt	ctgggcgatg	ctgcgttctg	gactccctg	240
tggatgaagt	tctggtatac	ggccctgggtc	gtgctcggca	gcaccgggtt	gggactggcc	300
gtagcgatct	tctttaaccg	tgaattccgc	atgcggaaaa	cggcacgttc	actggtgatt	360
ctgtcctacg	tgacgcgctc	tatttcaactg	gtatttgcct	ggaaatacat	gttcaacaac	420
ggctacggga	ttgtgaacta	cctgggcgtt	gatctgctgc	atctctacga	tcaggcgccg	480
ctgtggttcg	ataatcctgg	cagcagtttt	gtcctggttg	tgctgttcgc	catctggcgt	540
tacttcccg	acgcctttat	ctcgttccctc	gcaattttgc	agaccattga	taaatcattg	600
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cccgccatca	tgcgggtgct	ggccacggtg	gtcacgctgc	gaaccatctg	gatgttctac	720
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aaaaccgcct	ttgcgttcaa	tgacctgggt	aaagcagccg	ccatttccgt	tgtgctgttt	840
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taa						903

<210> 334
 <211> 645
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(525)

<220>
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<220>
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 <222>(544)

<220>
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<220>
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 <222>(609)

<400> 334						
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gcgaaagagg	cgatctcgct	gcacccgacc	attctgccgc	aggagtggac	gctacagcac	180
tacatcgaca	tctttaaccc	gctgatttct	ccgtttgtgg	attacttccg	taacagcatg	240
gtggtgtcgc	tgacctcctc	ggtcattgcg	gtgtttctcg	gcacgctggg	cgcatatgcg	300
ttatccaaac	tcgcgtttta	agggcgtagc	acgatcaatg	cgagcttcta	caccgtctat	360
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gacngnctga	aacgcctgca	aatcatcttc	cgcatcacc	tcccgcgtgg	caattccggt	600
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<210> 335
 <211> 459
 <212> DNA
 <213> Enterobacter cloacae

<400> 335						
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atgagtaccg	aagtggtaag	cgataaggat	ggcaccattg	ccgtgctgct	gggggcatcc	180
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aagctgaacg	gtaacgtttg	ggccacggaa	caagagctgg	aatacaccag	ccgcgttctg	360
caactgcaat	acgtcaaacc	gcaggctgcg	gatgctgcgc	caaaggcaga	gctgaagcct	420
caggcggaaa	gcaagccggg	agcggatatc	gcgctgtaa			459

<210> 336
 <211> 372
 <212> DNA
 <213> Enterobacter cloacae

<400> 336
 tgcactgctt ttgtgttctt ttattgggtg ttaatgctgt ggtggagtcg atgcggcgat 60
 cgtgttattt tacgcgttaa ttattgttat ttatctgtaa agggaggaga tatggtacgg 120
 gaaaaactga agacacctga aggcgcgaag ttctgtctgg cgttactggg tgtgtttatg 180
 attgctgctg catgcgtggg gcgagcaacc attgtcgggtg tgattgagca gtacaacatc 240
 ccgctatctg cctggacaac cagcatgttt gtccctgcaat cggcgatgat ctttgtttac 300
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 gaaaaacact aa 372

<210> 337
 <211> 410
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(372)

<400> 337
 ataccgcccg gtctaaaagg agagtttatc atgagtctgg aaatcaacca gattgccttg 60
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 gaaccaacgc ctaccgttgt cgagatgatg ggggagtgc atcgcgtcta cagcgcgaaa 180
 aataaagcct atggcttggt cagcgaagag agcgaactgg cggatagcct gcgcctgcaa 240
 cgtcagggcg aagaggattt cctggcattc agccgcgctg ctactggccg tctgcgtgac 300
 gagctggcga aatatccctt cgcgatggc ggtatcgtcc tgttctgcca ctaccgctgt 360
 ccggcggtag tntttccaca agagctggca atccgcgagg tcaataggga 410

<210> 338
 <211> 1875
 <212> DNA
 <213> Enterobacter cloacae

<400> 338
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 tgcagtccctc cgtttagcgac gaccaggcac actaagggaa acgaacaaca gtttatgggtg 120
 acgaatcgtc agcgtacccg tgaaaaagtc tcccagatgg tcagctgggg gcactgggtt 180
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 gtgattaacc cggatcagaa cgagaccgcg cgcgactggc agctgatgtt tatcagcgtg 540
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 ggttcgcacc tgatgtatat ctgggcagat gcgaacttct accgcccgat taccatgcag 720
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ctgcacgtca	gcacaccggc	aattgagtag	tgcagggcc	aagacctctt	tagcgccacg	1680
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ttgtccctgg	tgttgaacag	caacggcaat	taccagacgt	atagcctcga	aggtgagaag	1800
ctgaaagacc	agaaaccgca	gctcagtttg	ctgttgacag	tgctgacaga	cgagaagcgc	1860
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<210> 339

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 339

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gctccgtatc	cgcaagcgga	caaagggatg	aagcgccagg	ttatttcagct	ccgggctcag	180
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aaccagcatc	gtctgggctg	ccaactggaa	agcaaaaacg	tgggaaggctg	gggctatgac	300
tactatgtct	tgcacaaaag	aacctcgcca	gtctccacca	tgatggcgtg	cccgacgagg	360
aagaaagaga	agaaatttat	taccgctgat	ctgggtgata	acagtctgct	gcgctataac	420
agcaagctgc	cgatcgctgt	atatacgccg	gaaaacgtgg	atgtgaaata	tgcggtatgg	480
aaggcggatg	agacggtagg	acaagcggta	gttcgttaa			519

<210> 340

<211> 231

<212> DNA

<213> Enterobacter cloacae

<400> 340

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gtcaacgtac	tggaaaaaca	taaaacgcca	accgatctct	ccctgatggg	tttgggaaat	120
atggttacca	acctgatcaa	taccagcggt	gctccggctc	agcgtcaggc	gatcgccaaa	180
tctttcgcgc	aggttttgca	gtccctccgt	agcgacgacc	aggcacacta	a	231

<210> 341

<211> 1458

<212> DNA

<213> Enterobacter cloacae

<400> 341

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gtatggtggt	tatcaagttt	tatcctgatt	agcaccctta	atggctattt	cgataatcag	180
gaccgcgatt	ttctgacagg	taaacttcag	ctcaccgaag	agtttcttaa	aacagagacg	240
ttcaggaaca	aaacgggata	taagtcatta	tcagaaaaaa	taaacgatgc	gatggtgggg	300
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gccaaaaatt	ctgttggttc	agcgggtcctg	cttaataaag	cgggtgatat	tctcgactat	420
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acgccggaac	agggtaaaag	caaacatgtc	atcattacgg	ttgccacgga	tactgggtat	540
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acagcgatac	accttgagcg	tgacagggac	tgtgtgaacg	tgatgattac	gaatacagtg	1260
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<210> 342

<211> 732

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(297)

<220>

<221>unsure

<222>(306)

<400> 342

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caggtcagct	ag					732

<210> 343

<211> 711

<212> DNA

<213> Enterobacter cloacae

<400> 343

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caaaaaacag	gtcgttacct	gcagcaggga	ctgggtgagg	aaggctatca	ggccgatctc	120
tttaataatg	gccgcgatgg	tctcgggggc	gcgtcgaagg	gacagtatga	tttgataata	180
ctggacgtga	tgctgccttt	cctcgacggg	tggtcaaatca	tcagcgact	gagggagtcc	240
gggcacgaag	aaccggctct	gttttttaac	gcaaaaggaca	acgtgcggga	caaagtgaag	300
ggactggagc	ttggcgcgag	tgactacctg	attaagccct	ttgattttac	ggagctgggt	360
gcacgtgtaa	gaaccctact	gcgcggggca	cgctcgcagg	ccgcaacagt	ctgcaccatc	420
gccgatatga	cogttgatat	ggtgcgcggg	accgtgatcc	gttcggggaa	gaagatccat	480
ctcaccggta	aagaatacgt	tctgcttgag	ttgctgctgc	aacgcaccgg	agaagtgtta	540
cccaggagtc	ttatctcgtc	cctgggtctg	aacatgaatt	ttgacagtga	tacgaatgtg	600
attgatgtcg	ccgtgagacg	tctgagaagt	aaaattgatg	atgactttga	gccaaaactg	660
atccataccg	ttcgcgggtg	cggatatgtc	ctggagatca	gagaagagtg	a	711

<210> 344

<211> 413

<212> DNA

<213> Enterobacter cloacae

<400> 344

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gactttaagc	tggtctctgt	cgaaaagtca	tatcagcctg	gagcctgtgt	tgccccgttg	120
gcgcgggata	atggaattaa	tgacaatctg	ctgtttacct	ggcgccagcg	ttacagacat	180
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ctgcctgata	tggccctgtc	acaccatgct	gagcgcgact	atgaacccgc	cgctccagcc	300
tgcgcgcagg	ccatgacatg	cgaagtgact	gtcggcggtg	ccagcctgcg	tctgtccggg	360
gatttatcac	ctgcacttct	gaaaacgctg	atccgcgaaa	ctttggaaaa	acc	413

<210> 345

<211> 1230

<212> DNA

<213> Enterobacter cloacae

<400> 345

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aaatactggc	ggctcaagta	tcgtgtagcc	ggcaaagaga	agctgttagc	gcttgggtgtg	180
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gctgggggta	tcgatcctat	ggaagcgaaa	cgggaggaga	agattgcccg	tgaaattcag	300
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ggcaaaaaac	caatagccga	aatcaaaccg	cttgaactgt	tgaatgtgct	acggcgcatt	480
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caagtcttta	agcggatttg	ctataacgga	aaagtcaccg	ggcacggttt	ccggcacacc	1020
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cacgtcgaca	aaaactctat	acgaggaacg	tacaaccacg	cccagtatct	ggatggccgc	1140
cgcgaaatgc	tcagtggtga	tgccgactat	atggaggcgt	tgaaaaacgg	cgaaaatgta	1200
gtgcacggaa	cgtttgggaa	aagtgcctaa				1230

<210> 346

<211> 1227

<212> DNA

<213> Enterobacter cloacae

<400> 346

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ctgctggaag	cgcgtcgcaa	cggcttgagc	gaagcgatgc	tcgaccgtct	ggcgtgacc	180
ccggcgcgtt	tgaaaggtat	tgccgacgac	gtccgtcagg	tgtgcaacct	cgcgcacccg	240
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gcctccctgt	gcctgaagac	cggtaacgcc	gcgatcctgc	gtggcgggaa	agagacctgg	420
cgcaccaaac	ccgcgacggg	aaatgtcatt	cagcaggcgc	tggaggagtg	tggtttaccg	480
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acgcgcttta	ccgatggcgg	ccagtttggg	ctgggcgcgg	aggtggcggg	gagcacacag	1140
aagctgcacg	ccgcgggtcc	gatggggctg	gaagcgcgtg	ccacctacaa	gtggatcggc	1200
tttgggtgatg	ataccattcg	tgcgtaa				1227

<210> 347

<211> 399

<212> DNA

<213> *Enterobacter cloacae*

<400> 347

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gtgctgaagg	aagaagggtt	tatcgaagat	tttaaagttg	aaggcgacac	caagccggaa	180
ctggaactta	ctctcaagta	tttcagggt	aaagctgttg	tagaaagcat	tcagcgtgtc	240
agccgcccag	gcctgcgcac	ctataagaaa	aaagatgagc	tgccaaaagt	aatggctggg	300
cttggtatcg	cagttgtttc	tacctctaaa	ggtgttatga	ctgatcgtgc	agcgcgccag	360
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<210> 348

<211> 546

<212> DNA

<213> *Enterobacter cloacae*

<400> 348

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gtaaaaatcg	acgggtcagg	tattacgac	aaaggtaaaa	acggcgagct	gactcgtacc	120
ctcaacaaag	ctgttgaaat	taaaccatgc	gataacgctc	tgaccttcgg	tccacgtgat	180
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gataaacagc	tgatcgggtc	ggttgcagca	gatctgcgcg	cctaccgtcg	tcctgagcct	480
tataaaggca	agggtgttcg	ttacgccgac	gaagtcgtgc	gtaccaaaga	ggctaagaag	540
aagtaa						546

<210> 349

<211> 363

<212> DNA

<213> *Enterobacter cloacae*

<400> 349

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ctcaaaagag	tgggtgcaac	tcgcctgggt	gtacatcgta	ccccgcgtca	tatttacgca	120
caggtaattg	caccgaacgg	ttctgaagtt	ctggtagctg	cttctactgt	agaaaaagct	180
atctcagaac	aattgaagta	taccggtaac	aaagacgcgc	cagcagctgt	aggtaaagct	240
gtcgtcgaac	gcgctctgga	aaaaggcatc	agcaatgttt	cctttgaccg	ttccgggttc	300
caatatcatg	gtcgtgtcca	ggcactggca	gatgctgccc	gtgaagctgg	ccttcagttc	360
taa						363

<210> 350

<211> 927

<212> DNA

<213> *Enterobacter cloacae*

<400> 350

cagatggcta	agcaaccggg	attagatttt	caaagtgcc	aaggtggatt	tggcgagctg	60
aaacgcagac	tgctgtttgt	aatcggcgcg	ctgatttgtt	tccgtattgg	ctcttttatt	120
ccgatccctg	gtattgatgc	cgctgtactt	gccaaactgc	ttgagcaaca	gcgaggcacc	180
atcattgaaa	tgttcaacat	gttctctggg	ggtgctctca	gccgtgcttc	tattttcgca	240
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gctgttgtaa	gtctgggtcac	agggaccatg	ttcctgatgt	ggctcggcga	acagattact	540
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gcacagagca	cacattttacc	gctgaaagtg	aatatggcgg	gggttatccc	ggctatcttc	840
gcttccagta	ttattctgtt	cccggcaacc	atcgcgtcat	ggttcggggg	cggctcttcac	900
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<210> 351

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 351

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gtagtggttg	atggcaacgg	tgcggttgg	tttggttacg	gtaaagcgcg	tgaagttcca	180
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cgtgcaacta	ttgatggcct	ggaaaatatg	aattctccag	aaatggtcgc	tgccaagcgt	480
ggtaaatccg	ttgaagaaat	tctggggtaa				510

<210> 352

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 352

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gaggatactc	ctgctgttcg	tggtatggtc	aacgcggttt	acttcatggt	taaagttgag	180
gagtaa						186

<210> 353

<211> 438

<212> DNA

<213> Enterobacter cloacae

<400> 353

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tctcgttctg	gcggtggcgt	acgtcgcgg	ttcgagggtg	gccagatgcc	actgtaccgt	180
cgtctgcoga	agttcggcct	cacctctcgc	aaagcagcga	tcacagcgga	aatccgtctg	240
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attatcggta	tccagatcga	gttcgcgaaa	gtgatcctgg	ctggtgaagt	ttctactccg	360
gtaactgttc	gtggcctcgc	tgttactaaa	gggtcctcgtg	ctgctatcga	agctgctggc	420
ggtaaaattg	aggaataa					438

<210> 354

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 354

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atggcgcaaa	tcataatttaa	tagagaatgg	gttggttgagg	cagaactgac	tgcaacttacg	120
ggcctgagcg	agcgacaaat	aaaagctctc	cgcagtgggc	cctggccttga	aggtatacac	180
ttcaaacgcc	agtcaatgaa	aggcggagaa	accaaagcgc	gtctcctctg	gtacaactac	240
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<210> 355

<211> 1389

<212> DNA

<213> *Enterobacter cloacae*

<400> 355

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caatggccag	agattaaaaa	gcagctcacc	aaatggctgg	atactcctcc	agcgaagcgt	180
gagccggtag	atatcaatac	tgagacaaaa	accgacagcg	gcgccacgct	tggcggcgga	240
aatcagacag	accgcagccc	tgatctggtc	cacaacttgg	caaccctccg	cattgaaacc	300
gcacttggca	tcattgcggc	cgccatggac	tttgatattt	attccatccc	ggtagaaatc	360
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cgtgaactgg	tcagatcaga	tcacgctaag	ccagatccaa	aaaccgttgc	taccgcatgc	600
ggtagccgaa	ctacagagca	aaatgatgat	cagacccaac	ctgctgaaaa	ggacaaagct	660
gatttaaccag	cagtgtgccc	gggcgcgcgt	gcgcagctcg	acaaagaact	caatgaagca	720
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aaaccgaaaa	aagcagcaga	accagttcct	gaaacccaca	ccgcggcacc	actgaactac	1260
cgccagcagc	tcattccttgc	cgtatgcag	ggtatgtgtg	ccaacccttc	ctatcgctgt	1320
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ggtatctga						1389

<210> 356

<211> 1392

<212> DNA

<213> *Enterobacter cloacae*

<400> 356

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gtacaactac	cctgcataa	atcagttagt	gcaggagctg	taatgtcttt	tcccacgggc	120
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 <211> 522
 <212> DNA
 <213> Enterobacter cloacae

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 gcggcggtga accgctgtaa tgtcactgat cctgtgggga ctggatggta ttctggttcg 420
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<210> 358
 <211> 1221
 <212> DNA
 <213> Enterobacter cloacae

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<210> 359
 <211> 555
 <212> DNA
 <213> Enterobacter cloacae

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<210> 360
 <211> 309
 <212> DNA
 <213> Enterobacter cloacae

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<210> 361
 <211> 555
 <212> DNA
 <213> Enterobacter cloacae

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 gatcgtgatg ccgcgaatgc gctgactaat tgtgagattg tctgtggattc gtcgcagttg 300
 ccgcagctgg aagagggtga ctactactgg aaagacctta tgggttgcca ggtagtgacc 360
 actgaaggct acagcctggg gaaagtcacg gacatgatgg aaaccgggtc aaatgacggt 420
 ctgcgcatta aggcacaacc gaaagatgca tttggcatca aggagcgggt ggttccgttc 480
 ctcgatggac aggttatcaa gaaagtcgat ctactactc aaaccattga agtagattgg 540
 gatcctggtt ttttaa 555

<210> 362
 <211> 441
 <212> DNA
 <213> Enterobacter cloacae

<400> 362
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 gtcaacgaac tgcttccggt gatcgacagc ctggatcgcg cgttggaagt ggcgataaaa 180
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 aacgttcacc aggcattgac gatggtgga tccgaagacg ttgccgcggg taacgtgctg 360
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 gtggcgaaag cgaaagcgta a 441

<210> 363
 <211> 1389
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (301)

<220>
 <221> unsure
 <222> (314)

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gtaaaccgcc ttctgaaaca gttcgacgac atgcagcgca tgatgaggaa aatgaagaaa 1320
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<210> 364

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 364

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<210> 365

<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 365

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ctgatggtga ttgagcgtaa gatgttccac atcaccacag tggcggtggt gctgctgacg 660

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catgaaggct	ggcgcggtcg	ccgcgtggtc	tggttcaacg	ttgcgggtgc	gggcattctc	840
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<210> 366

<211> 1302

<212> DNA

<213> Enterobacter cloacae

<400> 366

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<210> 367

<211> 1095

<212> DNA

<213> Enterobacter cloacae

<400> 367

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<210> 368

<211> 693
 <212> DNA
 <213> Enterobacter cloacae

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<210> 369
 <211> 603
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (493)

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 tga 603

<210> 370
 <211> 993
 <212> DNA
 <213> Enterobacter cloacae

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 ccggttggtg ccgccatctg gttcgcgggt tactacggga tottccgctt cgcctacc 660
 cgcttcaacc tgaaaacgcc tggccgcgat accgatacgg ccaccagcgt tgaacaggcg 720
 gtggccggta ccgttgggaa atccggatat aacacgcggc ctattctggc ggcgctgggc 780
 ggtgcggata atattacctc totggataac tgcacaccc gcctgcgttt gtcggtggcg 840
 gacatgtcca aagtggatgc caacgcactt aaagetaaac gggctattgg cgtagtagac 900

ttaaatacagc acaattttgca ggctgctcatt ggcgcgcagg tacagtcagt gaaggatgag 960
ctggcaaccc tgatgcgaac cgtcgaagcc tga 993

<210> 371
<211> 1035
<212> DNA
<213> Enterobacter cloacae

<400> 371
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acgtcccttg ccgaagatgg cgtcgaaggca ctggaaaaaa tggccagcat ggcgcgggat 180
ctgatgatct gcgatctcga gatgcgcgcg atggacggat taatgctggt agaaaacctg 240
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gcgaagctgc ttcaggaact tcagccgcgg gtgcagcaaa atatctctca ttgcagagta 540
aattatcgcc agctggtagc ggctgaccag cctggactgg tgctggatat tgcgcgcctc 600
tcggattccg acctcgtttt ttattgcctg gatgttacct gagcgggaga taacggcggtt 660
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caggtgagta acggcgtgcc gttgggtacg ctgggaaata cttaccttaa tcaaattagc 960
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ttgtccacgg agtaa 1035

<210> 372
<211> 954
<212> DNA
<213> Enterobacter cloacae

<400> 372
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gtaaaaattg gactggcggt gggctcaggt gctgcccggg gttggtcaca tattggcggtt 120
atcaatacct taaaccagat ggggattgac gttgatattg ttgcaggatg ttctatcggg 180
tcgctggtcg gatctgcgta cgctgcgggt aagctcccgg agcttgaaag ctgggtgcgc 240
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gcgcctgtgc ctcaacaagg ctactggctc gttgaacgtg gcgtagtga tctgttccct 540
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gcggtgaccg caccgaacgc cattgaaatc atgacgacct ctattcaaat tcttgagaat 780
cgctcaagc gaaaccgtat ggctggcgat cctccggata ttcttattca accctattgt 840
ccacaaatct ctacccttga tttccaccgg gctgaggcgc ccatagcagc gggctcggtt 900
gccgtcgaaa agaaaataga tgaactgttg ccttttctgc gtacagcacg ttga 954

<210> 373
<211> 840
<212> DNA
<213> Enterobacter cloacae

<400> 373
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gttcttttca gaccgctatt agtggtgag actgtatact caacgcgtta ttcaatgcat 180
aaaagttcaa aacttgaaca gttcaggaga atttcaatgg ctgcccttaa ttcgaaagtc 240

agaaaggccg	ttatcccggt	ggcgggattg	ggtaccagga	tgttgccagc	gacgaaggca	300
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tgtattgcag	caggatatcac	cgaaattgtg	ctggtgacgc	attcatctaa	aaactctatc	420
gaaaaccatt	togataccag	tttcgaactc	gaagcaatgc	tggaaaaacg	cgttaagcgc	480
cagctgctgg	aggaagtgca	gtctatttgt	cctccacacg	ttaccattat	gcaggttcgt	540
cagggcctgg	cgaagggcct	ggggcatgca	gtattgtgcg	cacatcctgt	agtgggtgat	600
gagccggtcg	cggttattct	gcctgatgtg	atccttgatg	agtacgagtc	cgatctttcc	660
caggaaaaac	tggcggaat	gattaaacgc	ttcgacgaaa	ccggcagcag	ccagattatg	720
gttgagccag	tcgacgacgt	gaccgcttac	ggcgtggttg	actgcaaagg	cgttgacctg	780
caacctggcg	aaagcgtacc	gacgctgtgc	ttcaccacgg	gagctgacgg	agccggataa	840

<210> 374

<211> 891

<212> DNA

<213> Enterobacter cloacae

<400> 374

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caacgtaaag	ttctgcgcac	tatctgtccc	gatcaaaaag	ggctgatcgc	acgaattacc	120
aacatttgct	acaagcatga	actgaatata	gtgcagaaca	acgagttcgt	tgaccaccgt	180
accggtcgct	tctttatgcg	taccgaactg	gaaggcattt	tcaacgacac	aacctgtctt	240
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gccaaactac	gtggcttgga	cgctgaaatt	gccgccgtca	ttggcaacca	cgagacgctg	420
cgtacgctgg	tagaacgttt	cgacattccg	tttgagctgg	tcagtcacga	aggccatacc	480
cgtgaagagc	acgacaacct	gatggctgct	gcgattgaag	cgcataaccc	ggactacgtg	540
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attatcaaca	tccaccactc	cttctgtcca	gcctttattg	gcgcgcgcct	gtatcaccag	660
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gatgaaggcc	caatcatcat	gcaggacgtg	attcacgtgg	atcacacctc	cacggcagaa	780
gatatgatgc	gtgccggccg	tgacgttgag	aagaacgtac	taagccgtgc	gctgtatcag	840
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<210> 375

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 375

cgccttattt	tttgttccag	gaagagaatc	gtgtctcaac	tctgcccctg	tggtagcgct	60
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tcacacctta	tgcgctcgcg	gtatactgct	tttgtgatca	aaaacgcaga	ctacctgatt	180
aagacctggc	atccgtcctg	ccatgctgcc	gattttcgcc	aagagattga	agccggattt	240
gccaacaccg	tctggcaggg	cctcacccgtc	tttgaagccg	ctcccggccg	cgatgccaac	300
gagggctatg	tcagttttgt	cgcccgcctt	agcgaacaaa	acaaacccgg	cgccatcatt	360
gaacgctcac	ggttctttaa	ggacagcggg	caatggtatt	atattgacgg	cacacgtccg	420
caattcggtc	gtaacgatcc	ctgccccgtg	ggttcaggaa	aaaaatttaa	aaagtgttgc	480
ggcagtaaatg	cctga					495

<210> 376

<211> 222

<212> DNA

<213> Enterobacter cloacae

<400> 376

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cctcataaag	tgcgtcgtag	tccggattgg	agtctgcaac	tcgactccat	gaagtcggaa	120
tcgctagtaa	tcgtggatca	gaatgccacg	gtgaatacgt	tcccgggcct	tgtacacacc	180
gcccgtcaca	ccatgggagt	gggttgcaaa	agaagtaggt	ag		222

<210> 377

<211> 189
 <212> DNA
 <213> Enterobacter cloacae

<400> 377
 gagtctggac cgtgtctcag ttccagtgtg gctggtcac ctcctcagacc agctagggat 60
 cgtcgcctag gtgagccgtt accccaccta cttagctaata ccatctgggc acatccgatg 120
 gcaagaggcc cgaagggtccc cctcttttgg cttgcgacgt tatgcggtat tagctaccgt 180
 ttccagtgtg 189

<210> 378
 <211> 645
 <212> DNA
 <213> Enterobacter cloacae

<400> 378
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 atttcgctca ccgatcacca gaaaaatcag ctgggtggcct atgtcgatat gctgaacaaa 120
 tggaataaag cgtacaacct cacctccgta cgcgatccca acgagatgct gatttcgcat 180
 attctcgata gcatcgctgt ggcgcggtat ctgaacgggtg aacgttttat cgatgtgggc 240
 accggtccgg gcttgccggg cgttcggtt tctattgttc gaccggagag tcatttcacg 300
 ctgctggaca gcttgggcaa gcgcgtacgc tttttacgoc aggttcagca tgagctgaag 360
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 gacggtgtta tcagccgcgc gtttgccctc ctcaatgaca tgggtgagctg gtgcaaacac 480
 ctgccagcgg agaaggggcg tttttatgoc ctgaaagggc aacttcgggg ggacgaaatc 540
 gagcagcttc cggacgggtt tgcctgtcga tccattgaga aactccagat cctcagctc 600
 gaaggtgagc gtcactctgt gataattaag ccaaacactt tttaa 645

<210> 379
 <211> 411
 <212> DNA
 <213> Enterobacter cloacae

<400> 379
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 catctgaata accttcagct ggacctgctt acattctcgc tgggtgatcc acataacccc 120
 ccggccacct tctggacgat caacatcgac tccatgttct tctcgggtgt tttgggtctt 180
 ctgttccttg ccatgttccg tagcgttgc taaaaggcga ccagcgggtg tccagggaaa 240
 ttccagacgt tcatcgagat gatcatcggc ttctgcatg gcagcgtgaa agaactttac 300
 catggtaaga gcaaaactgat tgctccgctg gccctgaacg tgttcgtttg ggtcttcctg 360
 atgacctga tggacctctt gcctatccat ttcttacctt gggatcgggtg a 411

<210> 380
 <211> 1947
 <212> DNA
 <213> Enterobacter cloacae

<400> 380
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 ttttatcagg atccttttga cgtcatcacc attggcgggg gtcacgcagg cactgaggcc 120
 gcaatggccg cagcgcgaat gggtcagcag accctgcttt tgacacacaa tatcgacacg 180
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 gtgctttacc gtcaggctgt gcgcaccgag ctggaaaacc aaccgaacct gatgatcttc 420
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 ccgcgcgta ttgatgcgcg caccattgat ttcagcgtgc tggcacagca gcacggcgat 720
 aaccgatgc cgggtgttctc gttcatgggc aatgcggcgc aacatccgca gcagggtgcg 780

tgtacatca	cgcacaccaa	tgaaaaaaac	catgacgtga	tccgcaataa	tctcgatcgc	840
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tcacgtatct	ctggcgtcac	acctgccgcg	atttcgattc	tgtctggtgtg	gctgaaaaag	1920
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<210> 381

<211> 456

<212> DNA

<213> Enterobacter cloacae

<400> 381

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gctctcgccg	aagtgtgtaa	ggtgttgctg	acctttgctc	tactggtgat	ggcgctggcg	360
gtttttgaaag	tgggtattcat	gocgctgata	gcaacgtggg	ttttggtgct	ggtggtacaa	420
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<210> 382

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 382

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<210> 383

<211> 2508

<212> DNA

<213> Enterobacter cloacae

<400> 383

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tcgggtgagt	cgatctgtc	tcgcttttcc	gaaaacaacg	ccatgcctgc	cggcagtcag	180
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gtgctggatg	aacatggtga	atctgtcggg	tatgtcggac	aggccagcgt	actgtatatc	2400
cgtgctgaac	ggccgccacg	cgcgctcaac	gtgcactctc	gcggcggaac	gtgcgaaatc	2460
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<210> 384

<211> 1080

<212> DNA

<213> Enterobacter cloacae

<400> 384

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accgacagca	aatacggcac	catcctcgga	ttcagcaaca	acaagtatat	ggtgcggggc	300
gagatcacca	atccccggc	caataaaaac	ctgtctgcc	gcggtagcca	tacggcgctc	360
gagctgaata	caccgtttac	ggttcgcttc	acctcgctta	accagagcgg	caccacctcg	420
acgggggata	cggcgaacat	gagcgacgtt	ctgttcgtca	gcgacatgag	cgggttatct	480
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agcgggttca	agtggcctta	cgacaaccgc	gatatgtttg	gtcagccgat	gatcatcaaa	600
taocgcgcga	aactgactac	ctgttccttt	gataatgcgg	ggctgaccgt	ggcgctgcgc	660

acgctcggca	ttccccagct	cagtgcattc	tcacagccgg	ggctgacgcc	tttttcaactg	720
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gcggcgctgg	acgaacattt	cacccttccg	atggcggcgt	actattacgt	gtgggcaccc	1020
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<210> 385

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 385

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ccgcaccgtt	ttacatcttt	atgtaaaacc	ctcaacgtca	ggcgtgttct	gttgtgcccc	120
gagctgcatt	acgggctgtt	aaaaaaagt	ctggagatga	aatttgaatt	aaccatcagt	180
cagcaggatg	aattgactga	actgaaaaag	gaattacccg	cgttgctcat	ggcggacggg	240
caaaaaccgt	cgatctattc	gtggctcagg	cgggtaatgc	ggtccggctc	ccggggcgcg	300
tccatcctct	cggccagaga	gtgggaggtg	cttcatctta	ttgtggaagg	attttcaacg	360
acggagattg	cccgatcatg	aaaccgttcg	gtcagtacca	ttgcgacgca	gaagcataat	420
gcgatgaaaa	agctgaatct	ttccaaccac	agcgaactga	ttaagtattg	gcagacgggt	480
ggaaagatgg	aggaatag					498

<210> 386

<211> 1545

<212> DNA

<213> Enterobacter cloacae

<400> 386

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aaccgcgcta	acgcggcggc	aggttcgctg	cgtcagctcg	atccgcgtat	caccgcgaag	180
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cagctctcgc	actctccgga	ggcgggtgct	gcgttctatc	acaagggtga	agaagatcgt	360
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ctggtgattg	ccggggaagc	ggccggttcg	aagctggcaa	aagcgcagga	gcttggcattc	1500
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<210> 387

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 387

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ctgatgcgtg	aactgcgcga	gctggaagcg	cagcaccocg	aactgattac	gcccgattct	180
ccaacgcagc	gcgtcgggtc	ggaaccgctg	ggagctttca	gccagggtcg	ccacgaagtg	240
ccgatgctgt	cgctggataa	cgtgtttgat	gaagagagtt	ttctggcttt	caacaagcgc	300
gtgcaggatc	gcctgaagag	cgtcgacaat	ctgagctggt	gctgcgagct	aaagctggat	360
ggctctggccg	tcagtattct	ttatgagaac	ggcgtgatgg	tgcgtgccgc	aacgcgcggc	420
gacggcacta	ccggggaaga	catcaccacc	aatgtgcgca	ctattcgtgc	gatcccgtg	480
aaactgcgtg	gcgataacat	tcccgcoccg	ctggaattgc	gcggggaagt	gttccttccg	540
caggcgggct	tcgagaagat	caacgaagaa	gcgcgtcgta	cgggcgggga	aagtgtttgc	600
taa						603

<210> 388

<211> 951

<212> DNA

<213> Enterobacter cloacae

<400> 388

attaaacaga	tgaattattc	gttaacgtcag	cttcgcgttt	tgcgcaccgt	cgcgcaggcc	60
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gttaaggagc	ttgaaacgca	aacgggcgtg	aagctgctcg	accgcacgac	gcgagaagtg	180
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cgctatccgg	atattgattt	tgttttgcac	gacaggccgc	agcagtgggt	actggagagt	420
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gaggcccgca	cacgtgatcc	acttttttaac	gaaaccaata	atcagacgta	g	951

<210> 389

<211> 1020

<212> DNA

<213> Enterobacter cloacae

<400> 389

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gttattgaag	gactgaccac	ggcagctatt	gccctgctgt	tctttatgca	tggcgccaaa	180
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cagtctgcaa	ttgcctttac	ctcgctggcg	ggcggtaacg	tcgcggcggc	ggtttgttct	420
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tgccggtttg	tgctcggaca	cttatcccg	ccctggattg	gggagtttgt	ggcgaaacat	600
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gtgttgccgc	tgatgatttt	ccatcagatc	cagctgatgg	tgtgtgcggg	actggcgccg	960
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<210> 390
 <211> 1587
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 390
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 ttacagtttt actggagtta tcacaagcga gacgtcagat tgcatactct cattaccgat 180
 ttaagcgttt acatggagag ctatttcgat gagctcaaaa tgtcgattga tacgctccag 240
 ccactcacgc tgaacagctg cgaggaaagt agtgccgccg tgacctcccg ggccggccttt 300
 agcatcaacg tgcgcgcctt tttgctggtc agggataaac aggccttctg ctctcggca 360
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 caaccgcgata tcacgctcgg ggaataa 1587

<210> 391
 <211> 1881
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 391
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 tcgagccagg cgcagaccat caaagagagc acggcctttg ccgtcatttg cgagccgaag 180
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<210> 392

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 392

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gcgattgcgg	caatagaatt	tggtcacgct	ggcgccatgc	cgggcgccgg	cggcgaagga	180
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ccgctgcacg	agcgctattg	caggatgcta	tgggattatg	tccgtttcga	ttttggcgac	360
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ggcggttttg	cggcgcttac	gatgctgacc	aaaaacgcct	ttcttgatga	gatccgcaaa	780
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<210> 393

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 393

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ggcgatttag	tctgttcag	agcaggtcca	accggctgcac	acgttggcat	ctatatcggt	180
aacgatcagt	ttgtccatgc	ttccaccagc	agcgggtgtga	cgatttccag	catgaacgaa	240
ccttactgga	agaaacgcta	caacgaagct	cgccgcgttc	tgagccgtag	ttaa	294

<210> 394

<211> 1512

<212> DNA

<213> Enterobacter cloacae

<400> 394

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aattcacagg	actgggatgt	tatgaaaaag	ggattatcgg	tatggcctgc	gctatcaacc	120
gtggcttatg	gggtttttctc	tgcactgttt	tacgctttcg	gagttcatgc	tgacgatgac	180
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cagaatggta	cgcagcagaa	aaaatatacg	gtgcttaaca	gctacgtcca	gcatecgctg	780
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<210> 395

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 395

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ctgatggata	agctttatata	caaatcggac	gctgaactat	ttagggttgg	ctggacttat	540
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<210> 396

<211> 1209

<212> DNA

<213> Enterobacter cloacae

<400> 396

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<210> 397
 <211> 1161
 <212> DNA
 <213> Enterobacter cloacae

<400> 397
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 gccagtaatg tgagtatgcc gcttaatatata tcatcgatag cggtaagtaa tgatatacca 180
 gatggaacaa tcatatatca acaaaaaatat ataccagggtt attcaagtat tagcgttaac 240
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<210> 398
 <211> 1214
 <212> DNA
 <213> Enterobacter cloacae

<400> 398
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<210> 399
 <211> 903
 <212> DNA
 <213> Enterobacter cloacae

<400> 399

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<210> 400

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 400

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<210> 401

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 401

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<210> 402

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 402

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cgcactttca	ttggtatcaa	agaggaggag	atcgcgaaac	gccaggatat	cgtggtgaat	180
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gctgaagtgg	agatcgataa	acttcacgcc	ctgcgctacg	ccgactccgt	ctccatgacg	420
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<210> 403

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 403

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<210> 404

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 404

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<210> 405

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 405

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<210> 406

<211> 720

<212> DNA

<213> Enterobacter cloacae

<400> 406

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<210> 407

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<220>

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<222> (1008)

<400> 407

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<210> 408

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 408

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<210> 409

<211> 210

<212> DNA

<213> Enterobacter cloacae

<400> 409

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cgcgctcgt	ttgcaccgta	caatacaaaa	agtgaactcg	atgcgctggg	ttccgcgcgc	180
gaccgcgccc	tggaattact	ggtggattaa				210

<210> 410

<211> 1134

<212> DNA

<213> Enterobacter cloacae

<400> 410

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atttatcagg	gcacggggcc	ggatgcgggc	catcgctcag	gctggtataa	ccactacgga	1080
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<210> 411

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 411

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ggagcggcca	ccatggtgac	cgccctcctt	ggctttgtgg	cggtctctca	cgccctgaag	780
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<210> 412

<211> 207

<212> DNA

<213> Enterobacter cloacae

<400> 412

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atcgtctctg	aagggaacc	gacaaccgat	aatgataccg	ggatgatttg	tcttcacaca	180
cgccgctgga	agatccgata	ttgcgtt				207

<210> 413

<211> 462

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (278)

<220>

<221> unsure

<222> (403)

<220>

<221> unsure

<222> (424)

<400> 413

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aacgaaatta	agaaaggat	ggtactgaat	tacaacggca	aactgctgat	tgtgaaagat	180
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<210> 414

<211> 1272

<212> DNA

<213> Enterobacter cloacae

<400> 414

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<210> 415

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 415

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gaaattgagc	gtggcgaagt	taacctgggt	cggaacgacg	gcctgcatgc	cgcaggaaaa	180
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cgttttcagg	ttgtgcaggg	ccgtaccggc	attaacgtta	agctgaccga	gaaagacggt	360
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<210> 416

<211> 1167

<212> DNA

<213> Enterobacter cloacae

<400> 416

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<210> 417
 <211> 1755
 <212> DNA
 <213> Enterobacter cloacae

<400> 417
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<210> 418
 <211> 2496
 <212> DNA
 <213> Enterobacter cloacae

<400> 418
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cagaagatcc	atgaactgat	ggaaaacagc	atgaagctgg	acgttcggtt	gctggtggaa	2460
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<210> 419

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 419

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ggccatgctg	cgggtagccg	tgtataacgg	ggcggtgccc	caagcgcttc	tggaacaaag	180
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<210> 420

<211> 471

<212> DNA

<213> Enterobacter cloacae

<400> 420

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atggggctgc	cactgctggc	ggtctctggt	gttgaaagctg	acgacgttat	tggtaccctg	420
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<210> 421

<211> 663

<212> DNA

<213> Enterobacter cloacae

<400> 421

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aacggtgatg	tacaggttga	accgttctcc	tcgctgaaaa	agcagggcgt	ggataaactg	600
cgtcagaagc	tcgacagctg	gtttaacgat	ctggaaccgg	cgacagaagc	ggaagcagag	660
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<210> 422

<211> 650

<212> DNA

<213> Enterobacter cloacae

<400> 422

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cacctcacca	gtggcagaaa	atgccgttct	ggcacaagggt	gcgtccatgg	gccagccagc	300
tcaccagat	gggggtcgt	gcgtgcgtat	cgcttcgagt	tatcgttggg	gtccagcact	360
ataaactca	gtctgaagcc	aatcagcaac	ctgaagcgcc	agtgtttaat	acgttgccga	420
tgatgggtaa	agccagccc	gttagcctgg	gcgtaccggc	agatgcctcc	gcaagcggcg	480
gacagcaaca	gcaggtacag	gagcagcgcc	gtcgcattaa	tgcgatgttg	caggattacg	540
agttgcagcg	ccgtctgcac	tccgagcagc	ttcagtttga	gcaggcccaa	accagcagg	600
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<210> 423

<211> 1632

<212> DNA

<213> Enterobacter cloacae

<400> 423

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gatctcatcc cgcgtcagca gtttgacatt gcgagtcttc acacgaggct ggcaggatcc 1620
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<210> 424

<211> 492

<212> DNA

<213> Enterobacter cloacae

<400> 424

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gctcagccgc tgggtggcagg gcaaaaagtg gagctcggca tcgctgaagg tagcctgctc 240
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ttccagatgc tgttcggcac agatttggcc gccatgtgcg ggcccgcggt gggcgggcgtg 360
ggcggtttct ggcttgctaa aggcgtttcc ccaaggcttg ccgcccgga agcgtggcag 420
cccgttatcc tcagcgttgc actggcacc gaccaacttc gtgttgagac gctctcttct 480
aaggcccggt ga 492
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<210> 425

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 425

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tctgctaacc cctcggctga tgtttcatcc gggcggttgt tgcagcaaat gaatctggcc 180
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<210> 426

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 426

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agaggctaca gaaactctac tgaaatcatt attgatgaaa gcatgacggg tattgtcggg 180
cgtaatgact ttgggaaatc aacgcttctg gaagcgctgg ctattttttt tgaaacagaa 240
tga 243
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<210> 427

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 427

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caggccaatt	tctctgccga	tatcgcgcgt	gagatcagaa	cgcccatcac	caatctgggtg	180
acgcagactg	atatcgcact	gagtcaggat	cgaacacaga	gggaacttga	ggatgtcctc	240
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agagtgcagg	tggaatcgga	cgtacactca	acgcgtttta	tcttatccgt	gccagactg	780
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<210> 428

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 428

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caccatgaag	gggcaatagc	aatggctgag	accgagctca	aatacggaaa	agatccgaaa	360
atgagaaagc	tcgcgcagga	catcattaaa	gtcaaaaaag	gtgaaattga	gcagatgaat	420
aaatggcttg	atagtcaaaa	gtaa				444

<210> 429

<211> 702

<212> DNA

<213> Enterobacter cloacae

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atgggaaagt	agaccgtttc	ccctaccggg	ccgtcgaaat	cattagcggc	aatgaatgag	600
catgaaagag	ctgcagttgc	ccatgaattt	atgaataacg	gtcagtctgg	cccacatcag	660
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<211> 396

<212> DNA

<213> Enterobacter cloacae

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cgccttctcc	gggcgctcct	tctctctctt	ccttcccttt	ccgttggggc	gggcggtggc	180
cctgcgcctt	ttttcttctc	cgcctgtgcg	ctcccgtttt	ttctgccttc	ctcctccttc	240
ccgtcgtctg	cctactcggg	ctacaccatc	gacgagcacc	tggaatgct	gatgggtttg	300

catcacctcg acccgatat cgccgaggac gtggcgtttg ccgaatcccg cattcgccgg 360
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<211> 768
<212> DNA
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<212> DNA

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ctgatatac cacaatttgt ccgtccattc gttaactata tcaaaaacga ctttgtcgac 300
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<210> 434
 <211> 399
 <212> DNA
 <213> Enterobacter cloacae

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<400> 434
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ttcggccagg ctgctggcct cctcgcagtg ggtgccatcg tcgagccgca acagctcggc 180
aatctcgtcc agactgaacc ccagccgctg tgccgatttc acgaatttca cccgaaccac 240
gtccgctcc ccatagcggc ggatgctgcc gtaaggcttg tccggttccc gcaacaggcc 300
cttgcgctga tagaagcgga ttgtctccac gttgaacccg gccgccttgg caaaaacgcc 360
aatggtcagg ttttccaaat tattttccat atcgcttga 399

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<210> 435
 <211> 438
 <212> DNA
 <213> Enterobacter cloacae

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<400> 435
cgtgcgagat ttttcaggcg cacagccggg agtgtactca ggttttcagc atgcaggcca 60
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acagggccct ttttcagtga ttccagtaaa gacaggcggc tgcaatcagt tggccccagc 180
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cgcaacgtcg ctttttccct tacctctgaa atcaacggg tcagcgtagt ggctccgggg 300
agaataatac gatgttgcat aagccaccct gtcgccagat cgaaaagcag gccaggacgt 360

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tcgttgctta tccagctccg ggtatataaa agacgggtaa ggcgaaatgt ccagggccag 420
gcaaattcac gataactga 438

<210> 436

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 436

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gctcgggtct	caaccagtc	gcagtctctt	gatcttcagg	tcagagcact	caaagacgca	180
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ggcgtggcag	tccggttcat	tgatgacggg	atcagtaccg	acggtgatat	ggggcaaattg	420
gtggtcacca	tcctgtcggc	tgtggcacag	gctgaacgcc	ggaggatcct	agaacgcacg	480
aatgagggcc	gacaggaagc	aaagctgaaa	ggaatcaaat	ttggggggcc	cgggcaggcg	540
taccgtggac	aggaacgtcg	tgctgacgct	tcatcagaag	ggcactggtg	caacggaaat	600
tgctcatcag	ctcagtattg	cccgtccac	ggtttataa			639

<210> 437

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 437

ggcatagctg	accttgccag	gcctgcttcg	ccctgtagtg	acgcgatcaa	cgggcaggaa	60
acattccctt	ttcgtgcatg	gcaggcgcac	acgagttcag	acagcacggg	ttccatgcgc	120
gccaaagtcg	ccatcttctc	gcgcacgtcc	ttgagcttgt	gttcggccag	gctgctggcc	180
tcctcgagct	gggtgccatc	gtcgagccgc	aacagctcgg	caatctcgtc	cagactgaac	240
cccagccgct	gtgccgattt	cacgaatttc	acccgaacca	cgtecgccctc	cccatag	297

<210> 438

<211> 702

<212> DNA

<213> Enterobacter cloacae

<400> 438

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ttgaaccagg	agacggaaat	gtcatacagt	ggcgaacgag	ataactttgc	accccatatg	120
gcgctgggtc	caatggttat	tgaacagacc	tcacgcgggtg	agcgctcttt	cgatatctat	180
tcccgctctg	tcaaggaacg	cgttatcttt	ctgaccggcc	aggtggaaga	ccatattggt	240
aacctgatcg	tggcgcagat	gctgttccctg	gaagcggaaa	acccggaaaa	agacattttac	300
ctgtatatca	actgcgcggg	cgggtgtgatt	acggcgggca	tgtctattta	tgacaccatg	360
caattcatca	agccggatgt	cagcaccatc	tgtatggggc	aggcggcgctc	catgggggct	420
ttcctgttaa	ccgcaggggc	gaaaggtaag	cgtttctgcc	tgccctaactc	ccgcgtgatg	480
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gaaattctga	aagtaaaagc	gcgcattgaat	gaacttatgg	cgcagcatac	gggtcaacct	600
ctcgagcaga	tcgagcgoga	taccgagcgc	gacgcgttcc	tctctgcgcc	agaggcagtt	660
gagtaacggc	tagtcgactc	catttttgacc	catcgtaatt	ga		702

<210> 439

<211> 1332

<212> DNA

<213> Enterobacter cloacae

<400> 439

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acagataaac	gcaaagatgg	ttcgggcaaa	ctgctgtact	gctctttttg	cggcaaaagc	120
cagcatgaag	tgcgtaaact	gattgcccgg	ccgtccgtgt	atatctgcga	cgaatgcgtc	180

gatttatgta	acgacatcat	tcgcgaagag	attaaagaag	tcgcgcgcga	ccgtgagcgc	240
agcgcggttac	caacgccaca	cgagattcgc	caccacctgg	atgactatgt	cattgggtcag	300
gagcaggcga	aaaaagtgc	ggcggtggcg	gtatacaacc	actacaaacg	tctgcgtaac	360
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gtcattgggtg	gccagaccaa	gccgttactg	atttacggta	aaccggaagc	gcagcaggca	1320
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<210> 440

<211> 1695

<212> DNA

<213> Enterobacter cloacae

<400> 440

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cccttatttg	tagggcgggg	aaaatctatc	cgttgcctcg	aagccgccat	ggatcatgat	180
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gagcacttct	ctgcgaaggc	agagtacctt	gattcacccg	aacttgatga	gcgcgagcag	420
gaagtgcgtg	tacgcaccgc	gatcagccag	ttcgaaggct	acatcaagct	gaataagaaa	480
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ccgaagcaga	ttgagcgtaa	cgcgcttaaa	gccaacgagc	tgaccgttga	ggacagcgcc	1620
attgtcggca	ttattcgtaa	ctacaccctg	gaagcgggtg	gtcttcacca	cggggctggc	1680
aggatccgcc	cttag					1695

<210> 441

<211> 225

<212> DNA

<213> Enterobacter cloacae

<400> 441

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aggccacggg	caccggtttt	acgcgccatc	gctttcttgg	caatcgcgtc	caacgcttgc	180
tcacggaatt	ccagctcaac	gccttccaga	ttaaacagcg	cctga		225

<210> 442

<211> 192

<212> DNA

<213> Enterobacter cloacae

<400> 442

atcaacgcgt	cttcgctcag	ttcgttcagg	gtcgccacaa	ccggcagacg	gccgataaat	60
tccggaatca	aaccgaattt	gatcagatct	tccggtcaca	cctgcgccag	cagctggcct	120
tcgtttggtt	tttcagacgt	ggctttcacc	gttgccgcaa	aaccaatgcc	ggagccggtt	180
tccacacggt	ga					192

<210> 443

<211> 483

<212> DNA

<213> Enterobacter cloacae

<400> 443

gatgatagg	gtggtccgct	tcacaaaaga	ggactgcgct	cgctcggcgc	tctgccagcg	60
cacgctacaa	gcgtattatt	gaatatgctg	ttgtgttcaa	ggcccgggaa	accgggcttt	120
gttttttggt	catttttatcc	cctcttccct	ggggagaggg	ttaggggtgag	gggctcaggc	180
cgcaccgagc	tgcataatagc	accggggggg	attgactcgc	tgcgctcgcc	ctgcgggcag	240
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agctcttctt	caaatatggc	gggtgagggg	ggattcgaa	ccccgatacg	ttgccgtata	420
cacactttcc	aggcgtgctc	cttcagccac	tcggacacct	caccatattg	ttttgctgcc	480
tga						483

<210> 444

<211> 1119

<212> DNA

<213> Enterobacter cloacae

<400> 444

gagaagacag	cggtagtctc	cggcagtgat	gttaactcac	tatggagatc	gcgaatggtt	60
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tccggcagcg	atctcttcac	caccaaattc	tctccttcac	ctcaacaacc	tttttctacc	180
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gatgaatacc	aacaactcaa	ggtgctatcc	atgggaagac	agaaagcagt	gatcaaaagct	360
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<210> 445

<211> 186
 <212> DNA
 <213> Enterobacter cloacae

<400> 445
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 gtctgtccaa ctggctcgcg cagttgtcga accccggtcg ggggttctca ttccccgcaa 120
 aggcgtacaa catgcgaaaa aaaagcccgc attttcatgc gagctcttct tcaaatatgg 180
 cggtga 186

<210> 446
 <211> 270
 <212> DNA
 <213> Enterobacter cloacae

<400> 446
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 accggtaccc tgcttgaagg gatcttcggc taccaggaaa cgcgcagcgt cagcgaagtg 180
 gcgatgtact ttatctatct ggttccggcg ctgatcctgt tcgctatgcc gccgcgtacc 240
 ggctcgcaga cgtcgcgcgt tgcgcggtaa 270

<210> 447
 <211> 1155
 <212> DNA
 <213> Enterobacter cloacae

<400> 447
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 gtcaaagtca ccgtcaacga taaacagtgt gagccgatga ccatacaggc taacagcggc 180
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 ctgggtctgg attaa 1155

<210> 448
 <211> 1287
 <212> DNA
 <213> Enterobacter cloacae

<400> 448
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<210> 449

<211> 312

<212> DNA

<213> Enterobacter cloacae

<400> 449

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<210> 450

<211> 1809

<212> DNA

<213> Enterobacter cloacae

<400> 450

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<210> 451

<211> 615

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (527)

<220>

<221> unsure

<222> (554)

<400> 451

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gacgaagact	ggtccggcga	taaaagcgga	atcagcctgt	ataaagcggc	tgcaaaattc	420
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gcgcgcgact	ggagctttat	gccagggacc	tatcaggggg	cggaaancgg	tgctaatttt	540
gactacggcg	aatncggggg	cgtgagcttc	tcttatatgt	ggaacaacga	agttacaagc	600
gccgtggcac	attga					615

<210> 452

<211> 2001

<212> DNA

<213> Enterobacter cloacae

<400> 452

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gcagcattgc	tgtctcgatt	cgggcaaccc	gatcttctta	acgtgccgtt	tattgcccag	180
gcaggcggcg	caatttttga	caacctggcg	ctgattttcg	ccatcggtgt	ggcgtcaagc	240
tggtaaaaag	acagcgcggg	tgcgcggcca	ctggcagggg	ctgtcgggta	cttcatectc	300
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gacttcctga	atgctaacgc	gcgctccatg	ataagcccgg	tcgtgtgcag	caacatcgac	1920
gacttcagcg	gtctggtgat	ccaggcgcag	gggcaggtag	ttgcaggcca	gacgccactg	1980
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<210> 453

<211> 861

<212> DNA

<213> Enterobacter cloacae

<400> 453

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ttttccgttt	ccaggcagaa	cgcattggtt	gtgttgaaaga	ttttcacgat	agtaccggca	420
gccggagaga	ccacggtttt	gtccgtttgt	tttaccgcca	cgcgcgcacc	gaccgctttg	480
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ccaccacag	cggcaatgta	g				861

<210> 454

<211> 1101

<212> DNA

<213> Enterobacter cloacae

<400> 454

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ccagctgcgc	ggcatggttg	a				1101

<210> 455
 <211> 312
 <212> DNA
 <213> Enterobacter cloacae

<400> 455
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 ctggaatcgg gcgatccctg tctcgccatt ttgcagcaaa tcgcgcgcgt gcgcggcgct 180
 gccaatggcc tgatggggga aatggttgaa attcacctca aagatgagct ggtgacgggg 240
 gagaccaccc cggatcagcg ggctgtgcgg atggcggaag tcggccattt actgcgctct 300
 tatctaaaat aa 312

<210> 456
 <211> 312
 <212> DNA
 <213> Enterobacter cloacae

<400> 456
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 gcgatggctg gtaaaattca gctcgaccgc ttcattacgc accgcctgcc gctggagcag 240
 atcaacgaag ccttcgattt gatgcacgaa ggaaaatcta ttcgtaccgt tatccatttc 300
 ggcgacaact ga 312

<210> 457
 <211> 1551
 <212> DNA
 <213> Enterobacter cloacae

<400> 457
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 gacaacacaa catcgatgca ggcgcagcat aagctgagtt tcttgcatca catccggtcg 180
 gttccgctgt tttcctccat tctcggtggc attattctcc tgtttgcatt gagctcgggt 240
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 atccacgcgg gggcgggcag ccgtatcgcg gagatggagg cgatgaaaca aaacatcgct 420
 gaggttgaga cccgcacag gcagtcgcag gatggatttg ccgcctatat gaagcgcact 480
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 aaccacgaaa atgagaccgc gcgtccgctg gacgatgcct ataacgcggg gctgttgaag 660
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 cagggttccg gggaggtggt tgcagcgggc aataccatga atgaaatcgt cgaggcggtt 1500
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<210> 458
 <211> 501

<212> DNA

<213> *Enterobacter cloacae*

<400> 458

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agactgatca	gcataatcgc	cacgaatccg	tttgtaagac	ttaaccagcg	cgcgctactt	180
tttcccacta	acctatactt	tcagtctgac	acacgactgg	aggtttctat	gtgtggacgt	240
tttgacacaag	cccaaaccgg	tgaagagtac	ctagcttact	tcgccgatga	agccgttcgt	300
gacatagcct	atgaccacga	accaattggg	cggtacaacg	tggcaccggg	ttctaaagtc	360
ctgtttgtga	gcgaacacga	cgagcaatta	catcttgatc	ctgtattctg	gggttatccc	420
ccgggggtgg	gggataaaag	gccactgata	aacgcccgcg	tcgaaaccgc	ggccaccagc	480
cgaatgttta	agcctctctg	a				501

<210> 459

<211> 333

<212> DNA

<213> *Enterobacter cloacae*

<400> 459

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ggcagtacgc	catttgagcg	aggcgatgaa	gctgagggct	ttctaatagt	cacatctgca	180
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gctcgcgagt	ggatgcgaca	ggaggttaga	ggaaaagagg	ctgaacagat	cgctgccgac	300
ggagtatcga	cacgccaggg	cgaagtacag	cgt			333

<210> 460

<211> 429

<212> DNA

<213> *Enterobacter cloacae*

<400> 460

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ctgattaaga	agttcatggc	totttgcccc	tatattcgag	aagagcagtg	tgaagagaat	120
cgcttttttt	tcgactgcct	ggctgtttgc	gtcaacgtga	agcctgcacc	cgaaaaacgt	180
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agagcctga						429

<210> 461

<211> 507

<212> DNA

<213> *Enterobacter cloacae*

<400> 461

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tcttcacgcc	tgaaggccgt	cgctgtctt	ggctccggtg	tgcagtctct	gttaagcgat	180
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atgcatgatg	cttcagacga	agcgttgcgc	attgaactta	atcgttattc	attaaaaacg	300
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ctggaggtgc	ccttcagccc	ggtgtaccag	aattttgaca	aagcgtgaa	agagatcaca	480
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<210> 462

<211> 1143

<212> DNA

<213> Enterobacter cloacae

<400> 462

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<210> 463

<211> 1080

<212> DNA

<213> Enterobacter cloacae

<400> 463

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<210> 464

<211> 732

<212> DNA

<213> Enterobacter cloacae

<400> 464

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<210> 465

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 465

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<210> 466

<211> 564

<212> DNA

<213> Enterobacter cloacae

<400> 466

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<210> 467

<211> 183

<212> DNA

<213> Enterobacter cloacae

<400> 467

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<210> 468

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 468

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294

<210> 469

<211> 1785

<212> DNA

<213> Enterobacter cloacae

<400> 469

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<210> 470

<211> 225

<212> DNA

<213> Enterobacter cloacae

<400> 470

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<210> 471

<211> 720

<212> DNA

<213> Enterobacter cloacae

<400> 471

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<210> 472

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 472

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<210> 473

<211> 3678

<212> DNA

<213> Enterobacter cloacae

<400> 473

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<210> 474

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 474

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<210> 475

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 475

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gattgcgtta	aaattggcct	ctacataactt	ggatatcttg	ctcaaaaaac	gccctgggta	540

agctccgagt ctataattac cgcgcttcgc ttatctgaag ccaagaattc aaaatag 597

<210> 476

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 476

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cataaccacc	ttgagagcgt	tgcgctgcgg	tacgagaaga	tcacctggaa	acactgcgac	480
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<210> 477

<211> 1284

<212> DNA

<213> Enterobacter cloacae

<400> 477

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<210> 478

<211> 474

<212> DNA

<213> Enterobacter cloacae

<400> 478

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<210> 479
 <211> 948
 <212> DNA
 <213> Enterobacter cloacae

<400> 479
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<210> 480
 <211> 522
 <212> DNA
 <213> Enterobacter cloacae

<400> 480
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 ccggaagtg acagtaagaa cgttgatgtg tgggtttgca aaaatcctga cgaagaggac 480
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<210> 481
 <211> 243
 <212> DNA
 <213> Enterobacter cloacae

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<210> 482
 <211> 315
 <212> DNA
 <213> Enterobacter cloacae

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<210> 483

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 483

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<210> 484

<211> 2109

<212> DNA

<213> Enterobacter cloacae

<400> 484

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<210> 485

<211> 2613

<212> DNA

<213> *Enterobacter cloacae*

<400> 485

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<210> 486

<211> 768

<212> DNA

<213> *Enterobacter cloacae*

<400> 486

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<210> 487

<211> 759

<212> DNA

<213> Enterobacter cloacae

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<210> 488

<211> 231

<212> DNA

<213> Enterobacter cloacae

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<210> 489

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 489

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actatcagga	aaagagacag	gtttatgcgc	aggcttaccc	ctttattgct	ggtctcgctg	180
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atggttcgtg	gttccccgga	tgatgcagaa	gacgcaattg	aagcgcaggc	cgttgccgca	360
aaagcagatt	attacgtcat	cacgatgatt	gatgaaacca	ttattacggg	acagtgggtac	420
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<210> 490

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 490

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cagtcggccg	aattttgccag	cgcggattgc	gtcacggggc	tgaacgagat	tggtcagatc	180
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gatgaacagg	gcgcatacctg	gtatcgcata	gtccagatgc	aggaagatca	ccatgttaat	300
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<210> 491

<211> 1182

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

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<221> unsure

<222> (1176)

<400> 491

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<210> 492

<211> 1482

<212> DNA

<213> Enterobacter cloacae

<400> 492

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<210> 493

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (322)

<400> 493

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<210> 494

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 494

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<210> 495

<211> 369

<212> DNA

<213> Enterobacter cloacae

<400> 495

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<210> 496

<211> 2436

<212> DNA

<213> Enterobacter cloacae

<400> 496

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<210> 497

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 497

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<210> 498

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 498

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<210> 499

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 499

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<210> 500

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 500
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<210> 501
 <211> 978
 <212> DNA
 <213> Enterobacter cloacae

<400> 501
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<210> 502
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 <213> Enterobacter cloacae

<400> 502
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 aaggattttg gcatcggtac gccgcagcag aatgtgccgt acaccctgaa gggctgcggt 180
 tcgctcgact ggggcatgca gtcgaggctt tcgcgcattt tcaaccgca gagcaaccgc 240
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 ggtaactoga ttctgggcga actgtcgaac gagtgcgtgg cgggtggcgat ggaagacgcg 480
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 ctggcggtga cgggcgtggg gaaagagatg gcgcgtgacg ctcggtattt ttcgctggca 660
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 cagggagaag caaaatga 978

<210> 503
 <211> 1056
 <212> DNA
 <213> Enterobacter cloacae

<400> 503

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gtctccggtc	aggtgcagct	catcaataac	ttcgtcaacc	agggctataa	cgccatcatc	300
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gtcaagggtcc	tgacctggga	ttccgacacc	aaacoggagt	gccgcagcat	ctacatcaat	420
caggggacgc	cggaaacagct	ggggcgccctg	ctgggtggaga	tggcgggcaa	gcaggtcacc	480
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cagggtacc	agtatgaggc	gaagggaac	ggcatcgctg	tgctgccgga	gcgcgtgggtg	1020
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<210> 504

<211> 543

<212> DNA

<213> Enterobacter cloacae

<400> 504

aaaagtgacc	gccagctgcc	cgggtgccgat	cgttatcgcg	gggggcaaaa	agctgccgga	60
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ggggcgcaac	atcttccagt	ccagcgcgc	gctcgccatg	ctgaaggcgg	tgaagaaagt	180
ggttcacgag	aacatgagcg	ccgggaggc	gttcagttc	tggcaggaag	agaaacaggg	240
agaagcaaaa	tgaacgtgac	gctggtggag	atcaacatca	agcccgagcg	ggtggcggag	300
tttctggagg	tatttcgcgc	caaccacgag	ggggcgatca	aggagccggg	caacctgcgc	360
ttcgacgtat	tgcaggaccc	gcgggtgaaa	acccggttct	ttatctacga	agcctataaa	420
gacgaaaagg	cgggtgctgg	gcataagcaa	acccgcact	atctcgctg	cgtggataag	480
ctggaggagc	tgatgtcgga	gccgcgcaaa	aaacgcagct	ttgtcggatt	gttgccggag	540
taa						543

<210> 505

<211> 1338

<212> DNA

<213> Enterobacter cloacae

<400> 505

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tcggcgatgt	accagcagga	agttccgcag	tacggcacct	tgctggaact	ggtggcggac	180
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gaactggcgc	gocctgaatgt	tgaacgtcac	ggtgcgatcc	gcgttggcac	cgcgaggag	300
ctttccaccc	tgcgcgggat	cttcgccatt	atgggcgatg	acccggtcag	ctactacgat	360
ctctcccagg	cgggcgtgcc	cgtccactcg	acggcgtttc	gtccgacaga	cgatgcggcg	420
ctctgcogta	atccgtttcg	cattttttacc	tcgctgctgc	gcctggagct	gattgaaaac	480
gttgcgctgc	gcgaaagggc	ggcggagatc	ctctcccggc	gcaacatctt	tacgccgcgc	540
tgtotggaa	tgatcgacct	gcattgatgcg	cagggacact	ttaccgaggc	acaggcgcgc	600
gaatttgtgc	aggaagcctt	agaaaccttc	cgctggcatc	gccatgcgac	ggtcgatcag	660
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ttcctgcgcc	gtcaggggct	ggcttatttc	cgctaccgtc	tgaccccgac	aggtgaggcg	1140

catcgccacg	cgtttcgtcc	cggcgtcgat	ccgcaaccgc	tgatcgaacg	cggtctgggtt	1200
gtggcacagc	ccatcaccta	cgaggatttt	ctgcccgta	gcgcggcggg	gatcttccag	1260
tcgaatcttg	gctatgaaac	gcaggcgcg	atccacggaa	atgccagcgc	caatgccttc	1320
caagccgccc	ccctcccc					1338

<210> 506

<211> 960

<212> DNA

<213> Enterobacter cloacae

<400> 506

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gggcgagcgg	ctgaaaccct	taacctcagt	cagcctgcac	tctccaaaac	gctgaacgaa	180
ctggaacagc	ttaccggaac	ccgcctgttc	gatcgcgcc	gtctgggggc	tcagcttacg	240
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ggtcaggcgt	taaaccgtaa	agaggagccg	gccagcgaca	tcgtgcgcgt	gggcgcgctg	360
ccaacggcgg	cgctgggcat	actgcctgcg	gcgatcgcc	agttccaccg	tcagcaaaaag	420
cacgccacgc	ttcaggtcgc	gacctgaat	aacaccatgc	tgctggcggg	cctgaagtca	480
ggcgagctgg	atctgggcgc	tgggcggaag	tcgatccgg	aactgatgag	cggcctgaac	540
tacgagctgc	tggtccctgga	atcgctgaag	ctggctgtgc	gtccgaatca	tccctgtttg	600
caggacaccg	tgaccctgag	ccgtgtgatg	gagtggcgcg	tggtggtctc	accaaaagga	660
accgttccgc	gtcagaatgc	ggaagcgttg	ctgcaaatgc	agggctgcac	gctgccttcc	720
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ctgccggtaa	catcgcccg	cgcgggagaa	ccgattggga	tcctgacgcg	ggtagatgcc	900
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<210> 507

<211> 1038

<212> DNA

<213> Enterobacter cloacae

<400> 507

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ataaaagaag	agacgatttt	tacctgaaa	gcggggaccg	ggcggcaggc	gcttggtcag	180
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gaaggatgct	gtctgagcga	ttacctcagg	cagctgcgtg	acgcgccgta	catcaagcat	420
acgctgaaag	atgaccgcta	ccagaccgtg	gcagacgcct	taaaattcga	acatcccagag	480
tgggtggaag	gctggttctg	gcccgatagc	tggtatgtata	cggcaggcac	gacggatgtg	540
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gcgcaccccg	ccaaaacgcc	gtatctctat	tttgtggctg	acggaaaagg	ggggcacacg	960
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<210> 508

<211> 759

<212> DNA

<213> Enterobacter cloacae

<400> 508

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<210> 509

<211> 1299

<212> DNA

<213> Enterobacter cloacae

<400> 509

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gagtcacact	ggaaaagctct	ccttgccggg	cagagcgcca	ctcagccta	cgaccatttc	180
gatactagcg	cctatgcaac	gaaatttgct	ggcttagtaa	aggattttta	ctgtgaagag	240
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cctcacgaag	cgcgccagggt	tagcggtatg	gagtataccc	tgtgtaactc	cttcggcttc	1260
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<210> 510

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 510

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<210> 511
 <211> 660
 <212> DNA
 <213> Enterobacter cloacae

<400> 511
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 atggtcttca cccgcgagcc gggcggtaac cagctggcgg aaaaactgcg cagcctgggt 180
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 gaactggacc gcattgaaca ggaatctttt gatttcttta accgcacccg tgcgcgttat 540
 ctggagctgg ccgggcagga caagaccatt cgtaccatcg atgcgacgca atcccttgaa 600
 gacgttacgc gtgatattca gcagactgtt acgcagtggc tacaggagca gcaggcatga 660

<210> 512
 <211> 1008
 <212> DNA
 <213> Enterobacter cloacae

<400> 512
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<210> 513
 <211> 900
 <212> DNA
 <213> Enterobacter cloacae

<400> 513
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ccggatgacg	gttacaagac	cttcgtctgc	gtggaaaccg	cgtgcgtgac	cgcgccgcag	840
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<210> 514

<211> 1574

<212> DNA

<213> Enterobacter cloacae

<400> 514

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gcctatgcc	atgcggcaga	acggtatattg	atggctattg	gtgagccaaa	catggttgat	180
actgccctgg	agccacggct	ttcccgctctc	ttttogaatc	gggtggctgc	ccgatacccg	240
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<210> 515

<211> 774

<212> DNA

<213> Enterobacter cloacae

<400> 515

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<210> 516

<211> 184

<212> DNA

<213> Enterobacter cloacae

<400> 516

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<210> 517

<211> 933

<212> DNA

<213> Enterobacter cloacae

<400> 517

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<210> 518

<211> 288

<212> DNA

<213> Enterobacter cloacae

<400> 518

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tatcttaagg	aaattcgcctc	cctgtttgcg	aaggtcaaa	ttcgtgaagc	ggactcttcc	240
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<210> 519

<211> 1959

<212> DNA

<213> Enterobacter cloacae

<400> 519

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<210> 520

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 520

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<210> 521

<211> 2178

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (193)

<400> 521

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<210> 522

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 522

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<210> 523

<211> 1914

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1788)

<400> 523

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<210> 524

<211> 1011

<212> DNA

<213> Enterobacter cloacae

<400> 524

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gcgctcgggg	tcttatcctt	gctcggttag	cgcgtcccgg	tagcactgaa	aattttcctg	540
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<210> 525

<211> 987
 <212> DNA
 <213> Enterobacter cloacae

<400> 525
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 ttccgcgaaa ggatgattca gcattccggc gtgcagcgaa tctgcaaccg ggactactcg 960
 gcgctgttta cgcgcgccgc aatctga 987

<210> 526
 <211> 1116
 <212> DNA
 <213> Enterobacter cloacae

<400> 526
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 aaagaagctt acgaagtcct gaccgatgca caaaaacgtg cggcctatga tcagtacgga 180
 cacgcggcct ttgaacaggg cggcatgggc ggtggtggat ttggtggcgg cggcttcggc 240
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 gaagaagcgg ttccgcggcg caccaaagag atccgtatct cgacgctgga agagtgtgac 420
 gtttgcacg gcagcgggtg gaaagcgggg actcagccac agacctgcc aacctgtcac 480
 ggttccggtc aggtgcagat gcgcagggc ttcttcggcg tgcagcaggc ctgtccgcac 540
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 gaagtgccga tcaactttgc gatggcggcg ctgggcggcg aaatcgaagt gccgacgctg 840
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<210> 527
 <211> 318
 <212> DNA
 <213> Enterobacter cloacae

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 ttatccctgt cgacctgccg ctatgaggct caccgtccgg ctgctgatgc gcatttatca 180
 gggcgcatca ctgaactggc actggaacgc aggcgttttg gctaccgtcg taatttggcc 240
 aattgctgcc ccgtgaaggc cttcatgtta atcataagcg cgggtaccgg ctttatcacc 300
 tcagtggcct gggcgtaa 318

<210> 528
 <211> 294
 <212> DNA
 <213> Enterobacter cloacae

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gccatttccg atgccacgtt ttacatctgg cgtaagaagt atggcgggat ggaggtgcct	180
gaagttaagc gcctgaagtc gcttgaggaa gagaacgcca gactcaagaa gctgcttgcc	240
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<210> 529
 <211> 561
 <212> DNA
 <213> Enterobacter cloacae

<220>
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<220>
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<220>
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 <222>(27)

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caggtcacgc gtattctgga cagcattgca ctgtttcgag	240
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gttgagttgc gcttaatcca gccgggcaag ccaacgcaga	360
aacggacgat ttccgcgatga atgtttgaat gagcactggt	420
aggaaaatta ttaatgactg gcggcaggat tataacgaat	480
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gattccgacg ttactaactg a	561

<210> 530
 <211> 2418
 <212> DNA
 <213> Enterobacter cloacae

<400> 530	
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tcgatgtgcg gcgataattg tgtgcgtata tggtttggtc	240
agtgacgggg tatatgataa cgaactgaca ttaaaattcc	300
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cagatttttg ctcacataga tgggtgcatac cgagaaagt	420
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agaaaatcgg tgtatgagga gcctgatcga gaagtgacaa	540
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gataagcacg tccaggaacc agctggctgt tacgatgctg	660
tgcgcgtttc atcggtttaa agatatggat gttggcacia	720
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<210> 531

<211> 1680

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1654)

<400> 531

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gtgaccttta	ctcgcgtctg	aacaaacgca	cttgacgcaa	agttacaaaa	gcgattgagc	240
aagaaggatc	ttgaccgggt	gctggtggat	acttttcacg	gactcgttaa	gaagcaactg	300
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cgggctttga	aagaatccgg	tgtaacgatg	aagtttgctg	aagctgaatt	cgttattgat	420
gctatcggca	gagaaatgga	tacggatgtg	atttcagttc	ggcataacag	acaacagatc	480
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ggttcaaagg	gtcttgagtg	gaataaagta	ataataatga	gttgtaatgc	ggatcagata	1620
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<210> 532

<211> 321

<212> DNA

<213> Enterobacter cloacae

<400> 532

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gcgcccctggc	gtaagccgtg	gcgcgcggct	gcgggcagcg	gtctggccgg	tctgcccctg	180
aatgccacaa	ccggacgtca	ctatagcggg	gtgaatgtcc	tgtttctctg	gatgtcagcg	240
gaagaacagg	gttttcgcaa	taaccgctgg	ctgacttacc	ggcaggcgca	gccaggccgg	300
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<210> 533

<211> 900

<212> DNA

<213> Enterobacter cloacae

<400> 533

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tctgaactga	atattcagat	cagggaacgta	aaacatatta	aaacttccca	tattgaaaag	180
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catattaaaa	atggaatgag	ccgcgacgaa	gctgaagcat	tagtctctat	ggatttgagg	840
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<210> 534

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 534

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<210> 535
 <211> 192
 <212> DNA
 <213> Enterobacter cloacae

<400> 535
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 tgtgctctgg caaacaagct ggccagaata gcctggggcc taacggcacg acagcaaact 180
 tatgtagcat aa 192

<210> 536
 <211> 480
 <212> DNA
 <213> Enterobacter cloacae

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 catcgcacgc gacgcccctt ctaccacggc ttccggcgca tggctgttag cgcgatgtaa 480

<210> 537
 <211> 450
 <212> DNA
 <213> Enterobacter cloacae

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 aagtctattg tcgcggagtt taagcagtga 450

<210> 538
 <211> 1128
 <212> DNA
 <213> Enterobacter cloacae

<400> 538
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 gcagcgctga tctggagttc gttcgatgag cacttctgatg catcaggcgg cgatgggggg 180
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<210> 539

<211> 1515

<212> DNA

<213> Enterobacter cloacae

<400> 539

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<210> 540

<211> 1155

<212> DNA

<213> Enterobacter cloacae

<400> 540

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tctttattct	tccgtccggt	gggtttcgac	taccgttcca	agattgaaga	caccgctgg	360
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<210> 541

<211> 303

<212> DNA

<213> Enterobacter cloacae

<400> 541

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<210> 542

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 542

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<210> 543

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 543

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<210> 544

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 544

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<210> 545

<211> 576

<212> DNA

<213> Enterobacter cloacae

<400> 545

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<210> 546

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 546

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<210> 547

<211> 414

<212> DNA

<213> Enterobacter cloacae

<400> 547

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<210> 548
 <211> 612
 <212> DNA
 <213> Enterobacter cloacae

<400> 548						
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<210> 549
 <211> 2586
 <212> DNA
 <213> Enterobacter cloacae

<400> 549						
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<210> 550

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 550

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<210> 551

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 551

ttcagtggg	agacgggaag	cagtcocag	gtcgtgcgc	ctacagcctg	ccagaacaga	60
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ctatccctgc	tggcattttt	gccgctatct	caggcggttcg	ccaccgtctg	cgtaaatgaa	180
aatggcggtc	cgacggaggt	gtattacgac	ctgacggata	aattcaacag	ctccaataac	240
cagggtgggc	agattgtcac	actcagcgag	aagtctcagt	gggtgggtgt	taacgcgcgc	300
tgctctaagg	gaacgtccgg	gaacaccacc	aagcgcagct	atgttaccca	ttaccgggtc	360
acgggcacca	gcgatggcta	ccagtatctg	aagcttaacg	actatctgga	cggagcgatg	420
aaaatcaccg	acagctacgc	tggaaccttc	tatccaccca	gaaagtacat	tcagatgggg	480
agccatccga	acgtgtctaa	aaacaaaccg	ttgggtgtac	aggattccag	cctcgtcttc	540
cggtttaagg	tgacccgacg	ctttatcaat	atggtagtga	tccccgggc	gaccatgttc	600
cggttttacg	tcaccacgac	ctcctcgat	ccgtcacca	cgccgggtta	taccatcagc	660
tacagcggga	ccattcaggt	gcctcagagc	tgtgaaatta	atgcgggaa	tgtggtggag	720
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gaggggatct	cagcgcaaag	caaaaccatc	ggcataaaat	gcaccaacgt	cgaggcgaac	840
gccatgctca	cgatgcgtgt	tgaagcggag	aaggtttcag	gcagtaacgt	ggtttccgat	900
aacgcggatg	tgggttttgt	gattgccaac	agtaatggcg	tgccgctgac	gccaacaac	960
ctgaccagca	aaatcccggt	ccgtctggac	gacagcgctc	aggcacaggt	ggggatccgc	1020
gcgtggccc	tcagcgtgac	cggtaaaaaa	cctgccgag	ggcgttttac	ctctcgcggc	1080
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<210> 552

<211> 240

<212> DNA

<213> Enterobacter cloacae

<400> 552
 acgtatcttct tattcccgaa tatgcgcggg aagggttatt tacattttta aggaatagac 60
 atgaaactca gcaacattgc ttctactgtt attgcaactc tggccctggt cgcgggtgcc 120
 gctcacgcag aagatccggt agcgcctgta tctgtaaacg gtggtacggt gcattttaaa 180
 ggtgaattag tgaatgcgcg gtgttcagtg aatactgaac tcttcagagc agacggttaa 240

<210> 553
 <211> 498
 <212> DNA
 <213> Enterobacter cloacae

<400> 553
 ccgtcgcgat gctttgcgct ttgctccctt gcacacgcag agatggcgct tggggaaatt 60
 aacattcagt tatacggcaa tatagtggat tttacttgcg tggcggaggg ggacgacagc 120
 aataaaaccg tcacgatcgg cacttggtcc acgaaacagc tccgcacaac ggggagccgg 180
 acgcagcctg tgcgtgtcac cctgaagctg accggatgcc cgcggggggc agcttcggtc 240
 acatttacgg ggaagatgga cgggcatgat aacagcctgc tggcgtgaa tgatgccagc 300
 gcggccagca acgtgtccgt ggagatcctt gaccgggata aaacgcgcct cgcgttgagc 360
 caggccagcc agacgggtggc ggtggatgcg cagggaatg cagaactgtc gttttatgcc 420
 aattatatcg ccacggcgga taatccgcag ccgggcccgg ctgacgccga tgcaacgttc 480
 atgatcaatt ataattaa 498

<210> 554
 <211> 503
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (273)

<400> 554
 gatacttgcg aatattccca cggttgatcc cgtttttcag tgatttaaatt caattgcttt 60
 catcgcgctt ggtagtgaac attgaaaccc gcgcttcccc gatcattgac ttgctggacc 120
 gattacgccg ccacagcctg ttggcccggt acctgacacc atacatgttt ttccgcgccg 180
 atgattatga tgcctgcttg ttttgtaaag cggctggccc ttttcattgtg cttgcacgcc 240
 agcttacggc gttggatatg caacaaacct tgntggaagc accggcaccg gccggcaacc 300
 gcaaagagtg gttttcacgg gatgaatggc cgatcttaca ggcgttgtca cagggtagct 360
 ccttgctgca gatcgcgagc ttacagaacc gcccatatag ctgcattatt tacagtctca 420
 gctgcacctt ggcgaaactt ggactgaatt atcgctcatg gttgctacat cttctcaaca 480
 acctctcaga tttcacgtat taa 503

<210> 555
 <211> 276
 <212> DNA
 <213> Enterobacter cloacae

<400> 555
 cagcggcgct cgcttctgac aaaatacagg caatcccccc tttctaactg tacagacgga 60
 atcttctctc tgatggcagc aaagattatt gacggtaaaa cgattgcgca gcaggtgcgc 120
 tctgaggttg cggaaaaagt gaaggcgcgt aaagccgcgc gatttcgcgc ccccggtctg 180
 gccgttgtgc tggttggcag caacccggct tcgcaaattt atgtcggcag caaacgcaaa 240
 gcgtgtgaag aggtgggggt cgtctccgcg tottag 276

<210> 556
 <211> 636
 <212> DNA
 <213> Enterobacter cloacae

<400> 556

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gaagtccctgc	tacagaaaaa	taaaaacatc	caggtcaaac	tgaagtcagg	cgacagccac	120
gaagtgccttg	actgtatacg	caaccacccc	attgacctgg	tcattctcga	tattgaaatg	180
acggacacgg	atgggttcgt	attactgaaa	agaatcagga	acttaaataa	agacattaag	240
gttctttttcc	tctcttcaaa	atctgaagcc	ttgtacgcag	gacgcgccat	ccgcgccggg	300
gataatgggtt	ttgtcagtaa	gcgaaaagat	ctgggggaaa	tttataacgc	ggtggaaatg	360
atactgacgg	gctattcttt	cttcccttca	gaaacattaa	gttttataaa	ccatctgggc	420
tgcgggacgg	gcgcgcgtgt	ggatatgcc	ttatcgaatc	gtgaagtgc	ggttctgcga	480
tatctggcga	acggattatc	taataaggag	attgcggatc	aattattact	tagcaacaaa	540
acaattagtg	cccataagtc	taatatcttt	tccaagctgg	gcgtgcaaag	tatcgttgaa	600
ttaattgatt	acgcgaaagc	gcacgaatta	ctgtaa			636

<210> 557

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 557

cactcaatga	acttgcagac	atacgagtcg	acttcagcga	ttacgatgtc	agcgatatcg	60
aacgcgatat	tgaacgggtt	gagtccttta	cgcgtgacga	taccgatgac	gggggttgag	120
tgggcggata	aataatttcta	tttaccggaa	ggttcaagcc	acatcgccgg	tcgctggaag	180
acacaacccg	ttcagctggc	gatgctgaac	atgatgacaa	acgatgcgat	caaaatcgta	240
tctatccgta	aatcagcacg	cctcggctat	acaaaagtga	tggtcgttgc	gctgctgtat	300
tttgcagagc	ataagaagcg	cagctcggtc	gcataccagc	ccgtagatga	tgaggctgaa	360
gggttcgtat	ctgatgaaat	agatccggcg	atctgtgaga	tgccggttat	acaaaaata	420
ttcccggtt	gggacagcag	caacgaacgg	aacaatatca	aacgaaagga	aatgtcaggc	480
gcaatcctgg	atttttcgcg	agcaaatagc	ccagggaatt	ttcgtcgctt	aactaaacag	540
gtcgtcgccg	gtgatgaagt	cgacggctgg	ccgcttgaag	tctcgaagaa	aggcaagggc	600
gaagggtcgc	cgattgaaact	ggctctggta	cgtattaagg	gcgcgtcata	cccgaagcc	660
attttcggct	ctactccgac	cgttaccggc	aaaagccaga	ttgaaatgct	cgaggatggc	720
gccgatctgg	tcttccgggt	ttatctgcct	tag			753

<210> 558

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 558

ggagcagtta	tgacaacaga	aagctgtcag	ccggatgatt	ttttcgtcgg	tcctgacgtg	60
acaacaacta	ccggtatcat	ggcttcgggt	gtgaatatcg	cgaaatatac	accggtcatg	120
attgatgcaa	ctgccgggac	ttttaaatcg	tgggatggta	cgccaggaaa	agcagtgggt	180
attacagcaa	tggcagtc	tgccagcgct	ggccaggctg	agttttcgta	ctacaacgga	240
ggcacattcc	gtgccagtta	tctgaactgg	tcagctgatg	cggtgaagcg	aaaatcagca	300
tttgccggaa	cgccggtgag	catccaggaa	ttaa			333

<210> 559

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 559

ctaaacaggt	cgtcgccgg	gatgaagtcg	acggctggcc	gcttgaagtc	togaagaaag	60
gcaaggcgga	agggtcgccg	attgaactgg	ctctggtaag	tattaagggc	gcgtcatacc	120
cgaaagccat	tttcggctct	actccgaccg	ttaccggcaa	aagccagatt	gaaatgctcg	180
aggatggcgc	cgatctggtc	ttccggtttt	atctgcctta	gcgcgcaggc	ggcgtaaaat	240
gagctggctc	gcgtaagtgc	gatcatcgcc	tgtgaagaag	cgaaaggcg	cgagcagcag	300
gcgcgtgcgc	ttgcgcgat	tcttggcatg	acgctggatc	aggctaaagc	ggtcctggca	360
gcagcgccgc	aaaccgccc	ggcgcgcaat	gaaacagcgc	ttgatgcgct	gatgacaaaa	420
gagtcgccc	aagcggtggc	ttatatgccc	gctcaacaca	atcactctgc	agacggttct	480
gcagcgaaaa	tttactcct	ggttcaagca	ggtaaatcac	ttattgagga	gcagttatga	540

<210> 560
 <211> 1035
 <212> DNA
 <213> Enterobacter cloacae

<400> 560
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 cagccgcttt tcttgagcct ctttttttaa gagacgtata cgttcgatac tgaagacgtt 120
 tttctcgaca aaattcccgg cgaagtgtcg atggccgttt actgttcgcc actgatcaca 180
 ggcaaagtgc acagaacgcg tgggttttaa acgacgcact tcaaaccggg ttatacaaaag 240
 ccgaaacaca cagtcaatcc gcataccgtc atcaagcggg ctgccggtga gcatatcggc 300
 cagcctaaaa cgctgcaga acgtcgcgca gaaattatta tgcaaaacct gaaggatgaa 360
 gagctgtcca ttcagcagct ggaagagtac caggctgtgc aggcctgtgt gaaagggag 420
 tacacgatct ccgggcccga tatcgatacg acggaaatcg atatgcagcg cagcgttgca 480
 aataatatcg tgcagtcggg cagcactgca tggtcagcac aaaacaagga cacattcgat 540
 ccgagcaacg atatogaaga gtatgcagag catgcctccg gcacgatcaa cgttatggtt 600
 ctogatggaa aggcctggaa gacgcttaaa agcttcaaac tgttcctgta agcgtggat 660
 acgcgtcgcg gctcgaacag taagctcgag ctggctctta aaaacctggg cgacgtggtg 720
 agctttaagc ggtactacgg tgacacagcg gtgatcgtct ataaggcca gtacattgac 780
 ccgatacaa aagccaaaac gaaatatatg cctgacaaca cgatagccct gggtaattta 840
 cagtcocaaag gttatgcac ttatggcgcc gttcaggatg aagatgcgct tcgtgagggt 900
 attacagaag cgaccgcgta tccgaagatc tggactacta ccggcgaccc gtcaatcact 960
 cagactatga cgcaatcagc gccagcaatg gtcttgccag acgctgacgc gtttgtcatt 1020
 gtaaccctcg cataa 1035

<210> 561
 <211> 444
 <212> DNA
 <213> Enterobacter cloacae

<400> 561
 gagccgaaag gctctttttt ataccgggag acaaaaatgg ctaataaaac agaactgctg 60
 gcgcgtatca gtgatttaag cgcgcagctg gggcgtgagc tttcaacaac tggcacaat 120
 gaggcgctgc aggcggttat agacagtgtc gaagctgagc tgaagctact gaatgaagat 180
 gacggcgaaa cgctgcccct gcagccgctg ccgggtgggt caaattcagg aacgctgctg 240
 actgccagct ctctgacga aaatgatgaa gctgatgcag acggcgctgc gtatcgactt 300
 gtgaaattac gcgcgacgct tcatgtcgtt cattacgtta atcaaaagcc ggtgcgtgaa 360
 atcgtccctg ctggtcagtc aatctacgtt gatccggaag aggcgcgctt gctcatcgct 420
 gcaaatcagc tctacgcgct atga 444

<210> 562
 <211> 990
 <212> DNA
 <213> Enterobacter cloacae

<400> 562
 tttcttatcg tggcatttga agcatcacga atagcaaatg aggtctccat gattaagcaa 60
 aaaaccatca aaaatatgtt cgaactaagt ggtattggtt tacatagcgg cagcagcatt 120
 catatgaaaa tcatgccgcg tacgcgtaat agtggcatac ggttccgtag aacagattta 180
 aatccttcag ttgatattca gcttcgagct gacgaggttc atgacaccat gctggctaca 240
 agtctaatta atcctcaagg tattaggggt tcaacgatcg aacatttcct ttctgctgta 300
 tccagtctgg ggattgacaa tctcctggta gaactggatg cacctgagct ccccatactt 360
 gatggaagcg caagagaatt tattgattct cttatcaacg ctggttcgat agaacagtgt 420
 gcacttaaaa aatatcttct tattaataaa actgtgtcag ttaaagacgg tgataagtgg 480
 gctcttttca atccggactc taagttttcc gtggatttca cgattgattt caagcatcct 540
 ttaatctcgg ctgatactaa taaattaaat attgaaatgt cgaaagaaaa atatatagaa 600
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 gggcttgtac taggggctgg tttgaacaat gcgataggct tcgatgaata tagcgtcctc 720
 aatcctgaag gtcttcgttt taataatgaa ctagtctgtc ataaagtact tgatgcaatt 780
 ggagacctct ttgtttctgg gtataatatc atcgggtgctt accatgcata taaatctggc 840
 catgctttta ataataaact aatgcttgc tttataaatg ataccgatgc atgggaattc 900

gttaatttgc atgattacag cagggggaaa cttaaagtta atatgttgcc tgcgattaat 960
aaagaatgcc cagtatcatt aactatctaa 990

<210> 563
<211> 453
<212> DNA
<213> Enterobacter cloacae

<220>
<221> unsure
<222> (17)

<400> 563
tatcaccgaa tagcatntgg ggagagaatg agcactattg gtgatgcagc tgcgattatcc 60
ggggtttcgg ccaaaatgat tcgttattat gaggaggcag gattaattcc ttctgtctct 120
agaaccgcag ctggataccg gatatacaaa gatgtagatg tctataaatt acattttata 180
cgccgttgcc gagagctcgg tttttctctg tctcaaacgg gagatcttct ctctctttgg 240
ggaaatcatt cgcgccagag tgcggatgtg aaaaaattag ttgaatcaca tataaatgat 300
ttgaactcaa aaatagaaga acttcagcgt attgcatcga cccttacaac gctttcagat 360
tggtgcgcgg gtgatgataa accagattgt ccaattctga gggcactgta tctggcggag 420
acttcgcgta aggacaagga aaatagtcct tga 453

<210> 564
<211> 933
<212> DNA
<213> Enterobacter cloacae

<400> 564
ttaatgaaat tccctcattt ctttatacag cgacccattt ttgcaatcgt cctttcacta 60
tttatgctga tagcgggtgc cttagccttc tttcaattgc cactcagcga atatccttct 120
gtaactcccc caacagtgcg ggtgactgca agttatcctg gggcgaatcc taatgttata 180
gctgataccg tagctgctcc tcttgagcag gctatcaacg gggtagaagg gatgctatac 240
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ctgccatctg aagttcagca aatcggcgtt gtaacggaaa aaacctcgcc ggatatactc 420
atggtagttc atctgttctc accagataat cgataacaac cgctttatgt atctaaactat 480
gogatgttga acgtgcgtga tgagctttct cgcttacctg gtatcgctag tattgcgctt 540
tggtggggagg gtgaatatgc aatgcgagt tggcttgatc ctaataaaaat tgcttcocga 600
ggtttgaccc caagcgatgt cacttcagca attaaagaac aaaacgttca ggtagcggca 660
gggtcagttg gacaacagcc taatacttca tctcctctcc aggtcacagt aaatgcgtta 720
gggcgtctga caaccgagga gcaattcggc gatattatta ttaagtcagg aactgatggc 780
caggttactc gcctacgtga tgtagccagg attgagctcg gttcagataa ctattcggtta 840
cgaagtctgc tggataataa agatgctgta ggtatgcaga ttgtaatgac acctggagcc 900
aatgcgctgg acgtatcagc atctgtacgg tca 933

<210> 565
<211> 3639
<212> DNA
<213> Enterobacter cloacae

<400> 565
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aattttaacg gcaatcactg cttgcacaag gaacaacttc aattatcgaa agatcacttt 180
ttattggtga ggtttacaat gttaaataat attcccgat attgcaacgt ttgtcgttcc 240
cgctgcggga cgttgaatga ggtgattgag gacctcctct ttttggttaag gcctaacct 300
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tttaaaaatg agaatggggc ggaatctgtc gcttcgggtt ttactagccc aagcgggtaca 540
ccccttagtg atgcaattga atggttagaa cgttttgttc gtatctatgg cagcccaaac 600

accagctatg	ggacggagat	atgtaattgg	cacaaagacg	ttgctcatcg	ttggaccttt	660
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aatccagcca	atacatggct	agcgcaggct	aatgcgatag	ggactggtcg	gaataatggc	780
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gaaaggcata	tgtttaacca	ggaattcggt	cgtgactgga	ctaattggcc	tttactgatt	960
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acagaagaaa	ctcttacacc	tacagctgca	cttgaaagcg	atggtgaagt	cacattagct	1140
gatggcggtg	aaatatcctg	ccataccgca	ttttcctctt	ttaaaaatat	actgggcta	1200
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gatacttccc	tccgacaaca	ggcacttgag	gcgcttgagt	tttatgctca	tgtagatttg	1680
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aattatcaat	tgaagccact	cggtttgact	gttgagatgc	tcaggaataa	gctgaaggt	1980
tacgacatac	cacttgagca	taaagtcagg	aagtacgcct	taaaagatca	aaagaccggg	2040
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cggcacgggt	ataatccttt	acctgaatac	gtacaacctc	aggaatatca	gcgtaatgat	2160
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caggctcggt	tcagagctaa	ggtggaagaa	aaattatctc	acgaaacagt	tattgctgaa	2400
tttggtgggt	ggcaggggtg	tccgtatttt	ggaaaaccat	catatcctgt	tataggtgaa	2460
tttagcagta	attttaatag	cctaatacagt	ggggatagtt	atgatcctgt	aagtgggtgca	2520
ctgccactcc	gttcgttcag	atgccgtatt	cgtaggctga	atgaatttga	attagtaaga	2580
cgtccatggg	acggacgtag	aactttccaa	gttataagtt	tgaagaaaga	aactgataat	2640
gttacaaccg	tgacttttca	atctaaaagct	gaggggtttt	taccggatta	tgaaccaggc	2700
cagcatgtaa	caataagctg	ttacccactg	atcgattctg	aagatatcgt	aactagagcg	2760
tattcgttaa	caggccagc	atttgtagac	gctcgtaaaa	cttattctat	ttctgtaagg	2820
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aacactcggt	tgcaagttag	cagttttgtt	gaaataactc	cacctggagg	caacttcata	2940
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tttatctggt	atctggagtc	tattgatcct	gatgaaactg	gcoctgaaat	atggcttttc	3060
tatgccaatc	aaaatagtaa	gcaacatgcg	tttaagaaaa	gaatacagga	gttaagtagc	3120
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<210> 566

<211> 1299

<212> DNA

<213> Enterobacter cloacae

<400> 566

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<210> 567

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 567

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cgtaaaggcg	aatccagtat	cgtgacaccc	aacatgctcc	agcggcagtt	caatccggac	480
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<210> 568

<211> 291

<212> DNA

<213> Enterobacter cloacae

<400> 568

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cacagtcttt	acgcctggat	aaagaagtac	ggcccggtat	cttcactca	taatgaacag	180
tcagatgctc	aggccgagat	ccgcgctctt	cagaaagagt	tgaagcgggt	tacggacgaa	240
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<210> 569

<211> 2382

<212> DNA

<213> Enterobacter cloacae

<400> 569

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<210> 570

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 570

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ggctgcatgc	gcacgcgcga	tgaacgtttt	aactggcaaa	atttcagcga	cgcgcaaaag	180
caggaggtct	tacggctttg	ccgacagcgt	ctgctgcgta	aaattcgtgc	aaacaaagcg	240
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<210> 571

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 571

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cagctggcgg	actttataga	agagcatctc	gatctcggga	tcaccaacgt	cgatcatgct	180
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<210> 572

<211> 573

<212> DNA

<213> Enterobacter cloacae

<400> 572

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gcgctgatga	tccacgtggg	cgggcgataac	atgtccgatc	aacctaaacc	gcttggcggc	540
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<210> 573

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 573

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ctgtttaaag	ccgtgatggt	cggtttttgt	atctggctca	ttgcgcacgc	tctgctgcgc	180
gactggatgt	attccggtga	aatctggcac	ccgatgttaa	tggtatctctc	cctgtttacc	240
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<210> 574

<211> 2100

<212> DNA

<213> Enterobacter cloacae

<400> 574

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<210> 575

<211> 945

<212> DNA

<213> Enterobacter cloacae

<400> 575

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<210> 576

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 576

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<210> 577

<211> 1032

<212> DNA

<213> Enterobacter cloacae

<400> 577

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<210> 578

<211> 606

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (59)

<400> 578

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agtgggt						606

<210> 579

<211> 303

<212> DNA

<213> Enterobacter cloacae

<400> 579

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aac						303

<210> 580

<211> 438

<212> DNA

<213> Enterobacter cloacae

<400> 580

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ctggggaaaag	accgccagcg	cgacggtgcc	agcgttcttc	aggggaagcc	ggaggaagtc	180
cgggagctta	tcgacgcctc	gcctacgcc	aaaaagtaca	cctccggggg	gctgtccttt	240
gccgaacagg	acttaccgcc	cgggcagcgt	ttaaaacgcc	tgatggcgag	cttccagcgg	300
gttctgatgc	ccggactcga	taaagaccac	tacaccgtgc	tgtgggttga	gcaccgggac	360
aaggggcccgg	ctggagctga	acttcctgat	cccaaaccac	ggaactgctt	gacggcaaac	420
ggtccaacca	tactatga					438

<210> 581

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 581

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tggttaacag	aagatgagca	ccgcgctctg	ctggaaacgt	gcgacggtaa	acagctcgcg	180
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cgccaggtaa	acgccgggtg	cagtagcggg	ctcgaccgcg	tgacggctgt	cgccgcgctg	360
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gatgatcggt	aa					432

<210> 582

<211> 993

<212> DNA

<213> Enterobacter cloacae

<400> 582

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tccctggaag	aggtggcaga	aatctatctc	ccccctcttc	gcttgcttaa	cttctatatc	240
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gaagaagagg	ctatcagcgt	ggcgaccggg	ctgtggaatg	agatcaacta	cgtcaacctc	900
aaagagaaca	tcctgccgac	gcgcgaacgc	gcaagcctga	tcctcaccaa	gagtgagaaa	960
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<210> 583
 <211> 1185
 <212> DNA
 <213> Enterobacter cloacae

<400> 583
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 cctgaacgtc atgcgcaact gctggctgaa ctcggccttg ataagccgat gtggcagcag 360
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 gtgcagggcg gtgtactgct ggtcgcgacg atgattatc togtcaacct gctggtcgat 1140
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<210> 584
 <211> 912
 <212> DNA
 <213> Enterobacter cloacae

<400> 584
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 tatgtttcca toatgatcct gattgcggtg ttgcgaaacg tccttgcgcc gtataacccg 180
 gctgatcagc tcgcgcatgc gctgctggca cctcctgcat ggcaggacgg cggagcctg 240
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 gcacgcctgt cgtgctggtt tggctgcctc gttgtcgtac tgtcgtgat catgggatc 360
 gtactcggcc tggtgccagg ctacttcggc ggcattgttg ataacatcat catgcgcgtc 420
 gtcgacatta tgctggcatt accaagcctg ctgctggcgc tgggtctggt ggcgatcttc 480
 ggtccgtcga ttggtaacgc cgcgcttgcg ctgacgtttg ttgcgctacc gactatgtg 540
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 ccgtgattg ttcaggcgtc gctcggtttc tctaaccgca ttcttgatat ggccgctctt 720
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<210> 585
 <211> 1032
 <212> DNA
 <213> Enterobacter cloacae

<400> 585
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 gtaaaagcgc tggacggcgt ctccttcagc cttgaacgcg gtaaaacgct ggcggctcgtc 180
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gattatggtg	gacagctggt	ggcctgcttc	gcggtcgatc	aggatgaaaa	cggcgaaaaag	1020
ccgcatgcat	aa					1032

<210> 586

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 586

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ctgattgttg	ctcactccac	cgtgtacgag	ccagtgcgta	aagaagtga	gggctacgtg	180
gtcgateccac	tgggcaaaaca	ccacttcgaa	aacgtgtctg	ttgaataa		228

<210> 587

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 587

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gacgaaggca	caccgtttcg	cgcgtggac	cgtatcagct	acagcgtaa	tcagggcgaa	120
gtggtcggga	ttgtaggaga	gtcgggctcc	ggtaagtcag	tgagttoctg	ggcgattatg	180
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gataaatgcc	gcgcccagga	gccagagctg	aatctgctgg	ccgatggtcg	gcagtcacaaa	960
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<210> 588

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 588

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gttgatctcg	gcagcgtggg	ggtaagagcg	ctgggtggaac	gcagcgggat	tgccgcacat	180
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aaaaagcgta	acgcccga	agggatcgca	acgctctgta	ttggcggagg	gcaggggggtg	1200
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<210> 589

<211> 717

<212> DNA

<213> Enterobacter cloacae

<400> 589

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attgacagcg	gctcgaatgc	cgaccgtgtt	gccgtctcgc	accgctttga	taatggcttt	180
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ctggcctaca	aatgggataa	aaactgggca	ccgtatgtgg	aggtggggaa	cgtggggggtt	660
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<210> 590

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 590

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tcacatcgca	acottgaagc	tgaccttggc	tttgagctgt	tcgatcgctc	ggcgcgtcac	180
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agcgcgcgcc	tggatgagct	ggcgtatcc	ttaacggcgc	aaaaagaagg	ccccgtttta	300
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<210> 591

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 591

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attggcctga	cggaagcgcg	cgacagctac	ccgaccgata	ttggcgcgac	ccgtctgcct	180
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gaagcgcccc	ttgcgcgcgg	gccggtctgg	tctgcgccga	attacctgtt	actgctgagt	360
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gcgtcgaaat cgttgggtgca gctgaacgtg cgggggtggc cgaggctgat tgccatcgat 480
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 caggacgcac gataa 555

<210> 592

<211> 276

<212> DNA

<213> Enterobacter cloacae

<400> 592

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 gcgattgtcc tgctgatcac cgccttctgt gcgtatccct taacctactg gcgcataaaa 180
 gcgctggcgc aatttattct gtcgtcgaag acgaaaggca acgcagggat cagctcttca 240
 ccagcagggg ccggaagaat ccaacgcaat gcgtat 276

<210> 593

<211> 1428

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (713)

<400> 593

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<210> 594

<211> 1863

<212> DNA

<213> Enterobacter cloacae

<400> 594

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<210> 595

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 595

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<210> 596

<211> 222

<212> DNA

<213> Enterobacter cloacae

<400> 596

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<210> 597

<211> 1779

<212> DNA

<213> Enterobacter cloacae

<400> 597

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<210> 598

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 598

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<210> 599

<211> 425

<212> DNA

<213> Enterobacter cloacae

<400> 599

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<210> 600

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 600

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<211> 774

<212> DNA

<213> Enterobacter cloacae

<400> 601

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<210> 602

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 602

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<210> 603

<211> 3627

<212> DNA

<213> Enterobacter cloacae

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<210> 605
 <211> 1806
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 605
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<210> 606
 <211> 990
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 606

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<210> 607

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 607

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<210> 608

<211> 1236

<212> DNA

<213> Enterobacter cloacae

<400> 608

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<210> 609

<211> 896

<212> DNA

<213> Enterobacter cloacae

<400> 609

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<210> 610

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 610

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<210> 611

<211> 1629

<212> DNA

<213> Enterobacter cloacae

<400> 611

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<210> 612

<211> 1332

<212> DNA

<213> Enterobacter cloacae

<400> 612

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<210> 613

<211> 396

<212> DNA

<213> Enterobacter cloacae

<400> 613

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<210> 614

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 614

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<210> 615

<211> 414

<212> DNA

<213> Enterobacter cloacae

<400> 615

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ttccgggggg	atagtgcctt	ttataacctg	ctgtatcgta	ttgcagtcaa	tacggctaag	300
aattatttgg	ttgctcaggg	ccggcgctcg	ccttcaagtg	atgttgacgc	tatcgacgca	360
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<210> 616

<211> 915

<212> DNA

<213> Enterobacter cloacae

<400> 616

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<210> 617

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 617

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<210> 618

<211> 1557

<212> DNA

<213> Enterobacter cloacae

<400> 618

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<210> 619

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 619

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tggctgggac	atccgattta	tcgcccggtc	gatgacaata	ccgtggcctt	ctgtcatgaa	660
gggccgcacg	acctgggtcg	cgcccgcatg	tggctgggtc	acgaagatgg	cagcaacgtg	720
cggaagtga	aaacgcacgc	g				741

<210> 620

<211> 861

<212> DNA

<213> Enterobacter cloacae

<400> 620

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gagctgcgcc	gcctccatgt	tgaactgggt	aagctccagc	aatgggtggg	cgccaaaggg	180
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<210> 621

<211> 930

<212> DNA

<213> Enterobacter cloacae

<400> 621

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<210> 622

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 622

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aaagttactg	gtctgcaacta	tttttctgat	gatgctggta	gcgacggcga	caaaacgtat	180
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acctggacgc	agactgatgg	cttcatgacc	ggccgtacca	ctggcggttg	aacctaccgt	480
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<210> 623

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 623

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gccggaacaa	cagccgcgat	gctgggattc	gtcccaaaaa	tggcgctggc	tcaggcacgc	180
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<210> 624

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 624

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accgttttgc	gctaccggga	atategtgcg	ccggggctctg	acaaatggca	gcgtatttcc	120
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<210> 625

<211> 2460

<212> DNA

<213> Enterobacter cloacae

<400> 625

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<210> 626

<211> 717

<212> DNA

<213> Enterobacter cloacae

<400> 626

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aaaggcatga	ttgaagggaa	ggtgagccgc	cgctgggcgc	aaaaacacca	tccgcgctgg	660
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<210> 627

<211> 270

<212> DNA

<213> Enterobacter cloacae

<220>

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<222>(229)

<400> 627

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gctgaatttg	gcatcatggg	cgtgctgaca	gaactggccc	atgatacggg	catttcgatt	180
ccctctgccg	gaaatatgat	ttcgttttac	ccttttggcg	ttgtgatcng	cgcgcccatt	240
gtggcgctgt	tctccacaaa	ttttcgctga				270

<210> 628

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 628

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ggctgtaagg	cctgccaggt	ggcctgctcg	gagtggaaacg	atatccgcga	cgagggtgggg	180
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cgcttttagcg	aaaccgacca	gaacggcaag	ctggagtggc	tgatccgtaa	agacggctgt	300
atgcactgtg	aagatccggg	ctgcctgaag	gcatgcccg	ctgcgggggc	aatcattcag	360
tacgccaacg	ggatcgtcga	cttccagcag	gataaactgca	tgggtgcggg	ttactgtatt	420
gcgggttgct	cgtttaatat	cccgcgtctc	aataaagagg	ataaccgggt	ctataaatgc	480
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gataagctca	aagcgcgcgg	ctatgacaag	gccgggattt	ataaccgcga	gggcgtgggc	660
ggcacgcacg	tcatgtatgt	tctgcaccac	aatgaccagc	cggagctgta	tcataatctg	720
ccgaaagatc	cggcgatcga	tacatcaatc	aacctgtgga	aaggggcgct	taaaccgctt	780
tcagcggcgg	gctttatcgc	cacctttgcc	gggctgattt	atcaactacat	cggtatcggg	840
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<210> 629

<211> 297

<212> DNA

<213> Enterobacter cloacae

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<221>unsure

<222>(97)

<220>

<221>unsure

<222>(98)

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<221>unsure

<222>(99)

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 atcaactcttt atgacgttgc cgcgctggca ggcgttnnnn nnnnnnnnnn nnnnnnnnnn 120
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nggtccggca ggccatggcg 180

gcgctacact atgtgcccac ccgtggcgcg cagcagctgg ccgggaaacg caccgcacg 240
ctggggccga tcaccagtnt ttacctagcg gccgggacga tccaacgatt gcaactc 297

<210> 630

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 630

ccggggcagc ggtgctgttg ctgtggatcc cgctgcgtca gctgccgggg gctgggcaact 60
atcagtaatg tgatttgtat tgttcaggcg gcagatgcgt caatggcgct gatccctgag 120
ctcacatcgc tgcccgctgc catcaccctg ctgggtttccg gcattgtggt taacgccctt 180
gccaccggga tgtatatcgg cgcggttttt ggccgaggcc cgcgcgacgg cctgatgacc 240
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gtgttgatcg tcggctacct cctcggggga gcgtttggcg ttggaaccgt gctgtatgca 360
ttaaccatcg gcccgctgat ccagctctgt ttgccgtggt ttgccagag accgcgcatt 420
cagaaagctg cacagccgga gcggattgtt taa 453

<210> 631

<211> 483

<212> DNA

<213> Enterobacter cloacae

<400> 631

ctacagggtc aagcacatga agggggattc atgaaaattg gtgaattagc tcgtaaggcc 60
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cgagatattg aaaataatta tcgccattat gataataacc atctggaaaa attgttattt 180
atccgacgct gtcgctctct cgatatgacg catgaggaaa tccgcgcatt actactggca 240
atcaataata acggtaaaga atgtggacct attgacgaga taatcagtgc ccacctcgct 300
catgtccagc atcgtattaa tgaattaata gcgctagaaa aacaacttca agaacttaat 360
gatgtttgca atgcagaccg tagcgtagac gaatgtggga tagtccaaaa actgacagct 420
gaagatgaag atagagacct tcctctaact gtaccacacc accatctggg aggcgtacat 480
tag 483

<210> 632

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 632

gttatgaaca ttggtaaagc atcaagcgaa tcaggaatct ccgccaagat gattcgttat 60
tacgagcaaa ttggcttgat cctgctact ggctgactg aagctgggta tcgtgactat 120
gctcccaatg atatccatcg cctgattttt attcgaagcg ctgcgcacct cgggttttct 180
ctggaagaga tagagggttt gcttaagcta tggaatgata aatctcgtca gagctctgat 240
gttaaaccgt tggcgcagga acatattaat gatttagatc ggcgatataga aagtatgcgt 300
caaattggcag acacactcag agtggttaac caaagttgcg cgggagatga acgagctgaa 360
tgtcctattc ttcatagatt aacgattgct gatgatataa gtcattcggg taaacgagaa 420
ggtgcggtgc aacgtcgttc tcgtggaaac agagtgtcaa aagattag 468

<210> 633

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 633

aatttagtta taaggggaca tatgatcaca aaaacgtatg cggatagtgt ggtaaagat 60
atcgtccaat gggctgaaaa ttcactgaca tctactttac ttgtggagga aattgcagaa 120
aaatctggct attctcgatg gcattttcaa cgcattttta aacacgcaac cggaattgcg 180
ttaggtgaat atgttaaacc cgacgattac ctgtgctgcc gtagagttga aactaactac 240
taa 243

<210> 634
 <211> 1641
 <212> DNA
 <213> Enterobacter cloacae

<400> 634
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 tgtgttggaac gagtcgaagc cgccctaacg aaagttgagg gtgtggaaaag cgtaagtgtg 180
 aatcttgcaa ctgagcgtgc agacattctc ttgaatacac ctggtgaaag tatggcgcta 240
 atcaaaagcaa ttgaaaatgt ggggttatgag gtccccctaa cttctgttga attgtcagtc 300
 cagggcatga cgtgtgcatc gtgcgtaggg cgtgtcgaaa aggcgcttag agctgttgaa 360
 ggtgtaaagg atgcaacagt taatttagcg actgagaggg ccactatacg tggagtagcc 420
 ggaactgatg acctgattgc ggctatcgag aaagttggct acgaagccag cctggttgat 480
 acccggtggcc agaataatgt tgaggccgct gaaaaaaaag atgctgaaaa ggctgcattg 540
 aagaaagatt tagttctggc gaccatactt gcactaccag tctttattat ggaaatggga 600
 tcgcatctga taccgggaat gcaccaatgg ataattggata ccattgggct ccaggaaagc 660
 tggatatctcc agtttgtgtt aactctgctg gtgttagtta ttccgggacg gcgcttctac 720
 ctgaaaggta ttccggcggtt aataaggctt ggcccagaca tgaactctct cgtctccggt 780
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 gctgaaatgg ggatcttggt ccgtaagggg gaagctctgc aattgctcaa agatgctaag 1560
 gttgtagctg tagacaaaac tggcacctta actgaggggg cgccccgtaa tgacagacct 1620
 ggagttagcc gaagggtttg a 1641

<210> 635
 <211> 2556
 <212> DNA
 <213> Enterobacter cloacae

<400> 635
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 ctctctcata aggagcatgg tcatggaagt gacaaacatt tacatcgca gcaaggcat 240
 gtgaaagggt ggcatgcaca tgaaggatgc agccatgaac atagtcatac tgatgaagaa 300
 catgatcatg gtgaggaaga acatagtcac ggcgatcatc agcataaggg gtgtaacct 360
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 gtaaccata cacctgatcc gcttgaacct atcttggttg caattcgctc cttgggattc 660
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<210> 636

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 636

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<210> 637

<211> 866

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (21)

<400> 637

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aaggggag	cgactcgtc	gatcctcag	ttatcgcaac	cttcgaacag	ccattctctc	300
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gcgtgggtac	cggacgcgaa	atgtttggtg	cattgcggtga	gaaactctcc	ggtgcgggagc	840
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<210> 638

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 638

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cacgctgtcc	caatggcgaa	ggcgctggtt	gcgggtggcg	ttcgtgttct	ggaagtgacc	180
ctgcgtacgg	cctgtgcgat	ggatgcgatt	cgcgctatcg	ccaaagaagt	gccggaagcg	240
atcatcgggtg	caggtacggt	tctgaatgcg	cagcagctgg	cggaagtgac	cgaagcgggc	300
gcacagtttg	ccatcagccc	ggggtgacc	gagccctgc	tgaagccgc	aaccgaaggt	360
tctattccgc	tgatcccggt	tatcagcacc	gtttctgaac	tgatgctggg	catggactac	420
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<210> 639

<211> 2520

<212> DNA

<213> Enterobacter cloacae

<400> 639

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<210> 640

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 640

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<210> 641

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 641

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435

<210> 642

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 642

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<210> 643

<211> 849

<212> DNA

<213> Enterobacter cloacae

<400> 643

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<210> 644

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 644

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 <211> 1767
 <212> DNA
 <213> Enterobacter cloacae

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<210> 646
 <211> 822
 <212> DNA
 <213> Enterobacter cloacae

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<210> 647
 <211> 414
 <212> DNA

<213> Enterobacter cloacae

<400> 647

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<210> 648

<211> 360

<212> DNA

<213> Enterobacter cloacae

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<210> 649

<211> 633

<212> DNA

<213> Enterobacter cloacae

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<210> 650

<211> 231

<212> DNA

<213> Enterobacter cloacae

<400> 650

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<210> 651

<211> 2973

<212> DNA

<213> Enterobacter cloacae

<400> 651

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<210> 652

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 652

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aacaacgcag cgcgcgtttc gatcaccgtt ttcgaaaagg cagaccaacc cgggtgtcga 180
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ataccgcca ttttcatcac ttacctggac tggctcaaac agcagaatgc ggccgcctt 300
gccgcctata acgtcgacag tgagaagctg cagcaccggc aattttctgcc ccgtattctg 360

```

```

ctgggtgaat atttccacga ccggtttctc gctggtgctg ccgaggcgaa caacgctggg 420
tttcatatcg aagttcaccc caccgcagaa attcctgata ttaacgctga tgccaacgcg 480
tgccctttc attga 495

```

<210> 653

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 653

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aagcgacaag atataaacgc attaaagaat tttgattttc tggcagcgag ttttgcccg 180
atgtacgccc agggccagcc agttgatatc gatgccgtga ccggcaatat gagtaataaa 240
cagcaggcat ggttccggga gcgatatgac cactaccgaa agcaggctga gcgggcgaga 300
gtaatagaac tgcgatga 318

```

<210> 654

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 654

```

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ctgccgctta aactcctcac cgtcggtgat ttcagtaattg gaaaagagaa tcgcccatta 180
tcggaaaggg agaaaattaa cgtcaataaa aataacttca acagcgact ttcggaattt 240
aacccggaag tgaatctgac ggttcctaac acaatggccg gggatggctc ggaagaaagc 300
ataaaaactga atttctccga tattaaggat ttccgaacctg aacaggttgc ccgccagatc 360
cccagctcc gcgccatgct ggccatgct aattttattac gcgacctcaa atccaatctc 420
cttgataacg ccactttcag aaaagaactc gagaaaatto tcaaagacct ggcgctgtct 480
caggaattac gcgacgaaat gagtgcactg gccccgaaat aa 522

```

<210> 655

<211> 438

<212> DNA

<213> Enterobacter cloacae

<400> 655

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ggggatgccc tgagtatgat gacgtcaatc atggatacag atatgaaaac gagaattctc 60
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tgctctggct caaaagggtg catagcacac tgtacatcgg atggctcgtt tgtctgcaat 180
gacggaagtc tgagccagtc gaagcgattc tggtcaggtt atgggtgcctc cgaactgccc 240
cggcaggtaa aaccctcccc ctccgccagg aaagcgcaga cgaaaaagag aatagccgtg 300
aaaggccagg agcagcgtgt tgtagaaaac aatgcgcagt tcgatacaca accgcggcaa 360
octacatgcg cccctctcta tatggccaac aagcccggat tcacccattt acccatttgt 420
tcaggtaatc agtattaa 438

```

<210> 656

<211> 543

<212> DNA

<213> Enterobacter cloacae

<400> 656

```

aaagcgggta aggaacacct gcccataaga catgaacttt ttgaatattc ttttttactg 60
ttcaggaggt acatgatgac tctcagaacc tttcccggtg tgaacgatct ctccgactct 120
ctgtttgagg accgttttaa ccgtatcgat cgccttttta gccagctaac cggcagtaac 180
ccgttgccct ccacgccttc ttacaatatc cggcggctgg gcgataaccg ctatgaactg 240
acgctcagcg tgccgggctg gaaagagagc gaactggaaa ttgaaaccgt tggcggtcag 300
ctgaatatca gcggtaaacc tgaagaggag aaaaccgaaa acggcgaaga agggtggatc 360
catcggggta tcagccgcag cgacttccgg gccagctata gtctgccgga gcatgtgaaa 420

```

gtgaccggcg	cttcgctgga	aaacggctta	ctggcaattg	aattacacca	ggatatcccg	480
gaagaagaga	aaccgcagcg	catcgccatc	aacaacaacc	cggcgattga	acataagccg	540
taa						543

<210> 657

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 657

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tctcttaacg	ggaaactgca	taatattcaa	cgttcttttg	atgatatcgc	ttctggcagc	180
atcattcttc	tcgatatgat	ggaagcggat	aaaaaactca	ttcattactg	gcaagataat	240
ttaagcagga	aaaacaataa	tatccgcgta	ttgttattaa	atacgcctga	tgagtatcct	300
ttccgcgaaa	ttgagagctg	gccgcataat	aacggcggtg	tttacgtcac	tgaagaagaa	360
aaccgtgtcg	tggaggggtt	gcagggcata	ttgcgggggg	agtgttattt	ctcgcagaaa	420
ctggccagct	acctcattac	ccactccgga	aattatcgct	ataacagttc	ggaatcggcc	480
cttctgacgc	accgtgagaa	agagatcctg	aacaaactgc	gtattgggtg	ttcaaattatt	540
gaaatcgccc	gttcggttatt	tatcagcgaa	aatacggtta	agacgcattc	ttataatctt	600
ttcaaaaaga	tagctgttaa	aaatcgcaac	caggcggtgt	cgtgggcaaa	cgataacctc	660
aggcgttaa						669

<210> 658

<211> 450

<212> DNA

<213> Enterobacter cloacae

<400> 658

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aattttggcg	gcaacccgaa	taacggagcc	tttatgctta	accaggctca	ggctcaaaac	180
tcctataaaag	accccagcta	tgacgatgat	ttcggtatcg	agaccccgtc	agccctggat	240
aattttactc	aggccatcca	gtcgcgaaata	ttagggtggc	tattaactaa	cattaatacc	300
ggaaaacccg	gccggatggt	cactaacgac	tttatcgctg	atattgccaa	taaagacggg	360
cagcttcagt	taaattgtgac	agaccgaaaa	accggtaaaa	cgtcgacaat	ccagggtttcc	420
ggtttgcaga	ccagttcaac	tgattttctaa				450

<210> 659

<211> 450

<212> DNA

<213> Enterobacter cloacae

<400> 659

ctgttaaaaa	tcgcacgcag	gcgggtgctg	gggcaaacga	taacctcagg	cgttaatagc	60
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caggctgttg	aggtagaagt	tcccggaactg	ttaaccgacc	acaccgtcac	ctctgtcgga	180
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gttattttacc	agactttttt	attoccaacg	aaaagagact	tcgatcagaa	cgtcgctttc	360
gcgctggcac	aaacagaaga	agctattaac	cgcctacagt	tagacaaagc	ccttttgagc	420
acaggcgatt	tagcaaaaaga	tgagtttctaa				450

<210> 660

<211> 867

<212> DNA

<213> Enterobacter cloacae

<400> 660

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ggcttgtggg	atcttcagaa	taaaagtgaac	gtgagtaatg	cgggtgctggt	gaaatatcgt	840
gagatgtcgg	tgccgccaga	gtcataa				867

<210> 661

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 661

cggataaaaa	acatgaatga	gttttccatc	ctttgcgcgc	tgctgggcac	cttatattac	60
cgccagccgc	aggatccgct	gctgggtccg	ctgtttaccc	tgattcgtga	aggtaaactg	120
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tcgccattct	ggagaacgct	ggctccgctg	acgcgtgacg	ctatcgtctg	tatgtgggac	540
gagctggaag	aagagaacga	agagtga				567

<210> 662

<211> 579

<212> DNA

<213> Enterobacter cloacae

<400> 662

cttgaatcac	aaaaatcctg	caacgataca	tttcaacttg	cacgtaatgt	gcttctgata	60
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atgctggggt	tactgtttgg	ctacgccatg	aagaacagcg	gcctctggct	tgccgcccga	540
cgcgagaaga	gccagagcgt	tctctgcgta	agtaataa			579

<210> 663

<211> 801

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (158)

<400> 663

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tttgcggtga	cggaggtggg	gcagacattc	tatcagcact	gtaaagctat	gctggtggag	120
gctgaagctg	cggaggaggc	ggtggctgct	ttacaggntg	agccgcgcgg	tatggtccgg	180

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ggcgtgggcg	tggtagagct	gcccattttg	atgggtgaagg	atcagctggc	ttcaggtgaa	660
cttggtcggg	tgctgaatgc	ctgggaaccc	agacgggaag	tgatccatgc	ggtgtatcct	720
tcccggcgcg	gcctgctgcc	atcggtcagg	acgctggtgg	attttctcac	cgaagagtat	780
gcaaagatgg	ttgaagacta	g				801

<210> 664

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 664

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cgggacgggc	gctaa					435

<210> 665

<211> 951

<212> DNA

<213> Enterobacter cloacae

<400> 665

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gcggccgtga	cgcgaccggc	ggaggccgtg	gcgtacatct	cgcataccat	cagcgaataa	900
gagaagggca	acgcggtgac	cggacaggtc	gacagacagc	gaagctactg	a	951

<210> 666

<211> 774

<212> DNA

<213> Enterobacter cloacae

<400> 666

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cacaccgtcg	ccagtaccca	cgcttacagt	aacctccatg	attatatcgc	tcaggcgaag	120
ctgaaaggca	tcaaaactgtt	tgcgataacc	gatcacggtc	cggatatggc	ggatgcgccg	180
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atgctgacct	ctttagatct	gatacctcgt	ggcttccatg	agccgggtctt	tgcgccccag	360
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ctgggctctg	attcacacac	ggccttccag	ctgggggatt	tcagcgagtg	cctgaaaata	660
ttgcgggaacg	tgaatttccc	ggaagaacag	atcctgaacg	tcacgcgcgc	tcgtatgctc	720
gacttccttg	agtcgcgcgc	catggcgccg	attgatgaat	ttgccgatct	ttaa	774

<210> 667

<211> 1527

<212> DNA

<213> Enterobacter cloacae

<400> 667

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accttccagg	gaaatcatga	ttccggcgat	atthtccaga	ccaacgcgta	cgctgtggt	120
cccctgatcg	acggacttct	ggcgccaaaag	gtgacggggc	tgttggtcacg	ccgcgcagaa	180
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<210> 668

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 668

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<210> 669

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 669

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<210> 670

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 670

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<210> 671

<211> 1557

<212> DNA

<213> Enterobacter cloacae

<400> 671

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<210> 672

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 672

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<210> 673

<211> 1173

<212> DNA

<213> Enterobacter cloacae

<400> 673

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<210> 674

<211> 1188

<212> DNA

<213> Enterobacter cloacae

<400> 674

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<210> 675

<211> 858

<212> DNA

<213> Enterobacter cloacae

<400> 675

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<210> 676

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 676

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<210> 677

<211> 7962

<212> DNA

<213> Enterobacter cloacae

<400> 677

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<212> DNA

<213> Enterobacter cloacae

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<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 679

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<211> 426

<212> DNA

<213> Enterobacter cloacae

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<210> 681

<211> 1206

<212> DNA

<213> Enterobacter cloacae

<400> 681

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<211> 1170

<212> DNA

<213> Enterobacter cloacae

<400> 682

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<212> DNA

<213> Enterobacter cloacae

<400> 683

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<210> 684

<211> 1179

<212> DNA

<213> *Enterobacter cloacae*

<400> 684

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<210> 685

<211> 759

<212> DNA

<213> *Enterobacter cloacae*

<400> 685

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<210> 686

<211> 1176

<212> DNA

<213> *Enterobacter cloacae*

<400> 686

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<210> 687

<211> 966

<212> DNA

<213> Enterobacter cloacae

<400> 687

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<210> 688

<211> 879

<212> DNA

<213> Enterobacter cloacae

<400> 688

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<210> 689

<211> 663

<212> DNA

<213> Enterobacter cloacae

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663

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<210> 690

<211> 666

<212> DNA

<213> Enterobacter cloacae

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<211> 612

<212> DNA

<213> Enterobacter cloacae

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<400> 691

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612

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<211> 1335

<212> DNA

<213> Enterobacter cloacae

<400> 692

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<210> 693

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 693

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aatattgagt	acattcatga	gtttgaaaaa	tcttttcgcc	acccgcgtaa	ctggggcgcc	180
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<210> 694

<211> 858

<212> DNA

<213> Enterobacter cloacae

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<210> 695

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 695

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gagtgtcagg	tttaccgtat	tgaacctat	ctgggcaaag	agacggttac	tgaacttgct	660
ggcgtggcgt	tttgccaact	ccctgtttgt	gaacaaatgg	gacaaccgca	ctatcgacca	720
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<210> 696

<211> 759

<212> DNA

<213> Enterobacter cloacae

<400> 696

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cgcactatcg	accacgtgga	aattaccgtg	gcggaagagg	tgggcatcga	agcccggttg	180
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gtgcgcggcc	agtacaccgc	aggtttttgc	caggggaaaa	aagttcctgg	ctatctggaa	420
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attcagatcc	tgaacaaagt	gcggggtctt	gatcacaaac	acaacctgca	aaccaccaag	720
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<210> 697

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 697

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tccgagcgca	aagtggctga	agttattctc	gcgcgcgccg	ctcaggcgat	tcattcaagc	180
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gatgtcgtgg	tactcatctc	tcatacgggc	cgcaccaaga	gccagggtga	gctggcgcag	660

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cgccggggcg	caaaattccg	ggataacttg	aagcgggtca	aggaagccct	gaaagaatcg	900
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<210> 698

<211> 1554

<212> DNA

<213> Enterobacter cloacae

<400> 698

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aggcttcgca	gaaccaagat	cgtaaccacc	ttaggcccg	ccaccgaccg	cgataataac	180
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ggcaaatgtc	tcctcaacat	cggcgataaa	ttcctgctgg	acgccaacct	gagcaaaggc	420
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<210> 699

<211> 240

<212> DNA

<213> Enterobacter cloacae

<400> 699

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gtcagcgaacg	gcaagcctac	agaatcagac	tcaggcctgc	tgggctataa	agacgcaaat	180
ggtgtcaaac	agcagatcaa	taaagccgac	gttaaagaag	tctctgaaat	tccgcattga	240

<210> 700

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 700

agggagccat	ctatgaacag	tctttttaacg	ctggcgaagg	acttagagca	gaaatcgaaa	60
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gtcagaacgg	aactgaacga	aagcgagaag	agaatcagcg	ccgccatcca	cgaccacgac	180
cggatgctgt	cctcagccat	gagccagcgt	acgaaaggga	tgctgcgcac	ggtcagccag	240
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tggtggcagg	ggcagcagat	actcgacaat	tacacgacca	tccgggagca	gaagagcacg	360
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cgccgctgcg	tgagggtgaa	cccggacgcg	ggacggttcg	gagaggattc	gagctggatg	480
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<210> 701

<211> 213

<212> DNA

<213> Enterobacter cloacae

<400> 701

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tcgaaaaggc	tggacgagtg	ggagagcggc	ttcgcggaat	ggcggacgat	gtgtgggtctt	120
atgcaacggg	agaacgcagc	gctgagcggg	cgcgctcacc	acttgagcac	gcaggtgctg	180
agtttaagcg	agcagctgcg	ccggttgctg	ttaa			213

<210> 702

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 702

attagcgtga	tctggcagcg	cctggtgaaa	atgccggaaa	cgaagcagga	agccgctcag	60
gcgattacgc	ggggtttact	ggccttagcc	tcgtccgggg	agctgaaaac	gcgtcatgac	120
gtcactgagg	cgctggaaag	cgcaggtttt	gaggtgggtc	gcaccacaaa	aagcagcatc	180
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tcttttaacg	ctggcgaaag	acttagagca	gaaatcgaaa	gtgcagcaac	agactaccgg	300
cgagatgctg	aaagccgcat	tcagcgagca	cgataa			336

<210> 703

<211> 708

<212> DNA

<213> Enterobacter cloacae

<400> 703

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aacgacatcg	aggcacaccg	ggagcaggag	cgcgcagcgc	agcaccagaa	agcgtgagag	660
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<210> 704

<211> 3273

<212> DNA

<213> Enterobacter cloacae

<400> 704

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<210> 705

<211> 1095

<212> DNA

<213> Enterobacter cloacae

<400> 705

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<210> 706

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 706

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acaggcctga	ccgaacgaca	gattgagaag	tatcgccagg	gctgttgggt	ggaaggtgtc	120
cattttaaac	gggtgtctcc	ttctggcgaa	aaaaccttgc	gtggcacaac	ctggtacaac	180
tatccgagaa	ttaatcagtt	aataagggat	gcgtaa			216

<210> 707

<211> 210

<212> DNA

<213> Enterobacter cloacae

<400> 707

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aaatgcgggt	actgcggcaa	gacgggttaa	ccgggggaag	tagttaaaag	tacccttctc	120
tatcgcaacg	gcgcacagct	ggcgcgcaaa	gaaaaagaat	actgctctga	acgttgtgct	180
tcgtacgacc	agatggccca	cgaggcataa				210

<210> 708

<211> 1251

<212> DNA

<213> Enterobacter cloacae

<400> 708

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ccggcgaaca	tcaaaaaagc	cgggaacctt	cgggctgtga	tcgttagcga	aatcaacctt	180
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gctcttgcct	gggaagatat	tgactgggaa	aaaggtacag	cccatataaa	gcggaatctt	780
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gttttcatac	cccggatgcg	caaaggagaa	cagaaagcct	actactcttt	atcgagcato	1020
ggtgcgagat	tcaacgcagc	tgtaaaacgt	gctggtattc	gcgcgcggaa	tcogtaccat	1080
acgcggcata	cttttgcctg	ctggctttta	tctgccggcg	ctaaccctgc	tttcatagcc	1140

agccagatgg	ggcatgaaaa	cgcgcaaatg	gtttatgaag	tctacgggtgc	gtggattgaa	1200
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<210> 709

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 709

agccatggcg	cgctggcagg	cacacaggtg	agcgccttaa	tcacgcttac	cccgtgttt	60
acgctgttat	tttcagattt	attatcaatg	gcctggcccg	atgtcttcgt	caagccgatg	120
ctcaacctgt	tgggttatct	cgggtgcgtt	gtcatgggtg	cgggcgcgat	gtattccgcc	180
attggtcatc	gtctctgggg	gcgttggcgc	aaaaatgaag	cggttgtaat	agtccccgcg	240
tcaggcgaat	ga					252

<210> 710

<211> 1191

<212> DNA

<213> Enterobacter cloacae

<400> 710

gttacggaga	gtaaaatgaa	gtttgttgat	gaagcgacga	tcctggctgt	ggcagggtgat	60
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ggcgggtgacg	gtggggacgg	tggcgacgtg	tggctggagg	cggatgaaaa	cctcaacacg	180
ctgatcgact	acggtttcga	aaaatctttc	cgcgcgcgagc	gtggccagaa	cggccagagc	240
cgcgactgta	cgggtaaaacg	cggtaaagac	gtgacgatca	aagtgcgggt	gggtacgcgt	300
gtcatcgatc	agggtaacggg	cgaaccatg	ggtgatatga	ccaaacacgg	tcagcgctg	360
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cgtacccccg	gtcagaaaaac	catgggtacc	ccagggtgata	agcgcgacct	gcaactggaa	480
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gccagccagg	ttggcgtgaa	agatctctgc	tgggatgtga	tgacctttat	catcgagaat	1020
ccggttggtc	aggcagaaga	ggcgaacacg	cctgaaaaag	tcgaattcat	gtgggatgac	1080
taccaccgcc	agcagctcga	agagctggaa	gcggaagaag	atgatgaaga	ctgggacgat	1140
gactgggatg	aagacgacga	agaaggcgctc	gagttcatct	acaagcacta	a	1191

<210> 711

<211> 366

<212> DNA

<213> Enterobacter cloacae

<400> 711

atatattatag	cgcactctga	atcatcacgag	gatgtgcgcg	gaagcggagt	ttatatgtac	60
gcggttttcc	aaagtgggtg	taaacaacac	cgagtaagcg	aaggtcagac	cgttcgcctg	120
gaaaagctgg	acatcgcaac	tggcgaatct	gttgagttcg	ctgaagttct	gatgatcgca	180
aacgggtgaag	aagtcaaaaat	cggcgcttcct	ttcgttgatg	gcggcggttat	caaagctgaa	240
gttggtgctc	acggctcgtg	cgagaaaagt	aaaatcggtt	agtttcgtcg	tcgtaaacac	300
tatcgtaagc	agcagggcca	ccgtcagtg	ttcactgatg	tgaataattac	tggcatcagc	360
gcctaa						366

<210> 712

<211> 843

<212> DNA

<213> Enterobacter cloacae

<400> 712

gtaagggtttt	ctcggtccgg	taacggatta	aagccccgca	acgtgttgcg	gggcttttta	60
cattggaaac	cgggaaaatt	ttctgtaggg	aaaacgggca	tgaagcagca	ggccggcatt	120
ggtattcttt	tggcgctcac	taccgcaatg	tgctgggggtg	cgctgccaat	tgcaatgaag	180
caggtaactgg	aagtcattga	gccaccgacg	gtgggtgtttt	atcgcttcct	gatggcaagc	240
ataggcctgg	gcgccattct	ggcgcgtcaa	ggtaagctgc	caccgctgcg	catctttcga	300
aaacgcggtt	ggctgggtgt	actggctatc	gcgacggggcg	gtctgttcgg	taacttcatt	360
ctgttcagct	cttccctgca	atatcttagc	cctacagcgt	cacaagtgat	tggtcagctt	420
tcaccggctg	gcatgatggg	cgccagcgta	ttcatcctca	aggagaagat	gcgcggcacg	480
cagatcatcg	gggcaagtat	gctgctttgc	gggctgggtga	tggtctttaa	caccagcctg	540
attgagattt	ttaccgcctt	gacggattac	acctgggggtg	tcatttttgg	ggtgggcgca	600
gcaacggtct	gggtgagtta	tgccgtcgcg	caaaagggtg	tattgcgcgg	tcttgccctca	660
cagcagatcc	tctttttgct	gtacactttg	tgtacactgg	cattattgcc	tttagcgaaa	720
ccgggtgtaa	ttaccagcgt	cagcgactgg	caactggcgt	gcctcatttt	ttgtgggctg	780
aatacgctgg	tcggtttatg	cgcgctggct	gaagccatgg	cgcgctggca	ggcacacagg	840
tga						843

<210> 713

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 713

caaattgcaag	ctattccgat	gaccttacgt	ggtgccgaaa	aactgcgcga	agagctggat	60
tttctgaaat	ccgtgcgtcg	ccctgaaatc	atcgccgcta	tcgcggaagc	gcgtgagcat	120
ggcgacctga	aagagaatgc	tgaataccac	gcggcgcgctg	agcagcaggg	tttctgtgaa	180
ggcggtatta	aagatatcga	agcaaaattg	tccaatgcac	aggttatcga	tatcaccaaa	240
atgccgaata	atggccgtgt	gattttttgg	tcaaccgtta	ccgtgctgaa	cctggacaac	300
gacgaagagc	agacctatcg	catcggtggg	gatgatgaag	ctgacttcaa	acagaacctg	360
atttcgggtg	actcgccaat	tgcctgtggc	ctgattggca	aagagcagga	cgatgtggtc	420
accatccgca	cccctggtgg	tgaagtggaa	tacgaaatta	ttaaggttga	atatctgtaa	480

<210> 714

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 714

atggcacata	aaaaggctgg	cggtccacac	cgtaacggtc	gcgattcaga	agctaaacgc	60
ctgggogtta	agcgtttcgg	tggcgaatcc	gttctggcgg	gtagcatcat	cgttcgtcag	120
cgtggcacca	agttccacgc	gggtaccaac	gtaggttgcg	gtcgtgacca	cactctgttt	180
gctaaagcag	acggtaaagt	gaaatttgaa	gttaaaggcc	cgaacaaccg	taaatacatc	240
agcatcggtg	ctgagtaa					258

<210> 715

<211> 1095

<212> DNA

<213> Enterobacter cloacae

<400> 715

agatcgcatc	aaaaccgtac	gcggcggtgg	ttaccgtctg	gagagccaga	aatgaacagt	60
atgcgccggc	gattaatggt	ggtgctggcg	gttattctgc	tattttttca	actcattagc	120
gtagtctggc	tgtggcatga	gagccgcgag	cagatcggtt	ttctgggtgaa	cgaaacgttg	180
tccgctaaag	cacgcaacaa	ccatgtcgaa	aaagagatcc	gcgaagccat	tgccctccctg	240
ctggtccctt	cactggtgat	ggtcgggttt	acctgctctt	tctcattctg	ggcagtcaca	300
tggatcaccg	gaccactcaa	caaacttcgc	gccagccttg	cgaaccgttc	ggcggataat	360
ctgactcccc	tgccgatgta	ttctgatatg	gaagagatag	gcgcagtaac	cacgtccctc	420
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cagtccgggt	ccccgcaggc	cacgccactg	ataaacggga	tcgatcagct	gatgcacacg	600
gtggaacacg	tgtgatgct	ggcgcgctgc	ggacaggcga	tggccagcgg	ccattacgat	660

accgtgaact	ggactgagtc	gatcattgct	ccgcttagcc	tggagcatga	agccaaagag	720
catacggat	tatggccggc	ccacagcacg	ctgacggtag	agggggacgc	cgtcctgtta	780
cgtctgatgc	taaggaacct	tctggagaat	gcgcgccgtt	acagcccgcc	aggcacaatc	840
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ccgggtattg	atgaggcgca	ccgccagtcg	atcacccaac	ctttccgacg	tctcgaccag	960
cgctacggcg	gcagcggcct	tgggctgagc	atcgtagcgc	gtatcgtaca	gctccatcat	1020
ggtcatttaa	cgctggagaa	cggcgctgag	ggcgccctca	tcgccagctg	ttggttaccg	1080
acgaaaatag	gataa					1095

<210> 716

<211> 375

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (29)

<220>

<221> unsure

<222> (30)

<400> 716

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caacgtaagc	aaaaatatac	gatgaatctg	agtactaaac	aaaaacagca	ccttaaagggt	120
ctggcacatc	cgtcgaagcc	tgtagtgtat	cttggcaaca	atgggtttgac	cgaaggggtg	180
cttgccgaga	ttgaacaagc	gctggaacac	cacgagctga	tcaaggtgaa	aatcgccctc	240
gaagacagag	acactaaaaa	cctgatcgtg	gaagccatcg	tgcgcgaaac	cggcgccctg	300
aatgtacagg	tcacgcggtg	aacgcctggg	ctctatcgcc	catctaaaga	gcgcaaaatc	360
tcgctgccac	gttaa					375

<210> 717

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 717

ctagcgatga	aactactgat	agttgaagac	gatctgttat	tgcaggaagg	gttagcgctg	60
gcgctgggca	atgaggggta	cgccctggat	tgtgccgcca	cgcccgctga	agcagatgcc	120
ctgatccaga	gcgggtgaata	cagcctgggtg	atcctggatt	tgggactgcc	ggataaagac	180
ggcgcgacgc	tgcctctgca	gtggcgctcg	cgccgagtg	agaatcccg	attgattctc	240
accgcccgcg	atgccattga	agacagaatt	aacgggcttg	attctggcgc	tgacgattat	300
ctggtaaaa	ccctcgccct	tgcgagctga	caggctcgcg	tacgggcgtt	gatccgccc	360
tatcagggcc	acagcgacaa	cctgctgacg	gacggggata	ttaccctcaa	tctgcaaa	420
cagcaggtgc	tgcgccagtc	tcagcctgtg	gaagtgacct	caaaagagtt	cgctctgctg	480
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tactcctggc	aggacgatcc	aggatcaaac	acgcctgaag	ttcatattca	taatctgcgc	600
cgcaagctcg	gtaaagatcg	catcaaaacc	gtacgcggcg	tgggttaccg	tctggagagc	660
cagaaatga						669

<210> 718

<211> 1443

<212> DNA

<213> Enterobacter cloacae

<400> 718

cgcgagatta	tgcgattttc	cagttttatc	atcggtattga	ctaccagtat	aacgtacacc	60
gttcaggccg	cgaatgttga	tgagtacatt	aatcaactgc	ccgccggcgc	gaaccttgcc	120
ctgatgggtg	agaaggttgg	cgcgcaggct	cccagatttg	actatcacag	tcaacagatg	180
gcgctgcctg	ccagtaccca	gaaggtgatc	accgccctcg	ccgctctgct	ccagctcggg	240
cctgacttcc	gttttactac	cacccttgaa	accagaggta	acgttgaggg	tggcgaaactg	300

aaagggcgtc	ttatcgcccg	ttttgggtggc	gatccacact	ttaagcgcca	ggatgaccgc	360
aacatggttg	cggtactgaa	aaaatccggc	gtaacaaaaa	ttgatggcaa	cgtgctgac	420
gacacctcca	ttttcgccag	ccacgataaa	gcgcctggct	ggccatggaa	cgacatgacg	480
cagtgtttta	gcgccccgcc	agcgcgcgcc	atcgttgacc	gtaactgctt	ctccgtatcg	540
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gtcacgatgt	tcagccaggt	gcggacgctg	gcgaaaggct	ccccggaggc	acagtattgc	660
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tctcttcagt	accgcgcggg	ccttcacgct	gcgggcgtgg	atggcaaagt	ttcagccaaa	1260
acgggttccc	tgcaaggcgt	ttacaacctt	gcgggtttca	tcacgaccgc	cagcggacaa	1320
cgcattggcat	ttgtgcagta	tctttccggc	tatgccgtcg	aaccggctga	ccagcgcaat	1380
cgccgtattc	cactggtacg	tttcgaaaagc	aggctctata	aggacatcta	ccagaataac	1440
tag						1443

<210> 719

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 719

tgcatgggtct	ctggctggcc	gagcggaggaa	tgtctgatga	aatactcact	gatttacgct	60
gaccagcctt	ggctttatga	caacaaagcc	agtaacgggtg	cagcagaaga	tcactacgac	120
acgatgaaac	tgatcgacat	gaagcgcttg	ccggtttggg	acctggctgc	cgatgatgca	180
gttctggcta	tgtggtttac	cggaacccat	acccgagagg	ctatcgagct	ggctgaagcg	240
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gagaagcata	tcaacaaagc	acttcaggca	ggccgtgtgg	aagattttta	cgacttcctc	360
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gacttggtga	tcgccaccag	ggggaatgga	cttgaacgca	agtgtgccag	catcaagcag	480
gttatctaca	gcccactcgg	tgagcacagc	cggaagccgg	cagaggccgg	tttcgctctg	540
gagaagcttt	acggtgatgt	tccacgcac	gaactattca	gcogttgcgg	tgccgctggc	600
tgggaccact	ggggaaatca	atctgaatta	ccagctgttg	agcttatacc	ggcagttgcc	660
gttcccatga	aaaaacagca	ggagcgcgcc	gcatga			696

<210> 720

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 720

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ggtgtgagag	ccatactgac	acctgaaatt	gcgccaatgt	ctgggggtgg	tctgttccgg	120
cctggtaacg	aactgctctg	gctattccgt	cagggaaggg	tagttattga	gcaaccatct	180
gaagccatcc	agcatctgcc	atctggatta	atccctgaag	cccaccagcc	cctgactgac	240
gatgccaaaca	tgaaggctat	tttcgttaac	gagagggtca	ttcagcgagc	tggtgggttg	300
agtagccttg	atgcctggct	ggagagaaaa	tttgaatgcc	agtggcctca	cactgactgg	360
catgccactg	actttacggg	aatgcgccac	gctccgggga	gcattcgtct	ttgctggctg	420
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ctttcgcttc	ctgagttctg	ctggtggatg	gtacgtaatg	atctggctga	cottgttcc	600
gaatcagtg	cgagtaaagc	actcagaatc	aagccagaa	agcacagttc	agtgatgagg	660
gaaagcgaca	ttgtaccgtc	attaccggct	acgcaaatct	ttcaggagaa	ggcaaaaaag	720
atagtggcgg	tgaaggctga	tcctgaaacg	ccggatcttt	catgctga		768

<210> 721

<211> 531
 <212> DNA
 <213> Enterobacter cloacae

<400> 721
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 atggtagagc caagtctgaa agaagtagtt aaagcgatgt gcaaagcgta cccaggaggc 120
 cgtgaagcta tggccggtgc tcttgccatg tcagtaacgc agttcaacaa caacctgtat 180
 gagaagaatg gttgccgggtt cttcgaagtg aacgagctgg aggccatgga agacatctcg 240
 aatacgtccc tccctggcgga ttacttttgc cgtcgcctgt gcgcgctgct ggtggacggt 300
 cctcaacttg aagaccttga tctgtctgac ctgttttgatc gtgccatgag aacgtcagca 360
 gcgcgtggac gtgttgatac cgtgatccag agagctctcg aagatggagt aatcgaacgt 420
 catgaagctg aagaaatcaa cgaatatcac cgccgtcatc tggcagcgcg tgaagaagag 480
 atccgcgcga ttgtcgcgct gtttagccgt aagaaaagcc aaaaaaagtg a 531

<210> 722
 <211> 570
 <212> DNA
 <213> Enterobacter cloacae

<400> 722
 ggatggaatc ttcaaataca gtttcaagaa caccgagtac agcaaagtcc cggcggggctt 60
 cagaggagcg aactcatgag tcttctgaaa gatattcaaa ttttcatcgc cgctaactct 120
 ggcttaacga acaaagagat tgcggcatca atgccacagt acgacgttca tgctgttcag 180
 cgcggtgtat gccatctggt caaactgaat cgcgcgaacc gccagcataa cggcaagtgc 240
 taccagtatt ttgcaaaagc accgggtggg gaggttggcg aggggcgctt tgcactgaaa 300
 atcaaccggg ctgataaaacc agctgtacca gaacaggaag aaggtctaaa tccggctgtg 360
 accacaatga tggataaggc tcaaggcctg tttgaaaaag ggctctacca gcgggcagcc 420
 acgattctga tggatgcctt caatcgctct aagaacgaag agcagcggat gaagatactg 480
 attgagcgtc agcgttgctt gacgatggcg ccgaaaagtga aagcacctc tgatgcacgg 540
 tgtctggctg gccgagcgag gaatgtctga 570

<210> 723
 <211> 417
 <212> DNA
 <213> Enterobacter cloacae

<400> 723
 atggctgaaa aaacaggagg tgacgttatg aaactgggtg tcccgttccc gccgagcgta 60
 aacacctact ggcgcgcccc aaataaggga ccgctaaagg gccgccattt gattagcgcc 120
 aaaggcaggg cataccaaag cgcggcctgt gtgcgcattg tcgagcagct tcgcttcctt 180
 cccaaacctt caacggcacc tgctgccgtc gaaattatgt tgtaccacc agatgaacgc 240
 cgccgcgaca tcgacaacta caacaaggct ctgtttgatg cgcttacgca tgctggcatt 300
 tgggaggatg acagccaggt gcagagaatg ctggtggaat gggggcctaa agtgaatggc 360
 ggaagggtag agatatcgat aaccaagcat caaccagcaa tgggggtaat ggtgtga 417

<210> 724
 <211> 456
 <212> DNA
 <213> Enterobacter cloacae

<400> 724
 agcgaaatac ggcgaccagt taacgctgct gtttcggttt ttagatcgtg cgctggcaat 60
 cggcgattata gcatgaaaag tggagataac atgcgtgata ttcagatggg attggtagct 120
 tggggtaatt ggtcaaaata caaaatagaa gcagatgtag gttattctcc gattgcagca 180
 gggtttaagg ggcttcttcc agagagtggg gctatgccta agtgtacaga ggacgatgcc 240
 cttattattg atagttgcct cgctcggttg aaattgaagc gtcccgatga atacgaactt 300
 atctttgatc attacgtaaa ggggtgtttc aagcgaggaa tcggccgtaa acttaagtta 360
 tctgaaggga tggttcgaat taaattccag atggcagagg ggttcgttga aggttgttta 420
 gctatgttag atatcaggtt acaaattggac gagtaa 456

<210> 725
 <211> 936
 <212> DNA
 <213> Enterobacter cloacae

<400> 725
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 accacctccg gactggagcg tgacggcggt cgctggattt ataacacaac agagcagtgg 180
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 ccagcttacc tgaagtccgc taccactggc gcgaatgccg gaaggccagc gcgtgttaac 840
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<210> 726
 <211> 375
 <212> DNA
 <213> Enterobacter cloacae

<400> 726
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 gccaggggca ttaccgctcg caaaacggaa tgggatgcag atccagtga gatcatcaaa 300
 ggctgcttt ccggtggaga taaggccaga gataacgctg ttgaatggct gaaaaaacag 360
 ggagtgcagt tatga 375

<210> 727
 <211> 216
 <212> DNA
 <213> Enterobacter cloacae

<400> 727
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<210> 728
 <211> 1446
 <212> DNA
 <213> Enterobacter cloacae

<400> 728
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<210> 729

<211> 1386

<212> DNA

<213> Enterobacter cloacae

<400> 729

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<210> 730

<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 730

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gatgcagact	attcccagcc	cacagccagc	agtatcttcg	ccctggagga	tgaatcccct	180
ttcggctctt	atgaactgct	gatgcagatg	gtcagtgaac	atagcgaatg	catttcgcag	240
accgccataa	aaaatctcga	tgtcatctac	tctaacgacc	cggacgaact	gttgccgacc	300

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aaaggctcgg	ccgcagcggg	caccatgcac	gacctcgcg	gtgaactggt	ccctgagtgg	840
cagagccatt	tcagtgcgt	tctgacccgg	gaggtgcgtc	atgtctga		888

<210> 731

<211> 1725

<212> DNA

<213> Enterobacter cloacae

<400> 731

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gctgaaatgc	ccatggtccg	cagcgtcgac	cagttaagcc	cgaatcctga	taatccgcga	180
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cacaaagccc	gctctatata	tgaagagcag	atgggaaaaga	cggtttctgt	gcgtcagttg	540
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<210> 732

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 732

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cttgccctcac	ccggaaaggg	gaaagcctca	agggaaacgg	taagccgcgt	cctgctgatg	420
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cgggggaata	tctatgctca	gcacgatgag	cccctgacgt	tcagcgatgc	ggaaatgctc	540
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cagaatgccc	gcgaagtgt	cgacgatata	aaaaacgacc	ccaccatgcg	ccattatcgc	660
agccatcttg	cgctgatcga	atcgctctcg	gacagcccac	agtctcccag	ccagatggcg	720
aaacatcatc	accgaatacc	ctgtcccgcg	ccgggttcgg	aaaccgcacg	tcttcactac	780
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<210> 733

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 733

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<210> 734

<211> 1557

<212> DNA

<213> Enterobacter cloacae

<400> 734

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<210> 735
 <211> 3840
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
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<400> 735

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<210> 736

<211> 273

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (206)

<220>

<221> unsure

<222> (256)

<220>

<221> unsure

<222> (261)

<400> 736

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<210> 737

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 737

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<210> 738
 <211> 633
 <212> DNA
 <213> Enterobacter cloacae

<400> 738
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<210> 739
 <211> 588
 <212> DNA
 <213> Enterobacter cloacae

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 ccgactctgc tgtttaccaa cgcggggatg aaccagttca aggatgtgtt ccttggctctc 180
 gacaagcgta attattcccg cgcacacaacc tcacagcgtt gcgtgcgtgc gggcggtaaa 240
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<210> 740
 <211> 759
 <212> DNA
 <213> Enterobacter cloacae

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<210> 741
 <211> 516
 <212> DNA
 <213> Enterobacter cloacae

<400> 741

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gaattttcag	aaaaagttaa	aatccagcgc	tttttgctct	accgcggtt	cctgatggaa	480
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<210> 742

<211> 912

<212> DNA

<213> Enterobacter cloacae

<400> 742

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<210> 743

<211> 1095

<212> DNA

<213> Enterobacter cloacae

<400> 743

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<210> 744

<211> 240

<212> DNA

<213> *Enterobacter cloacae*

<400> 744

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gcctttccct	tgccttgat	ccctccctt	tccgtgctcg	ggctggcgct	gggcgatctg	180
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<210> 745

<211> 330

<212> DNA

<213> *Enterobacter cloacae*

<400> 745

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cttgaaaagt	tcttccgtaa	tggaaaaaca	acggcaggta	ttccttctga	aattattaac	120
gcgattctgt	gtcgacttga	aacgctggat	aatgtccaga	gtgagcggga	gttattatcc	180
aacagcttgc	gttatgaacg	cttaagaatg	acgtcaaacc	gttattcctc	cattcgagta	240
aactctaagt	atcgattatt	ctttgaatgg	aatgatggcg	cacataatgt	tcatttgtct	300
gcacatgact	ataaatcgct	catccattaa				330

<210> 746

<211> 1260

<212> DNA

<213> *Enterobacter cloacae*

<400> 746

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<210> 747

<211> 816

<212> DNA

<213> *Enterobacter cloacae*

<400> 747

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<210> 748

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 748

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aaattgcagc	aatgtaaggg	tgtaaaagag	gctcttgagc	gggaagagat	tcagttgtgg	540
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<210> 749

<211> 1881

<212> DNA

<213> Enterobacter cloacae

<400> 749

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aagaatgcac	caaaccctaa	aaagcagccg	gcggatctca	tggaggagtc	aattatcttt	180
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<210> 750

<211> 393

<212> DNA

<213> Enterobacter cloacae

<400> 750

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tttacccttt	catcatctac	tcgcgtctac	ttaagcgc	ttaggaataa	aggagtaaac	180
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tcgatcgcg	ttgttgaaa	tgagattgat	gcgtggataa	cccaacggat	tgaagagcga	360
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<210> 751

<211> 975

<212> DNA

<213> Enterobacter cloacae

<400> 751

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gacggcggtg	atcgtgggca	tcaggcgctg	ttgcagggat	tgctgaaaga	aggcgaggcg	180
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gggggtggact	acgtcctgtg	tgtacggttc	gacgcgtg	ttgccgcgct	gaccgcacaa	360
aattttgtca	gagacctgtt	ggtcaggcag	cttggcgctg	agtttctcgc	cggtggcgat	420
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<210> 752

<211> 2862

<212> DNA

<213> Enterobacter cloacae

<400> 752

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<210> 753

<211> 549

<212> DNA

<213> Enterobacter cloacae

<400> 753

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accgggcaac	aggtgaccca	aaacaagcga	gcaattttgca	tgtctaaatc	cgtacagagc	120
aacagcgcg	ttctcgttca	ctttacgctg	aagctggatg	acggctctac	ggccgaatcc	180
acccgcaaca	acggcaaacc	agccctgttt	cgtcttggcg	atacctccct	gtctgaagggt	240
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gatgccgcgt	ttggcgtgcc	aagtccggat	ctgatccagt	acttctcccg	togtgagttt	360
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gaaatgcctg	gcgtgatccg	cgaaatcaac	ggcgactcga	ttaccgttga	cttcaaccat	480
ccgcttgccg	ggcgactgtg	ccattttgat	gtagaagtgc	tggagatcga	tccggcactg	540
gaggcctga						549

<210> 754

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 754

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aacctcgccg	atagcgcaat	atgcgttggt	gcggcggtta	tcgtgctgga	aggcttcttg	480
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<210> 755

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 755

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gaagcggtgc	cgctggaagg	ccgcgaagag	aacattgtct	ttgaagtgcc	gaaagagttg	960
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<210> 756

<211> 384

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (276)

<400> 756

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<210> 757

<211> 1368

<212> DNA

<213> Enterobacter cloacae

<400> 757

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<210> 758

<211> 1818

<212> DNA

<213> Enterobacter cloacae

<400> 758

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<210> 759

<211> 324

<212> DNA

<213> Enterobacter cloacae

<400> 759

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gagtccttcg	atcagttcgt	gatcctgttg	aaaaacacgg	tcagccagat	ggtctataag	180
cacgcgattt	ctactgttgt	tccgtcccgt	cgggtatctc	atcacagcaa	taacgctggc	240
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<210> 760

<211> 1692

<212> DNA

<213> Enterobacter cloacae

<400> 760

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cactgtttta	ttttttgcgc	taattcattg	agatcgaggg	gctgtgacat	gacggaccat	180
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<210> 761

<211> 225

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (34)

<400> 761

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ccggatgtcg	aaattcactt	agattaccag	gcacaagggc	gtgaggcacg	catcagtgcg	180
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<210> 762
 <211> 954
 <212> DNA
 <213> Enterobacter cloacae

<400> 762
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 agcgttgatt cagccctcat ctaccgaggg atggacatcg gcacggcgaa gcccaacgca 180
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 caggggtggg acgtttttgca caggcaactg gaagagattg acccggttgc cgcagcgcgg 480
 atccacccaa acgatccgca aaggctttcc cgggcaactg aagttttttt catttcgggt 540
 aaaactttta cggaaactgac gcaaacgtca ggagacgctc tgcctatca ggtgcatcag 600
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 ggcgagattt catacgtatg aatggtttat cgaggtgttt gcgccacgag acagtttagc 840
 aagcgccaga tcacctggtt acgcggttgg aagggggttc actggttaga cagtgaaaaa 900
 ccacaacagg cgtaaacga agtgattgag gttattgttg atatcgctga ctga 954

<210> 763
 <211> 372
 <212> DNA
 <213> Enterobacter cloacae

<400> 763
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 gccggtgtcg aagcaatgca ggtgattacc ggtagccgta aagcgcgcga cccgaagtat 180
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 gttgtgctgt ttgatcatgc gctgtctccg gctcaggaac gtaacctgga agctctctgc 300
 gaatgccgtg ttatcgatcg caccggggtg atcttagata tttttgctca gcgtgcgcgt 360
 acccacgagg gt 372

<210> 764
 <211> 1251
 <212> DNA
 <213> Enterobacter cloacae

<400> 764
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 cccctcgatc tcaatgaatt agcgcaaaaa ataaaacagt ggggtgctga actgggcttc 180
 cagaaggctc gtattactga caccgacctc tctgccagt agcctaagct ccaggcatgg 240
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 accattcagc agcaactgtgt ttcgctgaat tttagaccct ttgtcgatcc tgcgcctatt 540
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<210> 765

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 765

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aaaggccgtg	cgtgtggcgt	aggcgaagtg	aaattcacccg	gtcaggttct	gcctaccgcg	120
aagaaagtca	cctaccgtat	ccatttcaaa	cgcacgttta	accgcgcgct	gattatgggc	180
ctggcggacg	gtgaagtgtc	ggtagatggt	cgcttgatct	ataccgcgaa	cgacctgaaa	240
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<210> 766

<211> 450

<212> DNA

<213> Enterobacter cloacae

<400> 766

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ggttttcagg	aaaccttcca	gccagtcagt	cgcttcgata	tccagggtgt	tcgtcggttc	180
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tgccagctcg	ttgagattct	tgctcgtcgg	gtccgctcatg	accagatgcg	aaatctcgtg	420
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<210> 767

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 767

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<210> 768

<211> 1257

<212> DNA

<213> Enterobacter cloacae

<400> 768

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<210> 769

<211> 231

<212> DNA

<213> Enterobacter cloacae

<400> 769

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agcatggaaa	ataagagtgg	agaggctaaa	gtgcagaagg	tcagaaactg	gtcgccgggtg	120
tggattttcc	cccatcgtga	ccgcgctgat	cggtgcattg	atcctgtttt	atcattacag	180
ccatcagggg	ccggaagtca	cgctaattac	caccaatgca	gaggggattg	a	231

<210> 770

<211> 579

<212> DNA

<213> Enterobacter cloacae

<400> 770

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cagcagaaa	atggctatga	cgaaatgggt	aaagtacttg	cgcaggggatg	ggcacaggag	540
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<210> 771

<211> 2025

<212> DNA

<213> Enterobacter cloacae

<400> 771

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gatcttgatc	tctacaccgg	cgtacagatg	atcgactgga	cagagatctt	caccccgagc	180
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gccgaactgg	gactgaaagc	acaagaaatc	agccaaaaaa	cgctgtctca	ggactttgcc	1980
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<210> 772

<211> 1908

<212> DNA

<213> Enterobacter cloacae

<400> 772

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<210> 773

<211> 1656

<212> DNA

<213> *Enterobacter cloacae*

<400> 773

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<210> 774

<211> 399

<212> DNA

<213> *Enterobacter cloacae*

<400> 774

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<210> 775

<211> 1074

<212> DNA

<213> *Enterobacter cloacae*

<400> 775

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tcaacggcgg caacttgtgc gtctcttggc accggtagcg aattaacaaa taataaaatc 180
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<210> 776

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 776

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gcttttgaat	gcgttcggcg	tactgctgat	gttattgaag	attcgattgc	agataaccgtc	420
gaaaacgagt	ttattgaccg	tcctattgat	ttgcacctcg	gcgatgacat	catcgaaaagt	480
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<210> 777

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 777

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<210> 778

<211> 1539

<212> DNA

<213> Enterobacter cloacae

<400> 778

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<210> 779

<211> 219

<212> DNA

<213> Enterobacter cloacae

<400> 779

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gtagtogata	tgtgcgcagt	cttccccgca	ggtaaagaaa	ttgttttgcc	agaaatatcg	180
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<210> 780

<211> 309

<212> DNA

<213> Enterobacter cloacae

<400> 780

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<210> 781

<211> 906

<212> DNA

<213> Enterobacter cloacae

<400> 781

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<210> 782
 <211> 843
 <212> DNA
 <213> Enterobacter cloacae

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<210> 783
 <211> 984
 <212> DNA
 <213> Enterobacter cloacae

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<210> 784
 <211> 699
 <212> DNA
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<210> 785

<211> 417

<212> DNA

<213> Enterobacter cloacae

<400> 785

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<210> 786

<211> 1662

<212> DNA

<213> Enterobacter cloacae

<400> 786

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<210> 787

<211> 720

<212> DNA

<213> Enterobacter cloacae

<400> 787

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<210> 788

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 788

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<210> 789

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 789

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<210> 790

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 790

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aaccgcttta	atcaacagga	tacctcgtc	gcgctggcag	tcaaagagac	attgcccgag	180
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aacctgaccg	cgcaggatct	ggctcgtcggg	ctggcggtt	ctggtcgtac	gccgtacgtc	480

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attctgatga	tattaaccgg	gctggatgca	gccgcggcca	gagccaggct	tgaagcccat	900
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<210> 791

<211> 1374

<212> DNA

<213> Enterobacter cloacae

<400> 791

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gacgaaaagc	ttgatattaac	gcgcctgaag	cagctccccg	gcgtgagcgg	gtacgttaaa	180
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<210> 792

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 792

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<210> 793

<211> 564

<212> DNA

<213> Enterobacter cloacae

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<210> 794

<211> 543

<212> DNA

<213> Enterobacter cloacae

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<210> 795

<211> 288

<212> DNA

<213> Enterobacter cloacae

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 aggatcagtt caatcgagcc tggcagcaac tcgcgtagct ttttctcaat ccagcacatc 240
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<210> 796

<211> 891

<212> DNA

<213> Enterobacter cloacae

<400> 796
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<210> 797
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 <213> Enterobacter cloacae

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<210> 798
 <211> 306
 <212> DNA
 <213> Enterobacter cloacae

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<210> 799
 <211> 1548
 <212> DNA
 <213> Enterobacter cloacae

<400> 799

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<210> 800

<211> 1167

<212> DNA

<213> Enterobacter cloacae

<400> 800

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atccatgggt	atgtctggct	gagtatggag	ctggcgcggc	agctggagtt	gttatcgcac	1140
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<210> 801

<211> 384

<212> DNA

<213> Enterobacter cloacae

<400> 801
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cagcgcgaaa tccaggacgt agagaagaag atccgtgaca accagaaacg tgtcctgctg 180
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atcgccagca tgaagagcga ttatgaagat cgcgttgatg actacatcat caaaaacgct 300
gagctgtcca aagagcgctg cgacatctcc aagaagctga aagtgatggg cgaaatcaaa 360
aacgtcgacg cgaaaggcga gtaa 384

<210> 802
<211> 930
<212> DNA
<213> Enterobacter cloacae

<220>
<221> unsure
<222> (100)

<400> 802
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ctogagagcg atgttaatat ccaaactcgtt gaccgcaccg ggcatcgcg cgttttcacc 180
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gatacattcc ctttgtccgt gcttaccocg ctcatgagc cgttctatca gcgccacagc 360
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gacagttctc gccocgagtg ccgcatttca tcgcagatgc tggatgagca ggaggccatc 660
accgtttttg attttaaaac caagctggag ctgcaataa ggggcctggg gtgcggttac 720
cttccccgtt atttagcgca gcggtttatt gacagcggag cgctggtgga aaaacaagtt 780
ttagcgcaga gcagtaacga atcgggtatg gtgggctgga atgaacagac cgccgggctt 840
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<210> 803
<211> 1182
<212> DNA
<213> Enterobacter cloacae

<400> 803
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gctggctcct gggatttgat ggattacacc acgggtcaaa tcttaacggc gggcaacgaa 180
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cctgagttct accacatgta cagcgagaag agcctgacct ggaacggcat caccagcag 660
aaccgcaacg gctgctgtg ggataagacc atgaacgtgg atggcctgaa aacgggacac 720
acctcgggag cgggcttta cctgattgcc tcagcgggtg acggtcagcg togaactgatt 780
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cgtgacaagg tggctcgcgca ctggccattg gttacgctgg aaagcggtga aaaggggtgg 1140

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1182

<210> 804

<211> 1371

<212> DNA

<213> Enterobacter cloacae

<400> 804

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ttcgatacat	tcggtatcgt	ttcaggccct	acggacgggc	atgtgccgac	ggcttacggc	180
tttgcaactga	ttgcgatcct	ctttaccgag	ctcagctacg	gtaaaactgg	gcgcggttat	240
cogtctgccg	gttccgccta	cacctatgcc	cagaaatcca	tcagcccgcg	ggtaggcttt	300
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gcaaaaaatt	attttgaagc	gctgggtgca	tcgattccat	cctggatgtt	cgtcgtggcg	420
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cgcgatggcg	tattcccgaa	aagcttcttc	ggctacgtgc	atccaacttg	gcgtaccccg	1020
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tatctgttcc	tgccgatgtg	tgggtctatg	accgtgggcg	cgtgtgggt	taacctggaa	1260
gagagctcaa	tgggtgcttg	cctgatcttg	gcaggtatcg	gcctgggtta	cctggcctgt	1320
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<210> 805

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 805

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aagacgggtca	agcagggtat	tgaacagctg	gtcatgtggg	tagatggctg	tcataattcag	180
cgcaggaggt	gggtggccgt	ttattatgac	aatccggatg	acgtgccggc	agaaaagctc	240
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gtgatgatga	ccgaaattgc	tgccggagag	tatgctattg	ccgccgcgcg	cgttgaaaaat	360
catgatttcg	ctactccatg	gtatcagttc	ttcaactccc	tgctggaaga	cagcaaatcc	420
cagattgcag	caaaaccttg	cttcgaacgc	tatctgaacg	atggcaatgc	tgacggctac	480
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<210> 806

<211> 195

<212> DNA

<213> Enterobacter cloacae

<400> 806

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tcacttttgg	agaaccgggt	aaaggatatc	aggaagaaca	ggatcgccgc	cacaatgagc	120
acgcctcgca	acgcgccgaa	acagatgcgc	agcaccctgt	ccgttctctga	cagaccgggt	180
ttctcgacca	gctga					195

<210> 807

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 807

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gggtcggttt	actccctctc	cottgagggg	gagggccgag	gtgaggggga	ggcagacgtt	180
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gtgattgggt	tttctgtgtc	ggttagcccg	atccgtggct	ttgttcgtga	agcgttatcg	420
ctggtaacct	ggggttggtc	tttctttggt	gccagtcatt	actacactta	cctgtctgtc	480
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<210> 808

<211> 1551

<212> DNA

<213> Enterobacter cloacae

<400> 808

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gatgctgcg	gtatcatcac	cattgatgca	aacaactgct	tccgtttaag	caaggcgaac	180
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<210> 809

<211> 759

<212> DNA

<213> Enterobacter cloacae

<400> 809

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cttgagctgg	ctatcagctc	cgtggtgctg	gcggtgctga	taggcctggc	gggcgcgggg	180

gcaaaattat	cgcgaacag	accgctggcg	ctgatatattg	aaggctatac	cacgctgatt	240
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aacggcgtaa	cggatgccat	cggcatggag	cagatcgata	tcgacccgat	ggtggccggt	360
attattaccc	ttggttttat	ctacggtgcc	tatttcaactg	agactttccg	cggcgcttac	420
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tgccgcctaa	tctatctggt	ctttacgacc	gtctccaatg	gtgtgctgct	tctgcttgaa	720
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<210> 810

<211> 464

<212> DNA

<213> Enterobacter cloacae

<400> 810

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tggagaagcc	gcagccgaaa	ccgcagcggg	ataaagcggc	cgagcaactg	gcagccgctt	180
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tcgtggggcc	ggatgcgtcg	aaagataagc	taaaaggttc	gcttggcgag	ctgaagcaaa	420
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<210> 811

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 811

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tgtggcataa	gacctgcaag	agcagcctgc	aacacaacac	acaacataaa	ccataataaa	180
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<210> 812

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 812

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ggtgctcggc	atctgtttcg	gcgcgttgcg	aggcgtgctc	attgtggccg	cgatcctggt	180
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<210> 813
 <211> 612
 <212> DNA
 <213> Enterobacter cloacae

<400> 813
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 gttgcaggcg tagaaaccca tctgggtgatg agccaggcgg cgcgtcagac cctctctctt 180
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 cagggggcgt ga 612

<210> 814
 <211> 804
 <212> DNA
 <213> Enterobacter cloacae

<400> 814
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<210> 815
 <211> 717
 <212> DNA
 <213> Enterobacter cloacae

<400> 815
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 tttacggcgt ttggcattgc ggcagtgtc tattttgatca tttcttacgt cctgatcagc 660
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<210> 816
 <211> 927
 <212> DNA

<213> Enterobacter cloacae

<400> 816

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<210> 817

<211> 1164

<212> DNA

<213> Enterobacter cloacae

<400> 817

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<210> 818

<211> 999

<212> DNA

<213> Enterobacter cloacae

<400> 818

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<210> 819

<211> 1401

<212> DNA

<213> Enterobacter cloacae

<400> 819

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<210> 820

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 820

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<210> 821

<211> 657

<212> DNA

<213> Enterobacter cloacae

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 cgtttttgcg tgcatttaat tccatgaaacg ctgcaacgta ctacgcttgg cgcaaaaaaa 540
 ttggggcagc gcgtaaatat cgaaattgat ccgcagaccc aggcggtcgt ggataccggt 600
 gagcgcgtgc tggcggcgaa agaggcggcg ataataaaga ccgtggaaga agaataa 657

<210> 822

<211> 1332

<212> DNA

<213> *Enterobacter cloacae*

<400> 822
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<210> 823

<211> 837

<212> DNA

<213> *Enterobacter cloacae*

<400> 823
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<210> 824

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 824

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gacatacgcc	agccgatggc	ttctcccagc	caggtggcgg	cgggaacgcc	gccgatatta	180
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acgctggcag	caacaaccga	gccagtcg	aagaaggcgc	catggttgag	gctggtaaga	300
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<210> 825

<211> 1395

<212> DNA

<213> Enterobacter cloacae

<400> 825

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gtaatggccg	gtggttacag	cgcacccgat	atggccgcgg	tggcgatcgg	aacctcaatc	180
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<210> 826

<211> 1032

<212> DNA

<213> Enterobacter cloacae

<400> 826

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gaaacggcct	tcaacatgct	gctggacagg	atcgtaaca	agcgtgaaca	gtcccagtc	960
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<210> 827

<211> 1290

<212> DNA

<213> Enterobacter cloacae

<400> 827

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<210> 828

<211> 1173

<212> DNA

<213> Enterobacter cloacae

<400> 828

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ggctcatccc	cctccgatcc	ccagataaag	catcccgaat	ttttcaaacg	cgtgttacag	180
gagggatcgt	tagggctggg	tgaaagctat	atggacggct	ggtgggagtg	tgagcggtcg	240
gatatgttct	tctccagcgt	attacgcgcg	ggtcttgaaa	aacagctccc	tcgctatttc	300
aaagataacct	tacgtatcgc	ctccgcgcgc	ctgttcaatc	tgcaaaagtaa	aaaaacggca	360
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gacatcggct	gtggctgggg	tggctctgcc	tgggttatgg	caaaaaatta	cggcgtcagc	600
gtagtcggcg	tcacgatttc	ggctgaacag	cagaagatgg	cgcaggaacg	ctgtctggga	660
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gcctgtgcgg	gcgcgttcgg	tgccgcgggat	atacagctgt	ggcaggtggg	gttttagtcgt	1140
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<210> 829

<211> 1091

<212> DNA

<213> Enterobacter cloacae

<400> 829

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ttatttcagc	cacggatcat	tatgttttcg	ctctttcagt	ataaaaaaca	gggtaagacc	180
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gatgcgggaa	cctcaatggc	ggaattgatg	acccttgcca	gcgataaaaa	tatgtctggc	360
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gccgtcacca	gcctgctggt	tatgctgctg	tataacgttc	aaattgcgct	ggctgacaat	1080
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<210> 830

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 830

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gaatccgata	tggttggtac	gccaacgcgt	gctctgaact	ttgtttacag	cgccaacacc	180
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accgaaatta	ccggccagga	caaattcgct	ttctacgttg	actccgctca	ggacaatgcc	540
ggtacggcga	aagagttcaa	agacctgacc	aacagcctgt	gggaaggggac	cgtgtctggt	600
gcgttccgcg	caacctgggg	ctaa				624

<210> 831

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 831

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gcgctggcca	ttaatgtggg	aaaagtcacc	accattattt	ctgcggatgc	tgactccacc	120
gccaaaggaa	taaaaaacga	agcagacagc	gtgcgcattg	ttctgttctg	cgcacagcgg	180
atcagcagcc	caatggatga	agggatcgct	attaatccgg	agaaagtggg	cgaactgttg	240

ctgacgcccc	cgcgcattggt	gatgcccgc	ggtaccagca	atatcgtaaa	attttactat	300
caagggaacg	ccgataacaa	agagcggtac	taccgcatta	ccttcacgga	tgaaggggta	360
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agcaccattc	tgggtggttc	gcccggggat	aagaagattg	atttcgtcta	tgtggcgga	480
aaaataacca	ataaaggga	cacctcgttt	cgcgtcaatg	cgaccgggac	ctgcctgaag	540
ccgaatccgg	aatccccgg	cacgcgctgt	agcaaaaact	tctacctgat	gccagagacc	600
tcgcgcgcta	tcgaggatat	caacggttacg	gataaccatt	ttcatctcgg	aatatgggac	660
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<210> 832

<211> 2601

<212> DNA

<213> Enterobacter cloacae

<400> 832

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gactcgcttt	atgcaactgt	ggagcagggg	atcaaaaattc	ccgtctatct	ggtgaataacg	180
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<210> 833

<211> 828
 <212> DNA
 <213> *Enterobacter cloacae*

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 aagaaggctc gggaggatca tggtttctct ggttcttcgg tgagtctgaa tgttgccata 240
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 gtcacgcca gtcaacatat cgactgtcaa catcagggtg cagatgctta ctattccagg 720
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<210> 834
 <211> 1740
 <212> DNA
 <213> *Enterobacter cloacae*

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 ccgctgatcc tccagttcgt tatggataat ccggtatcga aaaccacctg tgacggaaat 1680
 agctggtttg gtgaagtgac cgcgcaggga agaatagatg ttagcgcata ctggaattaa 1740

<210> 835
 <211> 660
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 835
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 tttcagcoga taaaaaacga taccagcgag cgtcagaatt ataccgtgtc gcttattcag 180
 gtagacgttc ctaaagagaa gggaaaagaa aocgaaataa aagacggcga agtcatgtat 240
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 ggcccgcag acaacaaaga gcgatactat cgcgtaaaat tcaccgagac gccgctccag 360
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 gtgagtaata ccgggaatac ctatttttaa tatgtttcct cggtcgggtg cagtacgcaa 540
 tacaacaatt caaaatatat tccaccgggg caacggctgg aaatagataa tgccgggcag 600
 gctgcaaggc ggatgattat ttatggcaat aaaatcattc cgctgaccac ctgcccgtag 660

<210> 836

<211> 1071

<212> DNA

<213> Enterobacter cloacae

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 tattgtcgtc cgtcctgtcg cgcccgccac gcgctgcgta aaaatgtctg cttttatcct 180
 gatgetcacc aggcgcgcga ggcggtttc cgcctctgta agcgtgtag gccggaccag 240
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<210> 837

<211> 1668

<212> DNA

<213> Enterobacter cloacae

<400> 837
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<210> 838

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 838

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gtttaccagt	tctaa					1035

<210> 839

<211> 393

<212> DNA

<213> Enterobacter cloacae

<400> 839

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gaattacgcg	gtaaaattca	ggcgacgtcg	gatgcgcagc	atcagctact	ctctacctat	240
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gagcgaagca	atggccgata	tcgtcacgga	agccatgcgc	gtgggaaaca	aaaccaacgg	360
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<210> 840

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 840

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caatacctgc	aaaaagatat	tcccgcacct	tttgtggatc	tctccacggg	aggcgagggg	180
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gtgatagccc	caaccgcgct	ggaggcggat	gcctgggata	ccggattgat	ggtgctcggc	540
acggagaagg	ccaaagaggt	ggtgcgtcag	gaaggggctgg	ccgtctatat	gatcactaaa	600
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<210> 841

<211> 672

<212> DNA

<213> Enterobacter cloacae

<400> 841

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ccaggcgatc	acccggtggc	gggggcggtt	cgctacaacc	tcacgttccg	ccaggcagcg	660
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<210> 842

<211> 1440

<212> DNA

<213> Enterobacter cloacae

<400> 842

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gctgagcaat	atgatgtcgg	cacgctggcc	gacgatattg	ctgaggtagg	tgcgtggtt	180
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gaaaacgtct	gggatgacct	tatcgatgag	atgagcgacc	gggacattct	tgacgcactg	360
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<210> 843

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 843

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ccaccgcggg	cagaatgtac	tgtacgccgt	gttgatggac	catcgggcca	atcaccagcg	120
cgacggaacc	tgcgcgcccc	gtcaccatgg	ccggacgccc	gccgagcagg	gaaagggcga	180
aacagagcac	cacggaggcg	ataa				204

<210> 844

<211> 977

<212> DNA

<213> Enterobacter cloacae

<400> 844

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gtggttaacc	gtcatctgcc	gaaagtgtcc	ggtcaatatt	cgactacgag	gcggcaagac	960
cgcgtaagggt	tggaagc					977

<210> 845

<211> 1401

<212> DNA

<213> Enterobacter cloacae

<400> 845

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atcgcgcgca	cggaagcctg	cccctaccag	cgaattgtta	tgtcattacc	ccactcgtct	180
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gtcgcggggc	tggatccgaa	agtgagtctt	atcgcctccg	tgggtgctctg	tttcgcccct	360
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tcgccagtcc aagaaaaata a

1401

<210> 846

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 846

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gcaaaactga	tgaagcaatg	gcgcgtttcg	aatcgtttga	acgtcgtatc	gaccacatgg	540
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acctga						606

<210> 847

<211> 255

<212> DNA

<213> Enterobacter cloacae

<400> 847

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tcacgcggtg	agctgtcgca	gagtgaacaa	cagcggctgg	cgcagctctc	tgccgaggca	180
aataaaatgc	gcgaacgtat	tcaggcgctg	gaagccatcc	tggacgcgga	acacccaaac	240
tggagggaac	ggtaa					255

<210> 848

<211> 615

<212> DNA

<213> Enterobacter cloacae

<400> 848

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ttacgcaacg	gctaa					615

<210> 849

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 849

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gcgcgtttcg	aatcgtttga	acgtcgtatc	gaccacatgg	aagcgggaagc	cgaaagccac	180
agcatcggta	agcagaaaac	cctggatcag	cagtttgctg	acctgaaggc	cgatgatgaa	240
attagcgagc	aactggctgc	gctgaaagcc	aaaatgaaac	aagacaacca	ataa	294

<210> 850
 <211> 429
 <212> DNA
 <213> Enterobacter cloacae

<400> 850
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 ggaacggtaa tggctggact gaatctgaat aaaaaactgt ggcggatccc acagcagggc 120
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 cgtgtggtca ccgtattgtc gattttcttc ggtctggcct ttattacact ggtggcatac 240
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 ccaaccagca gagatctcct gaacgcgggt gatgaacagc tgagcgcagg ggagaagcga 360
 ttgcgcgcga tggaacgtta tgtcacctcc gataccttta cgctgagaag tcgttttcgt 420
 cagcttttaa 429

<210> 851
 <211> 237
 <212> DNA
 <213> Enterobacter cloacae

<400> 851
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<210> 852
 <211> 996
 <212> DNA
 <213> Enterobacter cloacae

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<210> 853
 <211> 990
 <212> DNA
 <213> Enterobacter cloacae

<400> 853
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<210> 854

<211> 1041

<212> DNA

<213> Enterobacter cloacae

<400> 854

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<210> 855

<211> 1761

<212> DNA

<213> Enterobacter cloacae

<400> 855

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<210> 856

<211> 906

<212> DNA

<213> Enterobacter cloacae

<400> 856

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<210> 857

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 857

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<210> 858

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 858

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<210> 859

<211> 1341

<212> DNA

<213> Enterobacter cloacae

<400> 859

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<210> 860

<211> 2496

<212> DNA

<213> Enterobacter cloacae

<400> 860

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<210> 861

<211> 573

<212> DNA

<213> Enterobacter cloacae

<400> 861

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<210> 862

<211> 381

<212> DNA

<213> Enterobacter cloacae

<400> 862

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<210> 863
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 <212> DNA
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<400> 863

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 <211> 402
 <212> DNA
 <213> Enterobacter cloacae

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<210> 865
 <211> 2715
 <212> DNA
 <213> Enterobacter cloacae

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<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 866

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<210> 867

<211> 1377

<212> DNA

<213> Enterobacter cloacae

<400> 867

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<210> 868

<211> 423

<212> DNA

<213> Enterobacter cloacae

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<210> 869
 <211> 1377
 <212> DNA
 <213> Enterobacter cloacae

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<210> 870
 <211> 441
 <212> DNA
 <213> Enterobacter cloacae

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<210> 871
 <211> 1557
 <212> DNA
 <213> Enterobacter cloacae

<400> 871

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<210> 872

<211> 1644

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(253)

<220>

<221>unsure

<222>(264)

<400> 872

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<210> 873

<211> 1404

<212> DNA

<213> Enterobacter cloacae

<400> 873

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<210> 874

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 874

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cgctcgggtta	tctgggggtg	gaagagctgg	ccttcgatcc	atcttgttta	tggctgtgct	180
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<210> 875

<211> 1596

<212> DNA

<213> Enterobacter cloacae

<400> 875

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<210> 876

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 876

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<210> 877

<211> 1383

<212> DNA

<213> Enterobacter cloacae

<400> 877

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<210> 878

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 878

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ccgatggaga	agaagacacc	gtgcgcgagg	ccagtcagca	aacgggcaat	gaccagcggtg	300
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<210> 879

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 879

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<210> 880

<211> 192

<212> DNA

<213> Enterobacter cloacae

<400> 880

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caagaacaa	atttgttaca	acctgaagcg	cgatttgcac	ggttaaggctc	aaagaaagat	180
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<210> 881

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 881

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<210> 882

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 882

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gagaggatct	tgccctccggg	gtcgtttgog	agcctgggtc	aggcattacc	agcgggcaog	180
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<210> 883

<211> 1191

<212> DNA

<213> Enterobacter cloacae

<400> 883

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gttggattaa cccaaacgcc atggattggt gcggttaattg tgcttgtegc tttcctcctt 1140
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<210> 884
<211> 786
<212> DNA
<213> Enterobacter cloacae

<400> 884
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ctcggcgagc ggctcgccgc gtttcctgac ggcgcagctgc tggacttagg ctgcggggcg 180
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tccagtggag agtggcttac gtttatcacc gaagccggct tgatttcacg ctcatgata 600
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ttaactcagg cgatccgatt gtaccaggag agcgctctg ctgatgtgaa ggcgacttt 720
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gataa 786

<210> 885
<211> 1011
<212> DNA
<213> Enterobacter cloacae

<400> 885
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<210> 886
<211> 914
<212> DNA
<213> Enterobacter cloacae

<400> 886
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gtaaggagga ttagggtggc tgacttgta accgcaccgc ctgtattgcc cggaaaattt 180
gctttctttt ttgacctga cgggacgctc gccgggattg aaccgcatcc ggatgacgtt 240
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gcgccccatc	atgaggcggc	gatatcttcg	atagcaagaa	gcgtggccga	agcccatccg	600
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<210> 887

<211> 420

<212> DNA

<213> Enterobacter cloacae

<400> 887

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agggcgtctg	ttttgctact	atggcggcct	ttgaataagg	agaaccccat	gtcacaaaaac	180
ctgagcgccg	atcaggaact	ggtatctgac	gtcgtcgccct	gccagctggg	tatcaaacaa	240
atccttgatg	tgattgacgt	tatcgcgccg	ggtgaggtag	gcgaaaagat	gtcgacccaa	300
ctgaaaaaca	tcgatttcac	caaccatcct	gctgcggcgg	accgggttac	gtcccgcgcg	360
atccagaaag	cgattgcgct	gattgaactc	cgcttcacac	cgcagggtga	gtcacactaa	420

<210> 888

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 888

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ctgcggcggt	tacagattga	ggtggagacg	ctggcctgcg	cggagtcctg	tgcggtagtg	180
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gataataacc	tcattcagcg	caaggggctg	gggcacgcct	ttgactttgc	gctgacgctc	540
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cgctggttaa						609

<210> 889

<211> 1554

<212> DNA

<213> Enterobacter cloacae

<400> 889

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tatcaggagc	tgcatctcat	tcctgaaatg	accgtggcgg	agaacatcta	tctggggccag	360
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gagctgcgca	aagagggccg	catcattctg	tacgtttctc	accgtatgga	agagattttt	660
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cgcattgtag	tgatgcgtga	aggcgaaatt	gccggtgaat	tgctgcatga	acaggcgaat	1500
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<210> 890

<211> 1041

<212> DNA

<213> Enterobacter cloacae

<400> 890		
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gaaaatttaa	agctcggttt tctggttaaa cagcctgaag aaccgtgggt ccagaccgaa 180	
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actgaagtga	cccatgtggt gctgatcacc cgcgataact tcaaagagga gctggcgaaa 1020	
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<210> 891

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 891	
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gcgtggtggt	ccagaaaaag cctcaacggc actgccacct totttcgtac tcaggcgcaa 180
agtaacgtca	cgcacatgat gcgtgtcttt aactttttga aagctgtcgg ggcaaacctt 240
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aaaacgctcg	aagagtatga gcaacgctgt gcgaagctga gcaaaactggc tgatgaagcc 360
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caggatggca	tgctgctgaa gacgctcgca gatgaaatcc gcaacgcgaa acgtgcgggg 480
atttgtctgg	agcagacgga ccgccatctt ctcgacatag ctaccgtgca acaccactaa 540

<210> 892

<211> 1356

<212> DNA

<213> Enterobacter cloacae

<400> 892

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tttgtctttg	gtctgcaacc	cggtaaaccg	ccggttgacg	tgatgctcac	aattctcgcc	180
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<210> 893

<211> 1266

<212> DNA

<213> Enterobacter cloacae

<400> 893

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acgcgcgtgc	cggacatggc	aaaaagcttc	ggtgtacagg	ccgtggatct	gaatatcggc	180
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ggtggcgcg	tgatgggtgc	cgtgggtcgc	ctggccgtgc	tacgcaccac	gccaaaacat	420
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gccaatattc	tgttttcaac	cgcaacgcag	cgtcttgacc	acggggctgg	ggcatccgcg	1260
tgccggg						1266

<210> 894

<211> 240

<212> DNA

<213> Enterobacter cloacae

<400> 894

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cgtaaccggg	tccgcgcgag	caggatgggt	ggtgaaatcg	atgtttttca	gttggggtoga	120

catctttttcg	cgtacctcaa	ccggcgcgat	aacgtcaatc	acatcaagga	tttgtttgat	180
aaccagctgg	caggcgacga	cgtcagatac	cagttcctga	tcggcgcctca	ggtttttgtga	240

<210> 895

<211> 636

<212> DNA

<213> Enterobacter cloacae

<400> 895

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cgctacctga	ccttccttaa	aggtcgcgtg	ggcgcgaaag	tggccgattt	ctttatggac	180
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<210> 896

<211> 717

<212> DNA

<213> Enterobacter cloacae

<400> 896

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<210> 897

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 897

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<210> 898

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 898

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<210> 899

<211> 399

<212> DNA

<213> Enterobacter cloacae

<400> 899

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<210> 900

<211> 1776

<212> DNA

<213> Enterobacter cloacae

<400> 900

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<210> 901

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 901

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<210> 902

<211> 906

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (117)

<220>

<221> unsure

<222> (200)

<220>

<221> unsure

<222> (216)

<220>

<221> unsure

<222> (295)

<400> 902

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<210> 903

<211> 1644

<212> DNA

<213> Enterobacter cloacae

<400> 903

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<210> 904

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 904

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<210> 905

<211> 363

<212> DNA

<213> Enterobacter cloacae

<400> 905

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<210> 906

<211> 309

<212> DNA

<213> Enterobacter cloacae

<400> 906

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cgcgcgtaa						309

<210> 907

<211> 1488

<212> DNA

<213> Enterobacter cloacae

<400> 907

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<210> 908
 <211> 846
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 908
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 cgttag 846

<210> 909
 <211> 726
 <212> DNA
 <213> *Enterobacter cloacae*

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 accgaagagt tgttcaaaat gacgttactc ctgaaagggc acacagccta cctgtccgac 660
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<210> 910
 <211> 1536
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 911

<211> 1443

<212> DNA

<213> Enterobacter cloacae

<400> 911

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<210> 912

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 912

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gccttcacac	gcagcattat	ccgacgagca	tcctttgcgc	gacatggacc	ttataagttc	180
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cagcgtcgcg	tcggggcgtg	ttcctatcga	ccagcttaca	acctggccat	caaagcagtc	360
gataaccggc	gacagataga	cttttccagc	cggaagctgg	aactccgtaa	tatcggtcag	420
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<210> 913
 <211> 375
 <212> DNA
 <213> Enterobacter cloacae

<400> 913
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 tctgtctcct gctga 375

<210> 914
 <211> 1302
 <212> DNA
 <213> Enterobacter cloacae

<400> 914
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 gaatgggccc cgtctgcacgt tgcccgttgg gggaatggcc gggggcggct gctcttcacc 300
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 gctatacgtg atgtgaatac ctttaaaacc ggctggctgg ttctgggtgt gcttctgggtg 720
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<210> 915
 <211> 435
 <212> DNA
 <213> Enterobacter cloacae

<400> 915
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 ccaccatcac gagctgagct ggtaaaactc attgoggata tggggatcac ggtacgagcg 180
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 gtaacgccgc tgggtacccg gctatgccgc ccttctgaag tcgtgctgga tattcttccc 360
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 aaccggctga actaa 435

<210> 916
 <211> 624

<212> DNA

<213> *Enterobacter cloacae*

<400> 916

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catctgctga	ttgatgacgg	taaacacggc	gcgaactgga	atcatcgccg	cgcgcttgag	180
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gattacgctg	tgggtgatgc	atgggggtgc	tcagtgatct	atccgtgtta	ctcgctggtg	540
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cgccggcgct	ggaggtrtag	ctga				624

<210> 917

<211> 486

<212> DNA

<213> *Enterobacter cloacae*

<400> 917

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acgccgaagc	atttcgacaa	gcaggggaaa	tactggttta	aacggatggc	cgacgagctt	180
gatgctatcg	gtgtgatgtc	tcagcttgat	gccagagccc	ttgagctgct	ggttgaggcc	240
tataccgaat	accggcatca	ctgcgacacg	cttgaagttg	agggctacac	ctaccggacc	300
gaaacgcaga	gcggggatgt	gctgatcaag	gctcaccocg	ccgccatcat	gaaagctgat	360
gcctggaaac	gtctgcgtgc	catgcttggt	gagttcggca	tgactccagc	cagccgatcg	420
aaagtgaatg	caaaaggtcc	tgaagcgggt	gatccgctgg	ccgagtttat	gaaagcgagg	480
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<210> 918

<211> 1326

<212> DNA

<213> *Enterobacter cloacae*

<400> 918

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<210> 919
 <211> 408
 <212> DNA
 <213> Enterobacter cloacae

<400> 919
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 gaccacatca ccgocaaagc aaatgggggg accgatgacc tgtccaacct cgaaagcctc 360
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<210> 920
 <211> 1770
 <212> DNA
 <213> Enterobacter cloacae

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<210> 921
 <211> 876
 <212> DNA
 <213> Enterobacter cloacae

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<210> 922

<211> 1251

<212> DNA

<213> Enterobacter cloacae

<400> 922

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<210> 923

<211> 1227

<212> DNA

<213> Enterobacter cloacae

<400> 923

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<210> 924

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 924

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<210> 925

<211> 1449

<212> DNA

<213> Enterobacter cloacae

<400> 925

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gtcctgcaat	cggttgttat	tcaaattgaa	ggtgatgaga	aacgcgaatt	tgccggtttt	420
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<210> 926

<211> 879

<212> DNA

<213> Enterobacter cloacae

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 acgctgctgg tgggtgctggg actgtgtctg gtttgttcca ttgtcgtggc cggttctgcc 180
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 gaacgtatta ccgcacggct ggtggattta aaaaccgggg agttaatgga taaagaccgg 360
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 gggggcgcgc gtcccgcgca tgaatttgcc gttgatggcc tttccggcgc cagctcacc 780
 tcaaacgggtg tgcagcacag ctttgatttc tggatgggtg aactgggctt tggcccttc 840
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<210> 927
 <211> 1068
 <212> DNA
 <213> Enterobacter cloacae

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 tccgccaccc tgatggcgca ggagatccgc cagactatct tcaacgagct gaacctgacg 420
 gcatcggcgg gtgtcgcgcc ggtcaaatct ctgcgcaaaa tgcgctccga tttaaataag 480
 cccaacggcc agtacgttat cactccggaa gaggtttcgg cgttttttaa gacgctgccg 540
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<210> 928
 <211> 642
 <212> DNA
 <213> Enterobacter cloacae

<400> 928
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 aagctggaaa cggcggtggg catgacgctg gcggtaacgc ttggtgacagc tttttccagc 180
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 aacggcctgg gttacggcgt aatcctgttg acggttggtt tectgcgcga acttattggc 480
 agcggcaagc tgtttggcat tccggtgctg gatacggtac agaacggcgg ctggtatctg 540
 ccgaacggcc tgttctctgt ggcccaagc gcatttttca ttatcggttt gctgatctgg 600
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<210> 929

<211> 603
 <212> DNA
 <213> Enterobacter cloacae

<400> 929
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 aacttcatca cctttatcgg agtgattgcg gcgcttggtc agatcctgga gatgatcctc 300
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 aactgcgcga tttttggcgg tgtttccttt atgggttcagc gtgattacaa cttcagtga 420
 tcggtttgtgt atggcttcgg ttccgggtatc ggctggatgc tggcgattgt taccatggcg 480
 gggatccgtg aaaaaatgaa atatgccaac gtacctgcgg ggcttcgtgg cttagggatc 540
 acctttatca ccaccggcct gatggcgttg ggctttatgt ccttctccgg tgtgcageta 600
 taa 603

<210> 930
 <211> 216
 <212> DNA
 <213> Enterobacter cloacae

<400> 930
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 ttccggcatgt ccttaggctg gatcatcaag cgtaaaagca ttcagggcag ttgcggaggc 120
 atctcttcca tcggaatgga aaaagtgtgc gattgtccgg aaccgtgcga tgcgcggaaa 180
 aagcggatgg ctgcgcgagca gcaacgcatt atttag 216

<210> 931
 <211> 558
 <212> DNA
 <213> Enterobacter cloacae

<400> 931
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 aacaccgact ccgaataa 558

<210> 932
 <211> 942
 <212> DNA
 <213> Enterobacter cloacae

<400> 932
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<210> 933

<211> 1701

<212> DNA

<213> Enterobacter cloacae

<400> 933

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<210> 934

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 934

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ggcgaccggt	gggcgctggc	gctggatgaa	ggcaaacctg	tggccgcggt	gaatcagacg	180
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<210> 935

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 935

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atgggctgga	tgagcggcac	gctgggtgcgt	gttggccttag	ggttatgcgt	ggtttacggc	180
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<210> 936

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 936

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cacaacctcg	gagacagcgt	aaaagcgctg	acgctggagc	actatccggg	gatgaccgaa	240
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aaagcgccgt	tctggaaacg	tgaagcgacg	cgggaagggtg	agcgtggggt	ggaatcacgc	480
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<210> 937

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<400> 937

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<210> 938

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 938

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ctgcgcgagg	cggcacacga	agccggacac	cagattgttg	ataaagcgat	cgtcaaagaa	180
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<210> 939

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 939

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catgattaa						489

<210> 940

<211> 711

<212> DNA

<213> Enterobacter cloacae

<400> 940

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<210> 941

<211> 1297

<212> DNA

<213> Enterobacter cloacae

<400> 941

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tgggcgggga	agttttattcg	ggtgggaggg	gggggaaacc	cacacgggcg	gttggttag	180
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<210> 942

<211> 1155

<212> DNA

<213> Enterobacter cloacae

<400> 942

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gggtgatccg	cctgtgcaac	ccgaaatgga	aaccaggac	cgcgtagagg	cggaagatgg	180
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<210> 943

<211> 918

<212> DNA

<213> Enterobacter cloacae

<400> 943

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 <212> DNA
 <213> Enterobacter cloacae

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 gacgcggtac gcaccgtcag cgccgatatt gtctgcctcc aggaggtcat gggcgcgcat 180
 gaagtgcacc cgatgcattt cgaaaactgg cccgacacgc cccactacga gtttctggcg 240
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 cggtaa 306

<210> 945
 <211> 1344
 <212> DNA
 <213> Enterobacter cloacae

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<210> 946
 <211> 717
 <212> DNA
 <213> Enterobacter cloacae

<400> 946
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<210> 947
 <211> 717
 <212> DNA
 <213> Enterobacter cloacae

<400> 947

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<210> 948
 <211> 2085
 <212> DNA
 <213> Enterobacter cloacae

<400> 948

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<210> 949
 <211> 1425
 <212> DNA
 <213> Enterobacter cloacae

<400> 949
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<210> 950
 <211> 330
 <212> DNA
 <213> Enterobacter cloacae

<400> 950
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 gccgcgcgtc gcgctcgta gatgcaggta ggcggtaaag atccgctggt accggaagaa 180
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<210> 951
 <211> 1728
 <212> DNA
 <213> Enterobacter cloacae

<400> 951
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<210> 952

<211> 2130

<212> DNA

<213> Enterobacter cloacae

<400> 952

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2130

<210> 953

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 953

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ggccacggaa	cgggcgccgc	gtggagcaag	ctgttcacatg	aacgctatgg	ctttgaaaac	480
gcaacggaag	tggcgatggc	ctgcgcgacc	tttggcctgg	tgcttggcgg	gctgattggc	540
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<210> 954

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 954

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ctgatatacc	ttcgtttttg	gaatggcgat	gtaatctttg	acgcgccccg	gacgcggctt	540
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<210> 955

<211> 255

<212> DNA

<213> Enterobacter cloacae

<400> 955

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gcgctgctgt	ccagcaaagg	cgtaacgttc	aaggaaactgc	cgatcgatgg	tgacgcgatt	120
aaacgcgaag	agatgatcca	acgcagtgg	cgcacaacgg	ttccacagat	ttttattgat	180
gcgcagcaca	ttggcggctg	tgatgacttg	tatgcgctcg	acgcccgtgg	tggactcgat	240
ccgctgctga	gctag					255

<210> 956

<211> 1086

<212> DNA

<213> *Enterobacter cloacae*

<400> 956

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gctcttgcca	tcacgctggc	aagaaatgg	cacgacgtgg	tcctgtgggg	ccacgatcca	180
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aatgcgcg	aggcagcatt	gaccttatta	ggtcgtgcgc	gcaaggacga	gcgcagcagc	1080
aattag						1086

<210> 957

<211> 876

<212> DNA

<213> *Enterobacter cloacae*

<400> 957

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<210> 958

<211> 459

<212> DNA

<213> *Enterobacter cloacae*

<400> 958

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aacgcactgc	ataaagcagg	ctttgaaaac	gtaacggtgc	tgaagaagg	catctccggc	420
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<210> 959
 <211> 504
 <212> DNA
 <213> Enterobacter cloacae

<400> 959
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<210> 960
 <211> 519
 <212> DNA
 <213> Enterobacter cloacae

<400> 960
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<210> 961
 <211> 1587
 <212> DNA
 <213> Enterobacter cloacae

<400> 961
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 attgatgctg ctggcctgga agtgggtctg ccgcatcgtc agatgggcaa ctcagaagtg 240
 ggtcacgtta acctgggtgc gggccgtatc gtttatcagg acctgacgag cctggacgtt 300
 gaaatcaaag aacgtacatt ctttgccaac ccaacgctca ccggagcggg tgataaagcc 360
 gttgccgcag gcaaggctgt tcacattatg ggtctgctct ctgcggggcg cggttcacagc 420
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cctgttccac	tgatttatgt	gggtgataaa	tcagtgaag	cagtgaag	cggcaagctt	1500
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<210> 962

<211> 1293

<212> DNA

<213> Enterobacter cloacae

<400> 962

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gcacccgcc	atgoggatga	ccgcgatcag	cttaaatcca	ttcaggccga	tatcgccgcc	180
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aagcaggaag	aggccatttc	cgccgcgcgc	cgtaagctgc	gtgaaacaca	aaacaccctt	300
gccagctca	ataagcaaat	cgatgaaatg	aacgcgtcga	ttgcgaaact	ggagcgtcag	360
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<210> 963

<211> 966

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (875)

<400> 963

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gaaaatcagg	tgctggcgat	gccgtcagcc	atctctgtcg	ccgtcctgcc	taatgcgcct	180
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acccgcttct	tcacgggtgat	tggcgaaagc	atcancagca	gtacgctgg	taaaatacgt	900
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agataa						966

<210> 964
 <211> 417
 <212> DNA
 <213> Enterobacter cloacae

<400> 964
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 tgcacccagg caatgcgcca tctggttacc ttcgatgccg ccgatggaga agataccgcc 180
 ctgctgaact tcgcacagga acgcagtttc ttcgccaga gaggcggta cggtgacacg 240
 cagtaagact tcatacacat catccgccag ctgggtggat gcggtatcca gatcaagttt 300
 aacctctggc tgccagtctt tctggaaaac gtgcggcgca tttggcgctt cgaaagagac 360
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<210> 965
 <211> 606
 <212> DNA
 <213> Enterobacter cloacae

<400> 965
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 ggcgggggtg ccgcacacca gggattgctg aaattctcgc tgggtgctgc cgccgtcgcg 180
 ttgggcggta tgattggcga tcagctgctc tattttctgg ggctgcgctt tggcccagacg 240
 cttttgcaac gttttgccag gcatcaaaaag aaaattcgcc gcgccagcg gctgatccag 300
 cgacatcctt atctgtttgt gattggtacc cgctttatgt acggttttcg catcatggg 360
 ccgatactga ttggcgcgag tcgtttacca ccgaaaattt tcctgccgct gaacattctc 420
 ggggcgattg cctgggcggt gattttcacc acgcttggtt acgcgggtgg cgaagtgatt 480
 ggcccatggc tgcataatct tgaccagcac ctgaagcact gggcgtggtt gatcctggtg 540
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 gagtga 606

<210> 966
 <211> 432
 <212> DNA
 <213> Enterobacter cloacae

<400> 966
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 gcttcgctgc tgccgattac gataccggc agcattatcg gcatgctgat cctgtttgta 180
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 cgtacatgg ccctgctttt tgtgcctatc ggcttgggg ttatgcagta ttacgatgtg 300
 cttaaagcgc agttcggccc gattgtggtc tcctgcgcca tcagtacgct ggtggttttc 360
 ctggtcgtca gctggagttc acacattgtg catggcgaaac gtaaggctcg cggggagaaa 420
 acaaaaaaat ga 432

<210> 967
 <211> 360
 <212> DNA
 <213> Enterobacter cloacae

<400> 967
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 cgcgctgggc accgcacgct gcgcggaact ggattatcag gaaggggcat tcagctcgct 240
 ggcgctggtg atctgcggga ttatcacttc cctggctcgc ccgtttatct tcccgattat 300
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<210> 968
 <211> 894
 <212> DNA
 <213> Enterobacter cloacae

<400> 968
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 gtcacgacgc ttaaaccaggc aacggggctg gacgaagacg cgttggcttt cgccctgctg 180
 cccctggcgg ctgcctgcgc ccgcgtgac ctttccatt ttaacgtagg cgcaattgctg 240
 cgcggtgtga gcgggacctg gtacttcggc ggaaacatgg agtttctcgg tgcgaccatg 300
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 cagcgcgcaa tcttggtgta aaaggccgat gcgcgctgta tccagtggga cgcgaccgca 840
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<210> 969
 <211> 720
 <212> DNA
 <213> Enterobacter cloacae

<400> 969
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<210> 970
 <211> 765
 <212> DNA
 <213> Enterobacter cloacae

<400> 970
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<210> 971
 <211> 978
 <212> DNA
 <213> Enterobacter cloacae

<400> 971
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<210> 972
 <211> 537
 <212> DNA
 <213> Enterobacter cloacae

<400> 972
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 gctgcgcaac ccagatttgc gtccggcagc gcgatgatcg ttgacctgaa taccaacaag 180
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<210> 973
 <211> 930
 <212> DNA
 <213> Enterobacter cloacae

<400> 973
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 aacattttca ccgttgacgt ggacggtgct tttctctgct cgcaaatcgc ggccgctcag 540
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 atcccgttgg cagggccagg gcataccaaa gaaattgcc aacctggtgg gtggctgtgt 840
 gacagtgcag ccagctacac caccgggcag tcgtttatcg ttgacggcgg ttttatgctg 900

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930

<210> 974

<211> 645

<212> DNA

<213> Enterobacter cloacae

<400> 974

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aacgaaacgg	tcgcgcacat	ctatacccac	catgtcctgc	tgatggcagc	ggtgccgggtg	180
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ggcctgagct	tctccagctc	tacgcttgcc	atcggcgtag	tggtcctgga	ggcgctactg	600
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<210> 975

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 975

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gtggagccaa	ccggtctgtc	gatccataac	gtctcgacgg	ggcgtgattt	aacaaagctg	180
ctgatcgcca	gtaagcaata	ccgctgatt	ggtcagctca	acaccacccc	tgaggagatg	240
gcgaacttct	ccaaaccggg	cgtataaa				267

<210> 976

<211> 1431

<212> DNA

<213> Enterobacter cloacae

<400> 976

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gcaactgtaa	atacccaact	gcgtcatgcc	gactggccaa	aaagcgaatg	gtggaaagac	180
tttaacgact	cccagctcaa	cgcgctgata	gacaaagcgc	tgccggatgc	gccggatatg	240
caaattgccc	gtcagcgtat	caccctggcg	gaagcacagg	cgaagacggc	tgctcgtgct	300
gaggggtccac	aactggattt	ttccgcagat	gtggaacggc	aaaagatgtc	ggcagagggg	360
ttgatggggc	catttgcact	gaccgacccg	gcagcgggga	ccaccggccc	ctggtatacc	420
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1431

<210> 977

<211> 2559

<212> DNA

<213> Enterobacter cloacae

<400> 977

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<210> 978

<211> 237

<212> DNA

<213> Enterobacter cloacae

<400> 978

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cagtgggatg	ttcgcgattc	cgcattggcg	tatctcaccg	tgatcgatct	gccgtttctg	180

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<210> 979

<211> 1137

<212> DNA

<213> Enterobacter cloacae

<400> 979

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<210> 980

<211> 1614

<212> DNA

<213> Enterobacter cloacae

<400> 980

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<210> 981
 <211> 621
 <212> DNA
 <213> Enterobacter cloacae

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<210> 982
 <211> 957
 <212> DNA
 <213> Enterobacter cloacae

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<210> 983
 <211> 1290
 <212> DNA
 <213> Enterobacter cloacae

<400> 983
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ggcgtcgtgc	tgttcaacgc	cgtttattcg	tggctcagct	tatcccgggc	gctacgcccg	1260
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<210> 984

<211> 471

<212> DNA

<213> Enterobacter cloacae

<400> 984

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atctattcca	gccacacctg	gcaogtgaac	agccagatgc	cctcctggtg	gctgacgctg	180
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cagcatgtta	aaggcaaggc	ggaaaactgg	ccgaatctct	ccttctatga	gaaatacaac	420
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<210> 985

<211> 309

<212> DNA

<213> Enterobacter cloacae

<400> 985

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<210> 986

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 986

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<210> 987

<211> 423

<212> DNA

<213> Enterobacter cloacae

<400> 987

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<210> 988

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 988

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caaccgtgga	acggtctggg	atcacccgaca	caaacggcga	caggatcagc	gagaagacga	180
ttggcgccag	ccagaacagg	aaacgcagat	ccagccaggc	cataccaacg	gcccacacca	240
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<210> 989

<211> 1299

<212> DNA

<213> Enterobacter cloacae

<400> 989

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<210> 990

<211> 1491

<212> DNA

<213> Enterobacter cloacae

<400> 990

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<210> 991

<211> 277

<212> DNA

<213> Enterobacter cloacae

<400> 991

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<210> 992

<211> 405

<212> DNA

<213> Enterobacter cloacae

<400> 992

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<210> 993

<211> 2031

<212> DNA

<213> Enterobacter cloacae

<400> 993

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atctgggagc	aggagcgtaa	agtcattacc	gctgaagagc	gtatgcataa	agggcaggca	1980
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<210> 994

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 994

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<210> 995

<211> 1338

<212> DNA

<213> Enterobacter cloacae

<400> 995

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gaagacttaa	ccgcgcgtgt	gctggatctg	gcacgcgcaa	ttggctgtgg	ccagcgtggg	600
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<210> 996

<211> 525

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (16)

<400> 996

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<210> 997

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 997

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<210> 998

<211> 1149

<212> DNA

<213> Enterobacter cloacae

<400> 998

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<210> 999
 <211> 1275
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221>unsure
 <222>(374)

<220>
 <221>unsure
 <222>(403)

<400> 999						
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<210> 1000
 <211> 291
 <212> DNA

<213> Enterobacter cloacae

<400> 1000

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<210> 1001

<211> 900

<212> DNA

<213> Enterobacter cloacae

<400> 1001

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<210> 1002

<211> 312

<212> DNA

<213> Enterobacter cloacae

<400> 1002

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aagaactatt	ttgctcaact	gaacggtcag	gatgttaatg	acctgtatga	gctggctactg	180
gctgaagttg	aacagccact	gttgacatg	gtgatgcaat	acaccctggg	taatcaaacc	240
cgcgctgccc	tgatgatggg	catcaaccgt	ggtaccctgc	gtaagaaact	gaaaaaatac	300
ggcatgaact	aa					312

<210> 1003

<211> 2253

<212> DNA

<213> Enterobacter cloacae

<400> 1003

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cccctttcca	accgctcttg	cttaacgtct	cacacgagtg	aacagaccat	gctggttagc	180
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<210> 1004

<211> 1488

<212> DNA

<213> Enterobacter cloacae

<400> 1004

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<210> 1005

<211> 969
 <212> DNA
 <213> Enterobacter cloacae

<400> 1005
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 tgcccgccca aaaaggtgaa tcgcaagctt gcaggttcag cccttctgca ataccccgac 360
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 aatggcgaca ttactgacc gcttaaagcc agagctgtgc tcgactatac gggagctgat 660
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 tgttcgcatg ttccgggaatt gcatgaccac tacggccagg caaaagggtg ccgaattgcg 840
 cgtaaacacg tctcctggta tctccaggag cagctccaa atgaccagtt tcggcgcaaca 900
 ttcaacgcca ttgaggatgc cagcgaacag ctggaggcgt tggaggcata cttcgaaaat 960
 cttgcgtaa 969

<210> 1006
 <211> 233
 <212> DNA
 <213> Enterobacter cloacae

<400> 1006
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 aaactgccgg tggcgcaata tccgaccatt gcgcgccag cgggtggcgt gacagcaacc 180
 taccctggcg ctgatgcccc gacggtacag gacaccgtaa ctcaggttat cga 233

<210> 1007
 <211> 654
 <212> DNA
 <213> Enterobacter cloacae

<400> 1007
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 tttaacgcaa tatgggaaca gcaattgccg ctgcgtgaaa tcattcgtga caggctaattg 240
 ctttccgaaa atgacgaccc tttgttaatg cttcgtgaac aatttattgt tgcgctgcaa 300
 tatattgca gcaacccccg acagtatgcg cttttacaaa ttctgtatca taagtgtgaa 360
 tttcatgacg atgtgatttc agaattgtgaa atacgcaagc ggatcggttt aaacgatgat 420
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 attgaaactg cgtgattgt tttccatgcg ttttttagcg gagtcatata aaactgggtta 540
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<210> 1008
 <211> 918
 <212> DNA
 <213> Enterobacter cloacae

<400> 1008
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accataactga	tgccgacgct	gaatgccgac	tgtcccttg	acctcggttg	cccgattgat	240
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aactacgtac	aaaaacagac	cggctgtgat	gtgctgtgct	ggcagggcgc	ctgtatcggt	480
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aatgggctca	aagcgatttc	ggaggcgctt	gagaacgggtg	gcgcagcgca	tgagatccac	840
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<210> 1009

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 1009

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ggcggctatg	acctgtcgtg	gattgaagcg	gtgggtacgc	tgcccggttt	actctgtatc	180
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gaactgcaaa	tccgctggct	gccgttgcca	aaagccatcg	cctgggttcgc	ggcctgcgtg	420
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<210> 1010

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<400> 1010

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<210> 1011

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 1011

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ttaaccctgc	gcaacagcgc	cgggatgggtg	gttaacgtga	tggactgggg	cgcaacgtta	180
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<210> 1012

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 1012

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tcagtctgta	aagacgggaa	atgcccgagc	ccgaatgaca	aagtgggcag	cgatgccaat	420
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<210> 1013

<211> 954

<212> DNA

<213> Enterobacter cloacae

<400> 1013

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954

<210> 1014

<211> 1182

<212> DNA

<213> Enterobacter cloacae

<400> 1014

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<210> 1015

<211> 756

<212> DNA

<213> Enterobacter cloacae

<400> 1015

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<210> 1016

<211> 1218

<212> DNA

<213> Enterobacter cloacae

<400> 1016

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<210> 1017

<211> 1056

<212> DNA

<213> Enterobacter cloacae

<400> 1017

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gagacgcctg	ccaaacagac	gctgcgcgag	catgatccgg	actgtttcct	ctgcccgggc	180
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<210> 1018

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 1018

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<210> 1019

<211> 858

<212> DNA

<213> *Enterobacter cloacae*

<400> 1019

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<210> 1020

<211> 579

<212> DNA

<213> *Enterobacter cloacae*

<400> 1020

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<210> 1021

<211> 2640

<212> DNA

<213> *Enterobacter cloacae*

<400> 1021

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<210> 1022

<211> 456

<212> DNA

<213> Enterobacter cloacae

<400> 1022

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<210> 1023

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (991)

<400> 1023

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gtgatttggg	gctctatcct	cggcgttgca	ccgtttacgc	ttgttttacc	ctacgcaacg	960
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<210> 1024

<211> 1698

<212> DNA

<213> Enterobacter cloacae

<400> 1024

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<210> 1025

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 1025

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tttaacgata	cgaaacgcca	cagtgcggac	gtgaaaaaac	gtacgctgga	aaaagtggcg	300
gagatcgaac	gccatatcat	cgaattacag	gcgatgcgtg	agcaactggt	acagctggca	360
gaatcctgcc	cgggagatga	cagcgcggag	tgcccgatta	tcgacaatct	ttccggctgc	420
tgccaccgta	aaaccacgc	ctaa				444

<210> 1026

<211> 207

<212> DNA

<213> *Enterobacter cloacae*

<400> 1026

agaattggct	tccagagatg	ggagcctttt	ttgtatcgga	aattcattat	gagaacagct	60
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caatcactga	ttgattcatg	ggtgaagaat	aaccctgact	acatactctc	atttttcacc	180
acagccgcga	aggtcacgct	attgggtt				207

<210> 1027

<211> 735

<212> DNA

<213> *Enterobacter cloacae*

<400> 1027

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<210> 1028

<211> 228

<212> DNA

<213> *Enterobacter cloacae*

<400> 1028

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ggccaaagtt	atcagccctg	gcttagagct	caggacgtta	aatcccggtg	aaaccgttcg	180
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<210> 1029

<211> 861

<212> DNA

<213> *Enterobacter cloacae*

<400> 1029

acaataaaaac	tgtctgctta	cataaacagt	aatacaaggg	gtgttatgag	ccatattcaa	60
cgggaaacgt	cttgctcgag	gccgcgatta	aattccaaca	tggatgctga	tttatatggg	120
tataaatggg	ctcgcgataa	tgtcgggcaa	tcagggtcga	caatctatcg	attgtatggg	180
aagcccgatg	cgccagagtt	gtttctgaaa	catggcaaa	gtagcgttgc	caatgatggt	240
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<210> 1030

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 1030

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cagcgtggcg	ccgattatcc	gtttcagttt	gccatgatcg	cattcaatca	cgttggtccg	120
gtacttaatc	tgctcgtggt	caacgtcaga	cgggcacccg	ccttcgcggt	tgagcagagc	180
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ccaccgacta	tttgcaacag	tgccctctact	cctgcacag	gtttacgagt	aggtgatttg	720
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cattaa						786

<210> 1031

<211> 255

<212> DNA

<213> Enterobacter cloacae

<400> 1031

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ctcgccttca	ccgaagacct	tcagcccggt	ggaatcaatt	accagggtgtg	cgatttcacc	180
ccgggtgggc	gttttgaaac	tgacattaac	cgactttgcc	cgctctgtga	cacagctgta	240
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<210> 1032

<211> 1665

<212> DNA

<213> Enterobacter cloacae

<400> 1032

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tcatattccc	acgacaacct	gttctcatcg	atcttggggc	tgtgggacgt	aagcaccagc	1620
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<210> 1033

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 1033

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<210> 1034

<211> 821

<212> DNA

<213> Enterobacter cloacae

<400> 1034

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<210> 1035

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 1035

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<210> 1036

<211> 999

<212> DNA

<213> Enterobacter cloacae

<400> 1036

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<210> 1037

<211> 2148

<212> DNA

<213> Enterobacter cloacae

<400> 1037

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<210> 1038

<211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 1038

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<210> 1039

<211> 2715

<212> DNA

<213> Enterobacter cloacae

<400> 1039

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<210> 1040

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 1040

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<210> 1041

<211> 713

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (705)

<400> 1041

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<210> 1042

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<400> 1042

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<210> 1043

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 1043

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<210> 1044

<211> 1344

<212> DNA

<213> Enterobacter cloacae

<400> 1044

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<210> 1045

<211> 3075

<212> DNA

<213> Enterobacter cloacae

<400> 1045

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gctgaacaac	aatga					3075

<210> 1046

<211> 1551

<212> DNA

<213> Enterobacter cloacae

<400> 1046

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cgcagcgcca	tcagtgaacta	tatcgaaaac	gggaaacttc	ccgatgaaa	ggccagaacc	240
caggcctttt	ttgtttatcc	atcgctctct	gtcacctggg	acggtagcgc	cagcagcaat	300
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cgacctgcgc	tgttccgccc	ctacctggaa	gagcagctta	ccctgttgta	tcaggattac	420
ggcgcgcata	tcagcgttga	gcgcctccctg	cacgagatcc	cttaccctga	cgtgatagac	480
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aatccgctgc	acggcgagat	caaactgcgc	ggccaggcga	accgttttta	cgaaggggcg	1440
atctcagagc	accttcagat	tggtattcgc	gccatcgatt	tactgcgtgc	agagggcgac	1500
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<210> 1047

<211> 538

<212> DNA

<213> Enterobacter cloacae

<400> 1047

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ttttcacctc	attcgccagg	aagcctcacc	atgacgcgta	aacaggccac	catcgacgtg	180
cgtagcggat	tgaatgatga	cgagcagtac	ggctgcgttg	tcccgcgaat	tcactctctc	240
agtacctata	atttcacggc	atttaatgaa	cctcgcgcgc	atgactactc	gcgtcgcggc	300
aatcctacgc	gcgacgcgcg	ccagcgcgcg	ctggcggaac	tggaaggcgg	cgcagggcg	360
gtattaacca	ataccggcat	gtctgccatt	cacctggtaa	ccacagtgtt	cctgaaacct	420
ggcgatctgc	tggtggcacc	acacgaatgt	tacggcggtc	actatcctct	gtttgatatc	480
cctgctaaca	ctggcttcta	cctcgtcttc	ctacctctt	cttcgatcta	cactaccc	538

<210> 1048
 <211> 312
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1048
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 agacgacggg cgatttcggt tttaaccaca ccggtcgggc cgatcatcag aatatttttt 120
 ggcgtcactt cgtggcgaag ctcttcgtcg agctgcacgc gacgccagcg gttacgcagt 180
 gcgatagcca cggagcgctt ggcatgtgct tggcgcataa tgtgtttgtt cagttcgctg 240
 acaatttcgc gtgggggtcat ttcagacatg ggcatcctt acgctttaga cggtaattct 300
 tcgatgggtg ga 312

<210> 1049
 <211> 222
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1049
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 tgcggttaact ctatccagat ccgctctacc gtgggtcacg atctgaacct ggacgtgtgc 120
 ggcaaatgcc acccgctcta cactggtaag cagcgtgatg ttgcaaccgg tggcgtgtt 180
 gaccgcttca acaagcggtt cagcatcccg ggcgctaaat aa 222

<210> 1050
 <211> 765
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1050
 aattacactg cgctcgacat aaattcttat ttgccatttc aacagcgatg gctttcaggg 60
 tgtattttact ttgaggggaaa aaggatgaaa ctgaagcaac ttttattcgt gcttccatta 120
 ctatcgtgcg cggcgcaggg gggatatgtt gattaccgac acgagtatta cgacgatgga 180
 cgtaactatg accgtgtgta catgtcacac cgtttcggga cgggcttttg tgtggccgta 240
 gaggccgtct cagctcaga cgaagagcaa tctaatagat cgctcaataa tatggagagt 300
 aacagcaacg aatataactgc cagctaccag tttacctggc agggatttat ctggcagccg 360
 ggtgtcgcgg ttgaaatggg tgacgacatg gotattttata aacctattt acgcgtacag 420
 tataatatta atgaaagctg gtggacggcg ttccgttatc gtaccgaata taccgcgcgt 480
 aatgcagacg gtaagatga cagactggtg tatcgccggg aaatgtggct gggatataat 540
 attgataact ggatgtttga gctgaacgga atttataaat tcgccgacaa cgaagatctg 600
 tataacaaca aaaaagagga ttacgaatat aacttcgcgc tggcgtataa catcgattcg 660
 tgggtgccat tcgtggaggt gggtaatgtc tcttcgggct ataactgc taccactgac 720
 gaccgacaaa cgcgtctgcg tgcggctta ggttacaact tctga 765

<210> 1051
 <211> 1080
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1051
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 acagcaaccg tgtcccgcgc attgatgaac cctgacaaaag tctcccaggc gaccgaaaac 180
 cgggttgaaa aggcggcgct tgaggtcggt tattttccgc aagccatggg gcgtaacgta 240
 aaacgcaacg aatcccgcat catcctggtg atcgtgcggg acatctgcga tcccttcttc 300
 agcgaatatc tccgcggcat tgaagtcacg gccgcgcgcc agggctatct ggtgctgatt 360
 ggcgattgtg cccaccagaa ccagcaggaa aaaacgttca tcgacctgat catcaccaag 420
 cagattgatg gcatgctgct gcttggttca cgcctgccgt ttgatgccag cattgaagaa 480
 cagcgcgaatt taccgcggat ggcatggcg aacgaattcg cgcggagct ggagctgcca 540
 accgttcata tcgataacct caccgcgcgc ttcaacgcgc tgaactatct tcaggaactg 600
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attggccggg	aagcgatgct	gctttttgctg	gatcagctgc	acgggtcaaac	agttagcagt	1020
gggtcacggc	tactggattg	tgagctaatt	gtgcgcggct	ctaccaggc	attaacttaa	1080

<210> 1052

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 1052

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gtcagggtca	gcagcaaacg	caacagcagc	agtggacgca	gacgcagccg	gtacagcagc	120
cgcgttcaca	accgcagcag	cagacgcgta	ccgtacaaac	tcagcctgtc	cagcagcaac	180
cgaaggcgca	gccgcagaaag	caaacggcac	agccgtatca	ggatctgttg	cagacgcctg	240
cgcataccac	tgcgcaaacag	ccaaaaacgc	agcaggctgc	gccggtcacc	aaagagaccg	300
aggtgccgaa	gcagacggct	gagaaaaaag	atgaacgcgc	ctggatgggt	cagtgcgggt	360
cgtttaaagg	cgccgaacag	gcagaaacgg	tgcgtgctca	gctggcattt	gaaggatttg	420
actcacgcat	taccaccaat	aacggctgga	atcgcgtag			459

<210> 1053

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 1053

ccagggggtc	tgctcgtgac	aacaatagta	agtgtacgcc	gtaacggcca	ggtggttaatt	60
gccggtgatg	gccaggccac	gctgggtaat	accgtcatga	aaggcaacgt	gaagaaagta	120
cgtcgtcttt	ataacgacaa	agtgatcgcc	ggtttcgcag	gcggcacggc	tgatgccttc	180
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gccgttgagc	tggcaaaaga	ctggcgtaacc	gaccgcatagc	tacgcaagct	cgaagcgctg	300
ctggccgtgg	ctgacgaaaa	cgcctcgctg	atcatcaccg	gtaacggcga	cgtagtccag	360
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gcgctgttg	aaaataaccga	catgaacgcg	cgcgatatcg	cggtgaaagc	gttgatatt	480
gcaggtgata	tctgcatacta	taccaaccac	aatcacacca	tcgaagaatt	accgtctaaa	540
gcgtaa						546

<210> 1054

<211> 1074

<212> DNA

<213> Enterobacter cloacae

<400> 1054

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tccatcatcc	gcgatctgac	cgattcggcg	attaagatgg	tgcgcgtcca	ggcgattgag	360
aaaaaccgct	atcgcgccga	agagatggcc	gaagagcgta	ttctcgacgt	gctgatccca	420
ccggcaaaaa	acaactgggg	acaggctgaa	cagcagctctg	aaccttctgc	tgcgcgtcag	480
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cagttgcagc	ccatgttcca	gaacctgggc	gggcaaaagc	agaaagcgcg	taagctgaaa	660
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cagcgcgacc	tgctgcgcgt	ggtggaagg	tgcaccgtct	ccaccaagca	cggcatgggt	900

aagactgacc	acattctgtt	tatcgctccc	ggtgcgttcc	agattgccag	cccgtctgac	960
ctgatcccgg	aactccaggg	tcgctctgcca	atccgcgttg	agttgcaggc	gctgaccacc	1020
gaagatttcg	aacgtatcct	gactgagcca	atattaaccc	cgcggctgga	aaat	1074

<210> 1055

<211> 2325

<212> DNA

<213> Enterobacter cloacae

<400> 1055

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gaagattcga	tgcccgtcgc	tcacgttgcc	ctgcccgttc	cgtttccccg	cacctttgac	180
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aaacagcagc	gcgtggggat	cgtggtgtcc	gtcagcgaca	aaagcgaact	gccgcttaac	300
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cgactgctgc	tgtgggcggc	agattattat	catcatccga	ttggcgacgt	cctgttccat	420
gcctgcccga	ttatgctgog	ccagggttaag	agcgccagcc	acgcgccaat	gtggtactgg	480
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atccgtttac	agcagatcgt	cagcggcacg	ctggcgctga	tcaataccct	gccggaagcg	2280
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<210> 1056

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 1056

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aagagtgagc	aagtcaagaa	aatcacggtg	tccattctct	tgaagggtgt	gaagatctct	120
accgatgaac	gtacgcgtcg	tcagggtgaac	aacctgcgtc	acgccaccaa	cagcgaactg	180
ctgtgcgaag	cgttctctga	tgcgtttacc	ggccaaccgt	tgccgaacga	tgacgatctg	240
cgtaaagaac	gcagtgacga	aatcccggaa	gaggcgaagg	tgatcatgct	tgaactgggt	300

atcgacccgg agacctggga atactaa

327

<210> 1057

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 1057

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ccggcacctt	cgcgacgcaa	aaagagtagt	tcaaaaagca	agcaacgtag	cctgtctgct	120
gtctccccag	ccatggctgc	cattgctgcg	gcggtgctgg	tggcctttat	tggcggcctc	180
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gatcagctga	cggacgaaca	gcgtcaattg	ctcgctcaga	tgcaggcgga	catgcgccag	420
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cctgtccagc	agcaaccgaa	ggcgcagccg	cagaagcaaa	cggcacagcc	gtatcaggat	660
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gtcaccaaaag	agaccgaggt	gcccgaagcag	acggctgaga	aaaaagatga	acgccgctgg	780
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gcatttgaag	gatttgactc	acgcattacc	accaataacg	gctggaatcg	cgtagtgatt	900
ggaccgggtca	aaggcaaaaga	aatgcagac	ggcaccattt	cccgtttgaa	agtggctggc	960
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<210> 1058

<211> 2142

<212> DNA

<213> Enterobacter cloacae

<400> 1058

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atcgttggtt	tccagcgta	ggagataccc	gccctcatga	cgatgcaggc	ctttcagcga	180
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cgcacacatga	gcattttccc	actcccaggt	ttcgagacgg	ctgtaaggat	gcgcgcgcat	360
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<210> 1059

<211> 474

<212> DNA

<213> Enterobacter cloacae

<400> 1059

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<210> 1060

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 1060

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<210> 1061

<211> 1227

<212> DNA

<213> Enterobacter cloacae

<400> 1061

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<210> 1062

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 1062

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<210> 1063

<211> 1539

<212> DNA

<213> Enterobacter cloacae

<400> 1063

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<210> 1064

<211> 1188

<212> DNA

<213> Enterobacter cloacae

<400> 1064

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<210> 1065

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 1065

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aaagtggctg gggtagcagg attcgaacct cgggaatgcc gaatcagaat ccggtgcctt 240
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<210> 1066

<211> 246

<212> DNA

<213> Enterobacter cloacae

<400> 1066

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<210> 1067

<211> 246

<212> DNA

<213> Enterobacter cloacae

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<210> 1068

<211> 378

<212> DNA

<213> Enterobacter cloacae

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<210> 1069

<211> 588

<212> DNA

<213> Enterobacter cloacae

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<210> 1070

<211> 501

<212> DNA

<213> Enterobacter cloacae

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<210> 1071

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 1071

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<210> 1072

<211> 645

<212> DNA

<213> Enterobacter cloacae

<400> 1072

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<210> 1073

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 1073

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<210> 1074

<211> 1299

<212> DNA

<213> Enterobacter cloacae

<400> 1074

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<210> 1075

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 1075

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<210> 1076

<211> 636

<212> DNA

<213> Enterobacter cloacae

<400> 1076

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<210> 1077

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 1077

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aacgtcgcgc	ccggtaccaa	agttctgttg	ctgagcgaac	gagacgaaca	gttgacacct	180

gatcctgtcc	tgtggtcata	tgcgcccggg	tggtgggata	agccgccact	gattaacgct	240
cgcatcgaga	cgacggccac	cagcagaatg	tttaaaccct	tctggcagca	tggccggggc	300
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<210> 1078

<211> 1146

<212> DNA

<213> Enterobacter cloacae

<400> 1078

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<210> 1079

<211> 1266

<212> DNA

<213> Enterobacter cloacae

<400> 1079

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<210> 1080

<211> 981
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1081
 <211> 696
 <212> DNA
 <213> Enterobacter cloacae

<400> 1081
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 ggcgagaaa tcattgcaggc ggcgctgcac tgggcggagc aacaacaggt atcgacgctg 600
 cgggtcgcaa ccagatggg caacacgct gcgcttaaac gttatattgc gagtgggtgc 660
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<210> 1082
 <211> 1425
 <212> DNA
 <213> Enterobacter cloacae

<400> 1082
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<210> 1083

<211> 753

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222> (720)

<400> 1083

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<210> 1084

<211> 984

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222> (975)

<400> 1084

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<210> 1085

<211> 1281

<212> DNA

<213> Enterobacter cloacae

<400> 1085

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<210> 1086

<211> 1305

<212> DNA

<213> Enterobacter cloacae

<400> 1086

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<210> 1087

<211> 1086

<212> DNA

<213> Enterobacter cloacae

<400> 1087

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<210> 1088

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 1088

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<210> 1089

<211> 1095

<212> DNA

<213> Enterobacter cloacae

<400> 1089

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<210> 1090

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 1090

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<210> 1091

<211> 4371

<212> DNA

<213> Enterobacter cloacae

<400> 1091

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<210> 1092

<211> 2283

<212> DNA

<213> Enterobacter cloacae

<400> 1092

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<210> 1093

<211> 1071

<212> DNA

<213> Enterobacter cloacae

<400> 1093

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gaggagatcc gggatgatggg ggggacggatt gggggcggagg ataccgtctg a 1071

<210> 1094

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 1094

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catgacgttc	cggatgagta	cgccatccat	aaagagaaag	agtttacctt	caataatatt	180
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accttcgtca	gccagcgctg	ctggtttggt	gataaaagtg	aagtaaacct	gggggcaggt	480
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<210> 1095

<211> 1242

<212> DNA

<213> Enterobacter cloacae

<400> 1095

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ccaggcatgc	tggtctgtgt	tgagcagtac	aacgcaggta	ttgagtgggt	acctacatcg	180
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gggctgttca	gcctgttcaa	cctcgccaac	ggcgtgctgt	ggattgccct	gatggtggta	1200
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<210> 1096

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 1096

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gggtgaacca	ttccggctga	tccaagctgg	ggtaaaactca	ccggcacgcg	cgtccatcgc	180
cctattacga	tagttaaaga	atttgatcag	actacccgcg	ttctttaccg	cgccgtgtgc	240
gaagggagag	ttatgaagaa	ggggatcatt	aagatgtacc	gcattctgga	gtccgggatc	300

gaggccgaat	atttcaatat	cgtgatggaa	aacgttaagt	tcacgacagt	ggcacccttc	360
atgaccccta	acgggatgag	cagcaccat	cttgaaacgc	tcgaattgcg	ttacgaagca	420
atctcatgga	agtacacgga	ggggaatatc	atttaccgtg	acacctggaa	cgatcgctgc	480
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<210> 1097

<211> 1293

<212> DNA

<213> Enterobacter cloacae

<400> 1097

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aaagggctca	gtatcggtcg	gagcgccacc	attggcgccg	tgctggcgct	gatgagcggc	120
gtgatccaca	tcaacgatat	ccctgtggtg	tggaaatatc	tctggaatgc	gacggctacg	180
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ggctactatt	tcaggacggg	catcataatg	acgctgccag	ttctctttgt	gacgcttgcc	1260
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<210> 1098

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 1098

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gtgacgcgcg	tgggtacccg	tctgtgccgc	ccttctgaag	tcgttctcga	catccttccg	360
gacgcgcaaa	aaggggcatt	tacgaaggaa	gatggcggaag	tcgtcgttga	cgccaacggg	420
aaaaaaatct	cccgccagta	a				441

<210> 1099

<211> 1377

<212> DNA

<213> Enterobacter cloacae

<400> 1099

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gctagtgttg	tcgctattgt	tgtactttctg	gtgctgatoc	caatgacgct	aacttctcct	180
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ttacgcagcg	cgatgctggt	ggtattaggg	ttagtcatta	ttgcgcctct	ggtggcgcg	1320
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<210> 1100

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 1100

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agtaacgaga	ttatgttaga	aaatctgaac	tacgaactgt	tttacctgct	caacgccacg	180
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<210> 1101

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 1101

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ctccagctct	tcaaaacctc	ctccgacgaa	acgcgcctct	ccatcgatcat	gcttctgcgt	180
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gtctcgcgcc	atatggcctt	actgcgcgag	gccgggctgg	tcacgatcgt	tcgtgagggt	300
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aacagctgga	actgcctgcg	agaagagaca	cgtatgaagc	tgaaaaaccg	cctcccgggc	420
tcttgctga						429

<210> 1102

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 1102

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tggagaaggg	atatgagcgt	taaactgatt	gcagtcgaca	tggatggctc	cttccctgagc	120

gatgcgaaaa	cctataaccg	cgcgcgtttt	ctggcgcagt	acgcgcgcat	gaaagcgcaa	180
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<210> 1103

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 1103

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gccgtatccc	tgcttggcgt	gtctgaaatg	accattogtc	gcgatctgaa	caacgacagc	180
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<210> 1104

<211> 408

<212> DNA

<213> Enterobacter cloacae

<400> 1104

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atcatcaaga	cgacctgcc	taaagcgaaa	gagctgcgct	gcgtagttag	gccgctgatt	180
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ggttacactc	gcattctgaa	gtgtggcttc	cgtgcaggcg	acaacgcgcc	gatggcttac	360
atcgagctgg	ttgatcggtc	agagaaaagca	gaagctgctg	cagagtaa		408

<210> 1105

<211> 486

<212> DNA

<213> Enterobacter cloacae

<400> 1105

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cgggaagata	tttataatgc	gttgatgtgg	ctggataagt	tggctgatta	tcaggacggc	180
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gagtgtgaaa	ggctggatgc	cagctgcccg	ggattcattt	tattcctcga	gcagattcag	300
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gaatttgaac	tggaagatct	gaaatgggtg	atcctgatgg	tgctgttcaa	cattccaggc	420
tgtgaaaatg	cctatcagca	aatggaagaa	ttactctttg	aagtgaatga	aggatgctg	480
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<210> 1106

<211> 627

<212> DNA

<213> Enterobacter cloacae

<400> 1106

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atcgccatc	caacagaagc	cgttttcggg	gtcgggtgag	atcctgacag	cgaaagtcgc	180
gttaaccgtc	tgctggcgct	aaaacaacgg	cctgtcgaaa	aaggattgat	tttgatcgct	240
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gaaaccattt	tctctgcgtg	gcctggtccc	gtgacgtttg	tttttcctgc	acaaccgaca	360
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accgggcttc	ccccctgtcg	gacaaccgaa	gaagttctgg	cgagttcggg	gagtgatttc	540
ccggtagccg	tcggtgaaac	cggtggcgct	cttaaccgct	cagaaattcg	cgatgccttg	600
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<210> 1107

<211> 366

<212> DNA

<213> Enterobacter cloacae

<400> 1107

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ggatcgctg	aagatgttaa	gatcagtgag	ctgtctgaag	aacaaatcga	cacgctgcgt	180
gacgaagtgt	ccaaatttgt	cggtgaaggt	gatctgcgcc	gtgaaatcag	catgagcatc	240
aagcgctga	tggatcttgg	ttgctatcgc	ggtttgcgct	atcgtcgtgg	tctgccagta	300
cgcggtcagc	gtactaagac	caacgcacgt	accgtaagg	gtcgcgcgca	accgatcaag	360
aaataa						366

<210> 1108

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 1108

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cagcacgggtg	cgcgtaaacc	gcgtctgtct	gactatgggtg	tgcaattggc	tgaaaagcaa	180
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aacgttgtat	accgtatggg	cttcggcgcg	actcgtgctg	aatcacgcca	gctggttagc	360
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aatgacgttg	ttagcattcg	tgagaaagcg	aaaaagcaat	ctcgcgtgaa	agccgctctg	480
gagctggctg	agcagcgtga	aaagccaacc	tggttggaag	ttgatgctgg	caagatggaa	540
agtacgttca	agcgtcagcc	ggaacgtcct	gatctgtctg	cggacattaa	cgaacacctg	600
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<210> 1109

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 1109

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gaggtcagaa	cggaaggtgg	atttcgcctt	tatacggata	acgacctgca	acgccttcgt	180
tttatccgct	atgcacggca	actcggcttc	acgcttgagt	cgatccgtga	actgctgtcg	240
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ctggatgaag	ttgaaggacg	cattcaggaa	ctgcaagcca	tgcagcgatc	tctgcaaagg	360
ttaaattgacc	cgtgctgcgg	taccgctcac	agcagtgttt	attgctcaat	actggaagca	420
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<210> 1110

<211> 234

<212> DNA

<213> Enterobacter cloacae

<400> 1110

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gccattgagg	cattgcttca	cgacccactt	ttcagacagc	gagttgagaa	gaacaagaaa	120
ggaaaaggga	gttatcttac	taaaggtaaa	catgcacaac	ggggtaaatg	ggaggccagt	180
ggcaagcaag	ctaatcgctt	ttttaccact	ggcctttctg	tttctgtctc	ctga	234

<210> 1111

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 1111

ccggcgaaacg	ttttcgccag	ggataatgtg	atggaaacct	atgctgtttt	tggtaacccg	60
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cacccatatg	gtcgggttct	tgcgcctgtt	gatgcatttt	taccgacgct	aaatagcttt	180
tttgttgccg	gcggtaaagg	tgcgaacggt	acggtgcctt	ttaaagaaga	ggctttcggg	240
cgtgcggatg	agctgaccga	gcgtgcgtgt	cttctaccac	ggggcctggc	cggtcgcgta	300
attgaa						306

<210> 1112

<211> 393

<212> DNA

<213> Enterobacter cloacae

<400> 1112

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gtggctcata	tccatgcttc	tttcaacaac	accatcgtta	ctattactga	tcgtcagggg	120
aaacgcattg	gttgggcaac	agccggtggt	tccggtttcc	gtgggttctcg	caaatccact	180
ccgttcgcag	ctcaggttgc	agcagagcgt	tgcgctgaag	ccgtaaaaga	atacggcatc	240
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ctgaacgccg	ctggtttccg	catcacgaat	attactgatg	tgactccgat	ccctcataac	360
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<210> 1113

<211> 1008

<212> DNA

<213> Enterobacter cloacae

<400> 1113

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tttggccata	ctctgggtaa	cgcactgcgc	cgtattctgc	tctcatcgat	gcccgggttc	180
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gatgagaacg	cagctattag	catgcgtatc	aaagttcagc	gcggtcgtgg	ttatgtgccg	480
gcttctgccc	gaattcattc	ggaagaagat	gagcgcceaa	tcggccgtct	gctggtcgac	540

gcatgctaca	gccctgtaga	gcgtattgcc	tacaatgttg	aagcagcgcg	tgtagaacag	600
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ctgggtaaaa	aatctcttac	cgagattaaa	gacgtgctgg	cttcacgtgg	tctgtctctg	960
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<210> 1114

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 1114

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gtcacccccc	tggagttcat	tatgtgggtg	ctcgatcagt	ggctctgaacg	ccatattttgc	180
gatgcccaaa	acaaaggcga	gttcgaaaaat	cttcccggca	gcggtgagcc	gctgattctg	240
gacgatgatt	cacatattcc	ccctgaatta	cgggccgggt	atcgcttact	gaaaaacgca	300
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aaaggcattc	ataagaatga	cccgcggtac	tctgaaatca	gtcgtcggtt	ggcgctcate	420
gagctaaaac	tgcgccagac	gggaatgaat	actgactttt	tgcattggtga	gtacagtga	480
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<210> 1115

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 1115

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ccagtaacgg	tagcacagct	actcgaactg	gagttagcag	ggtggatcgc	agctgtaccc	1140
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<210> 1116

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 1116

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gggaaacacg	gtccgtttct	cggttggtta	cactatccgg	aatgtgatta	tgtccgtttc	180

ctgaagagcc	aggcggacgg	acatatcgtc	aaaattctgg	agggacagct	ttgtccgctc	240
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tacccggaat	gtgatcatat	ggaacaaatt	gataaaccag	atgaaacggc	aattgcctgc	360
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tcgtgcgata	gctatcctga	atgccagttc	gttatcaatt	tcaaaccagt	agcgggctgc	480
tgccataatt	gcgattatcc	gttacttata	gaaaagaaaa	ccgcgcaagg	cttgaaacgc	540
ttttgcgccca	gtaaacaatg	tggaaagccg	gtttcggcgg	atcaaatacag	tgaataa	597

<210> 1117

<211> 1323

<212> DNA

<213> Enterobacter cloacae

<400> 1117

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cctccactgc	aacaaaaggt	ttccgataaa	gataaagcgc	tgcttcagga	gctgtgcttt	180
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<210> 1118

<211> 1410

<212> DNA

<213> Enterobacter cloacae

<400> 1118

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<210> 1119

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 1119

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gacggcaatc	cgtttgagct	ggaagccgac	gatctgctgg	cgatttgcat	tcagcatgag	420
atggatcacc	tggtcggtaa	actgtttatc	gattacctct	cacctctgaa	gcaacagcgt	480
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<210> 1120

<211> 972

<212> DNA

<213> Enterobacter cloacae

<400> 1120

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<210> 1121

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 1121

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ggtgcggcgt	tcggtaagat	cgtttcatca	ttagtgcgcg	acattattat	gccgcggtta	180
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ggcgatatcc	ctgcggttgt	aatgcactac	ggcgtattca	ttcagaacgt	atttgatttc	300
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459

<210> 1122

<211> 408

<212> DNA

<213> Enterobacter cloacae

<400> 1122

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cgttttgtcg	ccgccaacgt	tcgcggggcg	ggcggcgaga	ttgacctgat	catgaaagac	180
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gcccgcata	atgggagttt	tgatactgtg	gattggcgtt	tcgatgtggg	agccttcacc	360
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<210> 1123

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 1123

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gatgtggaga	tcgcgattcc	ttcgcacogt	agcgcgcgca	tcaggagat	gcataatgctc	540
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<210> 1124

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 1124

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<210> 1125

<211> 1173

<212> DNA

<213> Enterobacter cloacae

<400> 1125

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<210> 1126

<211> 1185

<212> DNA

<213> Enterobacter cloacae

<400> 1126

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<210> 1127

<211> 2169

<212> DNA

<213> Enterobacter cloacae

<400> 1127

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cgtgcactgc	tgaagaagg	gaaaaccag	caggccgcgc	agctgttcag	ccagctgcgc	300
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<210> 1128

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 1128

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<210> 1129

<211> 339

<212> DNA

<213> Enterobacter cloacae

<400> 1129

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<210> 1130
 <211> 291
 <212> DNA
 <213> Enterobacter cloacae

<400> 1130
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 gtagttgaca gcattgctgt taaacgtcgt ggtgctgtac gtaaagctaa actgtactac 240
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<210> 1131
 <211> 996
 <212> DNA
 <213> Enterobacter cloacae

<400> 1131
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 ttcgaagaac ataaggatca cgtggactgg ttatga 996

<210> 1132
 <211> 1134
 <212> DNA
 <213> Enterobacter cloacae

<400> 1132
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<210> 1133
 <211> 387
 <212> DNA
 <213> Enterobacter cloacae

<400> 1133
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<210> 1134
 <211> 1554
 <212> DNA
 <213> Enterobacter cloacae

<400> 1134
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<210> 1135
 <211> 1599
 <212> DNA
 <213> Enterobacter cloacae

<400> 1135
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<210> 1136

<211> 1161

<212> DNA

<213> Enterobacter cloacae

<400> 1136

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<210> 1137

<211> 933

<212> DNA

<213> Enterobacter cloacae

<400> 1137

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agtgcagaag	agaaggcgct	ctactgggcg	gatatacctg	aaggggagat	ccatcggtac	180
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gattataacg	gcgccatget	gatgegtate	gacaacgacc	tgacgccgaa	agtgatccag	480
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aagcgcgaag	agtttgcgcg	gttttagcgag	ggagacggta	ttcccgcacg	tgccggcaatg	660
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tttgccggcg	acgatatgaa	aacgctgttt	atcaccacca	cgccgggaaaa	tatggaggcg	840
gaggagctgg	cgaaataccc	gctttccggg	gccatcttca	ccctgccagt	aaatgtggca	900
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<210> 1138

<211> 750

<212> DNA

<213> Enterobacter cloacae

<400> 1138

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taccagcttg	cccgccagcg	cctgaataac	gtcgggtgta	cccaaattct	cggcggagat	660
cgtgtacct	tcaccgaaaa	gggtgatttt	ttctcctatc	gccgcgacaa	gacgacaggc	720
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<210> 1139

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(1028)

<400> 1139

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atgagcgct	tgctgaatca	ggaaggggga	tcggtagctc	ctttattaac	gtccgctggc	180
attaatgcc	gccagttacg	caccgccatc	gatcaggcgc	tgagccgttt	accgcaggta	240
gaaggtagcg	gcggcgacgt	gcagccgtcg	caggatctgg	tgccgctgct	gaacctttgc	300
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gcgcttgaat	cacgcggtac	cttaaccgac	ctgctgaaat	ccgccggtgc	aaccaccgct	420
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<210> 1140

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 1140

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caactggaag	cggttgataa	tcgctatccg	tttggctcgt	attcgagca	ggtacagtta	180
gatcttatct	acgcctacta	caaaaatgcc	gatctgccgc	tggctcaggc	aacgatcgat	240
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gaccgtgacc	cgcaacatgc	gcgtgatgct	ttcaatgact	tctccaaact	ggtgcgtagc	420
taccggaaca	gccagtacat	taccgatgcc	actaagcgct	tgggtgttct	gaaagatcgt	480
ctggcgaaat	atgagtactc	cgttgccgaa	tactacacc	gccgtggcgc	atgggttgcc	540
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ggcctgaagc	tgatgaaaa	tgctgatcgc	cagatgcaga	tgacggctca	ggctgacaaa	660
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<210> 1141

<211> 396

<212> DNA

<213> Enterobacter cloacae

<400> 1141

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cgtctcgcca	aactggataa	atggcaaaaa	catttgatta	atccacatat	catcctgtcc	180
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cggcagctca	ataaagtgc	acacaaaggt	gaagcacgct	gcgccgcaac	ctcggtgaaa	360
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<210> 1142

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 1142

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tcaattactc	tcatgttatt	gtcgtgatt	ttgtcgggtt	gccagatcaa	tccttatgct	120
tttcagcctg	gctggaccag	cccgactgg	ttcactgccg	gtaaagaaga	cgctatgaat	180
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cgaggggaat	atcttcgtgg	ctacgctgac	ggacagaaaa	aaatatgcga	agagggcttc	300
attcacgcct	ggggattagc	gggaaaatca	tttctgcc	gctgcgatac	aactgaaaat	360
gcagtaaac	tgtatgaatc	ctggcaacaa	ggaatggatg	aaagtatgcg	ttccagcagg	420
ctgaattga						429

<210> 1143

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 1143

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atttttagtg	ccctgcaaa	ggcaggctcg	ttcactgaaa	cggataaatc	agtacgttcg	180
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tgtctgataa	tagagcacia	ccaggctcagg	ttttccgtaa	atctggatgc	gctggcgcgc	540

agtggcgtaa gagtcaatcc ggatgtatta atgctcgcaac ggaataagaa gcatgaataa 600

<210> 1144

<211> 1179

<212> DNA

<213> Enterobacter cloacae

<400> 1144

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<210> 1145

<211> 1242

<212> DNA

<213> Enterobacter cloacae

<400> 1145

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<210> 1146

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 1146

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tcctatggct	ttaacgaact	gaatggcgac	tgggtctctg	gcctgtcaga	taagatcctg	180
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tgggcgaagg	gcgcgaacat	cccgcgagc	aacctcacca	cgcggggctt	aggcaaaaaa	420
taccctgtca	gcagcaaccg	cactgcacag	gggcgcgctg	aaaaccgccg	ggttgcggtg	480
gtcatcagca	cgccttaa					498

<210> 1147

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 1147

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<210> 1148

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 1148

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aagctgcata	tcagcaagc	cgtgtttcac	cactatcatg	atgtccatgt	tcgcgccgaa	180
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<210> 1149

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 1149

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aaagctttct	tttcggcgcc	actgaaaacg	ctcctcgatc	tgctgccgga	acgtgcgctg	300
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<210> 1150
 <211> 1158
 <212> DNA
 <213> Enterobacter cloacae

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 gatgcgtggc tggttgccgc gtcacatgat cccgtcaccc agcgctgaa attcctggta 240
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<210> 1151
 <211> 801
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1152
 <211> 1014
 <212> DNA
 <213> Enterobacter cloacae

<400> 1152
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 gcgaaaagcc atgcgttgct ggagaagcgt ttcccggaga ccaaattctc atgggtcgag 240
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<210> 1153

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 1153

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aaagaacagc	gcgcgcgaact	ggtattaagt	cttcaccacg	ggactggcag	gatccgagta	300
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<210> 1154

<211> 2718

<212> DNA

<213> Enterobacter cloacae

<400> 1154

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caagctaaat	accgccacga	ctaccgtgcg	ccggaatacc	tgataagcga	tatcgatctg	180
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<210> 1155

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 1155

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<210> 1156

<211> 1404

<212> DNA

<213> Enterobacter cloacae

<400> 1156

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<210> 1157

<211> 1107

<212> DNA

<213> Enterobacter cloacae

<400> 1157

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<210> 1158

<211> 437

<212> DNA

<213> Enterobacter cloacae

<400> 1158

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<210> 1159

<211> 1599

<212> DNA

<213> Enterobacter cloacae

<400> 1159

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<210> 1160

<211> 1491

<212> DNA

<213> Enterobacter cloacae

<400> 1160

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<210> 1161

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 1161

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cagccgcttc	aggtactcaa	ggcctgcggc	gcggtggatt	acttctgtca	gaacggccac	300
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<210> 1162

<211> 1686

<212> DNA

<213> Enterobacter cloacae

<400> 1162

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<210> 1163

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 1163

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<210> 1164
 <211> 702
 <212> DNA
 <213> Enterobacter cloacae

<400> 1164
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<210> 1165
 <211> 2076
 <212> DNA
 <213> Enterobacter cloacae

<400> 1165
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<210> 1166
 <211> 759
 <212> DNA
 <213> Enterobacter cloacae

<400> 1166
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<210> 1167
 <211> 255
 <212> DNA
 <213> Enterobacter cloacae

<400> 1167
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 cggcaaccgc ctgcgcggtt gtcagaagcc agcccgcgcg tgcaccagc accgacgttt 180
 tgccgctccc ggcgcctgcc agcactaaaa gagactgctc gccattcacc acggcgcgcg 240
 cctgggcagg attga 255

<210> 1168
 <211> 1197
 <212> DNA
 <213> Enterobacter cloacae

<400> 1168
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 gatgcgggtc gtgatgtaca atttatagag cagttccgtc aggcgcgcca tcaccgggtg 1140
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<210> 1169

<211> 348
 <212> DNA
 <213> Enterobacter cloacae

<400> 1169
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 tcccttgatg aaccgtcagc agacgatctg gccgttgacg cagagcttcg cgccgcgccc 180
 tggatatcatg tggttatgga gggcgacgat ggtcagcctg tccataccta tcttgccgaa 240
 gcgcagctga gtggtgaact acaggatgag catccggaac aaccactat ggacgagctt 300
 gctcagacca tccgcaaaca gttacaggca ccaagactgc gtaactaa 348

<210> 1170
 <211> 453
 <212> DNA
 <213> Enterobacter cloacae

<400> 1170
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 accatcgccc tgtggcgggt aggaagccga gttgtccgg tcgaagtcgc gcaagccgcg 420
 cgtgaagcca atgcccgctc tegttttcag taa 453

<210> 1171
 <211> 2178
 <212> DNA
 <213> Enterobacter cloacae

<400> 1171
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<210> 1172

<211> 483

<212> DNA

<213> *Enterobacter cloacae*

<400> 1172

cgaggttaacc	tcacggataa	gattatggaa	ctgacaacac	gcacacttcc	ggcgcgcaag	60
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catcagcctc	ttttacagca	tcatgccctt	tctgctacgg	gaacaaccgg	caacctgatc	180
caccgcgaaa	ccggtctgga	agtgaatgcc	atgctgagcg	gcccgatggg	gggtgaccag	240
caggtaggcg	ctcagatttc	agaaggtaaa	attgacgttc	ttattttctt	ctgggatccg	300
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aacattccgg	tagccaccaa	tctttcaacg	gcagatttca	tcattgaatc	gccgcagttt	420
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<210> 1173

<211> 672

<212> DNA

<213> *Enterobacter cloacae*

<400> 1173

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agcagcagcg	cgacgtgaa	acccgcaggc	gcgaacaccc	tgaccggcgt	ggccgcagtg	420
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gccagcaaca	gcacggcgga	aggcaaagcg	cagaaccgcc	gcgttgaaat	tacgttgagt	660
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<210> 1174

<211> 585

<212> DNA

<213> *Enterobacter cloacae*

<400> 1174

cctatgcaac	gttgcggctg	ggtaagccag	gatcagcttt	atatcgatta	tcacgacaag	60
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cagcaggccg	ggctgtcgtg	gatcacctgt	ctgaaaaagc	gtgagaacta	tcgcaaagcc	180
ttccaccagt	tcgatccggc	tgcggttgcc	gccatgaccg	acgacgacgt	acaaaagctg	240
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cgtgcttatac	tggcgatgga	gcaaaatggc	gaaccctttt	cagcattttg	ctggtcgttt	360
gtggataacg	agccgaaggt	gacgcaggcc	gccacgcttg	cagagatccc	aacgtcgacc	420
ccgcctcag	atgccctgtc	gaaagcgctg	aaaaaacgcg	gctttaagtt	tgtgggcacc	480
accatctgtt	actcctttat	gcaggcctgc	gggctggtca	atgaccacat	tacgggctgc	540
ttctgccatc	cggagggcc	ccatgatccg	caaatggcaa	agtga		585

<210> 1175
 <211> 1170
 <212> DNA
 <213> Enterobacter cloacae

<400> 1175
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 aaggtattct cactaaattc agggaaatca gcgatgatca aaccaaccgg ggccaccatc 180
 agcgacgtgg cgaaagccgc caaaaccggg aaaaccagca tttcacgcta cctcaacggc 240
 gagaaacacc tgctgtccga tgcgctgctg gcgcggtatc aacaagccat tgcgatctc 300
 gactaccgtc ccagcctgat ggcgcgccgg ctcaagcggg gacgcaccgg cctgattggg 360
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 gccaccactg ccaccgagca cctgattgaa cagggtttcg aagccattct gttcctgagc 720
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<210> 1176
 <211> 942
 <212> DNA
 <213> Enterobacter cloacae

<400> 1176
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 ctgaatgtcg ctaccggcct tgcgcggctg gggctgaatg tcggctgggt gagccgcgtg 180
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 aatggaaacg atcccatcgt ggagtatttc cgcaaaggct cagcggcaag ccatctctcc 360
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 gcggcgccgc tctcgccag ctctacgat ttactcgatc acgcggcttc ggcaatgaaa 480
 gcgcagggca aaaccatctc ctttgatccg aatctgcgcc cgggtgcttg gaaaagcgaa 540
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<210> 1177
 <211> 1338
 <212> DNA
 <213> Enterobacter cloacae

<400> 1177
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 tacagcctgg cgtacctgga tcgtgccaac ttcagtttcg catccgcgcg cgggatcaac 180
 gaagacctcg ggatcaccaa aggggtctcg tccctgctgg gcgcctctt cttcctgggg 240

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ggcgacgcgc	acgcctga					1338

<210> 1178

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 1178

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agcccgaaa	ccgtggcaca	gcacgcgcac	gcgtttgcc	gcgcgagg	cctgctgggt	180
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gaaacacgct	acaacatggc	ggcgaccgcc	gtggataacc	tgattgccgc	gctcggcggt	960
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<210> 1179

<211> 507

<212> DNA

<213> Enterobacter cloacae

<400> 1179

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ctcactttgc	atggcgaaaca	gatcggagct	aaatccaagc	tgcttcagaa	cagcaaacac	180
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acagcgcaac	gagagcttcg	tggcggtatc	gcaggagtag	ccgcggttag	ctacaagatt	300
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ccagtcgctg	gtttcgcgca	taacgaagac	cacgtaagta	tcattccagcc	cgtcagccgg	420
agcctggtag	gtgaaactttt	tgggtgggtt	aatcagcgat	ttcacatcgc	tggattcgtc	480
cgcctgagcc	caggcataaa	gacctaa				507

<210> 1180

<211> 552
 <212> DNA
 <213> Enterobacter cloacae

<400> 1180
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 ggctgggtcaa tgaccacatt acgggctgct tctgccatcc ggagggccac catgatccgc 120
 aaatggcaaa gtgagaacac cgcgccgctt ttgagtctgt ggctggagag caccaccgag 180
 gcgcatccgt ttatcgacgc aagttactgg caagcgaatg aagcggtagt gcgggatgaa 240
 taccttcccg ccgccgagac ctgggtctgg gaagaaaacg gtaccctgtg cggttttatc 300
 agcgtcatgc agttccagtt cgtgggggcg ctgtttgtcg ccccggcgtt catcgaaaag 360
 gggattgggc gtgcgctgct gaaccacgtt cagcagcact acccgtatctt aaccctggag 420
 gtgtaccaga aaaacgtgcg ggcgggtgaat ttctatcatg ctacagggtt tcgcatcgaa 480
 gacagcgctt ggcaggatga taccacaacac ccgacgtgga tcatgagctg gcaggcggat 540
 caaacgccgt aa 552

<210> 1181
 <211> 231
 <212> DNA
 <213> Enterobacter cloacae

<400> 1181
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 tggaaggagg gcggtatctg taagaacggc gccttaaacc tgctgaccca agatctcccc 120
 agctcgaagc tggggaatgg ctgcgcgggg aatacggcgc tggcatgggt ggagaaatat 180
 gaggggcccg cgcttaccct tacggcgctt gatccgcctg ccagctcatg a 231

<210> 1182
 <211> 375
 <212> DNA
 <213> Enterobacter cloacae

<400> 1182
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 ggctgccatg ctgcttctgg cctgggtgggt gtttcagtct gcctgctttt ttgtcacacc 120
 gctttttgct ggcaacagga atatatcgtt tcagatgcac aaagtaatac gacggaacgt 180
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 cgcacccaga atgcttacgg ggtttaccct gaacgatccc tccggttcgg atgcggaaac 300
 cgttctgagc gttggctgga attttcccggt ggccgggacat ttcaccaccg ggcccgtcat 360
 ggcgtggcgc actga 375

<210> 1183
 <211> 324
 <212> DNA
 <213> Enterobacter cloacae

<400> 1183
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 gaccagggtg atgagaaagt cgtgaccaag ccgtcaaacc ctttgcaacc gctgatcccc 120
 gcggcgcagg tctttactca gcagttggtc caggtgggtg actttattag tgaacaaggt 180
 acgcagggtg gctttgtctc taacggtatc cagttcccg cctcccagca ggcgagccag 240
 tataacgcgc tgatcgggtc gctcgcgtcc cagcatcagg cctttagcca ggccctggagc 300
 gcagcgggtc ctgctacgga ataa 324

<210> 1184
 <211> 294
 <212> DNA
 <213> Enterobacter cloacae

<400> 1184
 ccccttcctt atcgcttaaa aatctgtaac gcaatccatc aagccggaag gcacaatata 60

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gctgataaag	gtttcggtt	catcacacct	gacgatggct	ctaaagacgt	gttcgtacac	180
ttctctgcta	tccagaacga	tggctacaaa	tctctggatg	aaggtcagaa	agtttccttc	240
accatcgaaa	gcggcgctaa	aggcccagca	gctggtaacg	ttgtaagcct	gtaa	294

<210> 1185

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 1185

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cgacggaaacg	ttatacatgg	gacgcgatc	accaacctcg	ttatgaagat	attctcgcg	180
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gatacaacca	ccacgcagtc	gcttacogac	cccctctggc	atgccagcgt	gaactcattg	420
ggttggcgtg	ttgatacgca	gtatggtgat	ttacacctct	gggcgaagat	cagctataac	480
cagcaaactg	aagaagaata	tttatatacg	ctgggattga	gcgccaatt	ttaa	534

<210> 1186

<211> 1287

<212> DNA

<213> Enterobacter cloacae

<400> 1186

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gcggtgctgt	tcagacgagt	ggaaggttat	ttcgaacacc	tcactgtaag	aaatggaatt	180
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totaactggc	tgtcggcggt	aggtctttat	gcctgggctc	aggcggacga	atccagcgat	720
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<210> 1187

<211> 2232

<212> DNA

<213> Enterobacter cloacae

<400> 1187

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<210> 1188

<211> 1224

<212> DNA

<213> Enterobacter cloacae

<400> 1188

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<210> 1189
 <211> 1194
 <212> DNA
 <213> Enterobacter cloacae

<400> 1189
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 aatggatatt tgaagatctt ctggccagaa tctaataaat tcatacaatg ttaa 1194

<210> 1190
 <211> 858
 <212> DNA
 <213> Enterobacter cloacae

<400> 1190
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 gactcattaa gcggaacgga tatcatggcc gctatgggca tgacgcagga acgggcagca 180
 ttgggttaca gcgcttttct cggaagatg ggtatcagca acaatgaccg ggagagggcg 240
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 tattctcgca gcgcgcgcag cgtgaaacag tgtgactgct gctcgggtca gggattcatt 420
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 ttttacgata agctaatac caaatttgac atcgaagagg catgggccga tgcgcagttg 840
 aagcagataa caaaatag 858

<210> 1191
 <211> 699
 <212> DNA
 <213> Enterobacter cloacae

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 aaccgaagcc aggacgacgt tgacgaaatc cgccgccagt ggggtgctggc cttcaaagaa 240
 aacgggataa acaccatgga gcaggttgaa gcggcgatgc gtatggtgctg tgcgcaggag 300

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<210> 1192

<211> 312

<212> DNA

<213> *Enterobacter cloacae*

<400> 1192

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tacgccacta	ctggtacagg	tttacctgcc	gagctgatcc	atttaatttt	tttaagagtt	180
tcccagatca	atgggtgtgc	acactgcata	gatatacata	ctcgcgatct	tatcaagagt	240
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<210> 1193

<211> 486

<212> DNA

<213> *Enterobacter cloacae*

<400> 1193

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gctggcatgg	aagtcgtaca	caggcgagag	cctgaccttc	cggaggcacg	taaagtcgcg	180
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gacaataaaa	tagcgatggc	caggatggag	ggcatcttgc	gaaaagaacc	tgttcagaca	360
ggggaaccgg	taggttatta	tgtcttcttc	gctgatcctg	atggtaacac	acttgaactt	420
tcttatggtc	agaaagtcgg	gatcgaggct	tttcgtcatt	atgatacagt	gcctgcactc	480
cagtaa						486

<210> 1194

<211> 474

<212> DNA

<213> *Enterobacter cloacae*

<400> 1194

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aaggcgagat	tctggctgga	tgaactgccg	gttgctgact	atcgcgttgt	gaaaatgcct	420
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<210> 1195

<211> 894

<212> DNA

<213> *Enterobacter cloacae*

<400> 1195

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<210> 1196

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 1196

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<210> 1197

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 1197

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ccgggagggtc	gtatggccga	cctgtcgaa	gggtatacca	aggctcgctaa	cgagatccaa	180
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aagcggctgc	gtgcaaccgg	aacggcaaa	ccatcccggg	gcggcatcga	cctgcttaac	960
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<210> 1198

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 1198

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aaaagactta	gcaagcagtt	tgatggttgc	cagattacga	ttaagcgtgc	cagtaatgat	180

ggttttgactg ttttcggggg cgacaagaaa gaggtcgaac atatcgtgca ggagacttgg 240
gaaagcgcgg acgagtgggt ttatttaa 267

<210> 1199

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 1199

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gccatttccg atgccacgtt ttacatctgg cgtaagaagt atggcgggtat ggaggtgcct 180
gaagttaagc gcctgaagtc gcttgaggaa gagaacgcc a gactcaagaa gctgcttgcc 240
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<210> 1200

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 1200

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<210> 1201

<211> 938

<212> DNA

<213> Enterobacter cloacae

<400> 1201

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<210> 1202

<211> 1101

<212> DNA

<213> Enterobacter cloacae

<400> 1202

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1101

```

<210> 1203

<211> 1401

<212> DNA

<213> Enterobacter cloacae

<400> 1203

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1401

```

<210> 1204

<211> 1485

<212> DNA

<213> Enterobacter cloacae

<400> 1204

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```

<210> 1205

<211> 399

<212> DNA

<213> *Enterobacter cloacae*

<400> 1205

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```

<210> 1206

<211> 492

<212> DNA

<213> *Enterobacter cloacae*

<400> 1206

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acaggcgcg cgaagtgtct ggtgaagaat gaacgggcta ttgcgtttta ccatcgccac 420
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<210> 1207

<211> 2250

<212> DNA

<213> *Enterobacter cloacae*

<400> 1207

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<210> 1208

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 1208

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<210> 1209

<211> 492

<212> DNA

<213> Enterobacter cloacae

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<210> 1210

<211> 1140

<212> DNA

<213> Enterobacter cloacae

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<210> 1211

<211> 1203

<212> DNA

<213> Enterobacter cloacae

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<210> 1212

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 1212

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<210> 1213

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 1213

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<210> 1214

<211> 243

<212> DNA

<213> Enterobacter cloacae

<220>

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<222> (150)

<220>

<221> unsure

<222> (159)

<400> 1214

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gcaaaaaaac tggcgtttcc gcaccccccn taccctaaant ggacagcaat aggcgttaac 180
tggcttgccg gttttgattt cgaaattaag gttatcgcca ggatccctac gcccgcgaat 240
taa 243

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<210> 1215

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 1215

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<210> 1216

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 1216

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gctgagctgg cgttcacctc ccagaacgac aagctgaaag gccgtgttga agaatttgcc 180
gcgcagctgg gttccagcat tgttctggaa tgtgacgttg cacaagacga aagcattgat 240
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<210> 1217

<211> 1941

<212> DNA

<213> Enterobacter cloacae

<400> 1217

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1941

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<210> 1218

<211> 1225

<212> DNA

<213> Enterobacter cloacae

<400> 1218

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<210> 1219

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 1219

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taa						243

<210> 1220

<211> 351

<212> DNA

<213> Enterobacter cloacae

<400> 1220

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tgcggtgggg	cagtaaaaaga	cggcattatt	gagattcagg	gcgataaacg	agatttaatt	300
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<210> 1221

<211> 870

<212> DNA

<213> Enterobacter cloacae

<400> 1221

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<210> 1222

<211> 1407

<212> DNA

<213> Enterobacter cloacae

<400> 1222

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<210> 1223

<211> 915

<212> DNA

<213> Enterobacter cloacae

<400> 1223

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<210> 1224

<211> 1323

<212> DNA

<213> Enterobacter cloacae

<400> 1224

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<211> 587

<212> DNA

<213> Enterobacter cloacae

<400> 1225

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<210> 1226

<211> 2334

<212> DNA

<213> Enterobacter cloacae

<400> 1226

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<211> 2142

<212> DNA

<213> Enterobacter cloacae

<400> 1227

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 <212> DNA
 <213> Enterobacter cloacae

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 <212> DNA
 <213> Enterobacter cloacae

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<212> DNA

<213> Enterobacter cloacae

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<211> 795

<212> DNA

<213> Enterobacter cloacae

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<210> 1233
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<212> DNA
<213> Enterobacter cloacae

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<210> 1234
<211> 501
<212> DNA
<213> Enterobacter cloacae

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<210> 1235

<211> 1695

<212> DNA

<213> Enterobacter cloacae

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<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 1236

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<210> 1237

<211> 1383

<212> DNA

<213> Enterobacter cloacae

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<210> 1238

<211> 1347

<212> DNA

<213> Enterobacter cloacae

<400> 1238

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<210> 1239

<211> 411

<212> DNA

<213> Enterobacter cloacae

<400> 1239

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<210> 1240

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 1240

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<210> 1241

<211> 732

<212> DNA

<213> Enterobacter cloacae

<400> 1241

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<210> 1242

<211> 264

<212> DNA

<213> Enterobacter cloacae

<400> 1242

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<210> 1243

<211> 933

<212> DNA

<213> *Enterobacter cloacae*

<400> 1243

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<210> 1244

<211> 342

<212> DNA

<213> *Enterobacter cloacae*

<400> 1244

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<210> 1245

<211> 1293

<212> DNA

<213> *Enterobacter cloacae*

<400> 1245

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<210> 1246

<211> 1287

<212> DNA

<213> Enterobacter cloacae

<400> 1246

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<210> 1247

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 1247

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<210> 1248

<211> 765
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 1249
 <211> 555
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1249
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 aatgaactgg ctcatgcccc catgaccagc caggattatc caacctttaa tttccttcag 420
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<210> 1250
 <211> 1281
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1250
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<210> 1251

<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 1251

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<210> 1252

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 1252

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<210> 1253

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 1253

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agtaaaggcg	cggcgagcta	tctgctccag	cagggttacg	aggcgggata	cagcgtcgat	180
ggcggttcg	atgocctggc	tcgtcatttc	ccggcagaag	ttgaatacgc	gtttgagcgc	240
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<210> 1254

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 1254

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<210> 1255

<211> 2433

<212> DNA

<213> Enterobacter cloacae

<400> 1255

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<210> 1256

<211> 2091

<212> DNA

<213> Enterobacter cloacae

<400> 1256

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<210> 1257

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 1257

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267

<210> 1258

<211> 2760

<212> DNA

<213> Enterobacter cloacae

<400> 1258

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<210> 1259

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 1259

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tccgcgctgg	aaaccattat	ttcgggtgtgc	ggtctggtcg	gggtgctgct	gttgaatatg	180
gtggtttga						189

<210> 1260

<211> 1053

<212> DNA

<213> Enterobacter cloacae

<400> 1260

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gatgaaaagg	cgtaacgtcc	gtcattcg	caggcgcttg	aagcgggcat	taattttttt	180
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gaaatggcca	gacgcgatga	gatcgttgtg	gcgacaaaga	ccttctttcc	gtggcgcaac	300
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<210> 1261

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 1261

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<210> 1262

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 1262

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ctgaaaagtag	tggaagatgc	cggactaaaa	acgacgatat	ccagcattcg	cgggggacag	180
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gccagcgta	ttatccgcga	agtgtatgaa	agtgatggga	ttgtcgcagc	cgtctgccac	420
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<210> 1263

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 1263

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ggcctttaag	cccggataaa	gaaaattgcc	gtaggtttcc	attgtcctca	gtgcatccgg	180
caatga						186

<210> 1264

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 1264

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ggttatcgca	acgtgttgca	gaactactca	tttccgttta	atcgccagtt	ggtattaaca	180
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gtacagcgca	ttaaaagcat	cgttgagggt	cgtccgcttc	gcgaaacgga	actgccaccg	480
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<210> 1265

<211> 1068

<212> DNA

<213> Enterobacter cloacae

<400> 1265

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<210> 1266

<211> 453

<212> DNA

<213> *Enterobacter cloacae*

<400> 1266

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<210> 1267

<211> 909

<212> DNA

<213> *Enterobacter cloacae*

<400> 1267

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<210> 1268

<211> 1290

<212> DNA

<213> *Enterobacter cloacae*

<400> 1268

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<210> 1269

<211> 975

<212> DNA

<213> Enterobacter cloacae

<400> 1269

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aacagcggga	ccgaacctgg	tggagcgatg	atttttcgat	cgggcgcatt	cgcgccggca	960
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<210> 1270

<211> 561

<212> DNA

<213> Enterobacter cloacae

<400> 1270

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<210> 1271

<211> 894

<212> DNA

<213> Enterobacter cloacae

<400> 1271

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<210> 1272

<211> 1335

<212> DNA

<213> Enterobacter cloacae

<400> 1272

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ggttcggggc	agctgctgag	cgacctgata	tccgggcgga	cgccggcaat	tccgtttgac	1260
gatttgagcg	ccgcacgcta	tcaatcaggg	tttaccat	cgctccaca	acacctgcac	1320
ggcgcgcata	attaa					1335

<210> 1273

<211> 1080

<212> DNA

<213> Enterobacter cloacae

<400> 1273

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tcaccggttg	agctgtgggg	caacgaggtt	aaaattgatg	atgtggccgc	tgcggcgggc	1020
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<210> 1274

<211> 633

<212> DNA

<213> Enterobacter cloacae

<400> 1274

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aagcgggcca	tgacgtggat	gccgatcagc	gaacaagccg	ggaaggcctg	ggcgctgagc	180
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cgctacatgg	gctggaagg	acagccatcc	accagcgagc	tgaaaaacc	ggagcgtaat	360
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gatgaattct	tcgagcacgt	tgtgaagaat	catccgtcag	cacaggctcc	acgttatatac	600
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<210> 1275

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 1275

cccagagaca	gtctgtcatc	tatcgaggag	ccatctggcg	tgagtagcta	cagtgagcag	60
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<210> 1276

<211> 939

<212> DNA

<213> Enterobacter cloacae

<400> 1276

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caaaccgtta cgctgccgct gggcgcccg ggcacacctg tacacgataa ttcaggcagt 900
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<210> 1277
<211> 552
<212> DNA
<213> Enterobacter cloacae

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<400> 1277
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tttgggaaggt aa 552

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<210> 1278
<211> 1752
<212> DNA
<213> Enterobacter cloacae

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gaggcggagt ag 1752

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<210> 1279
<211> 1581
<212> DNA
<213> Enterobacter cloacae

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<400> 1279
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<210> 1280

<211> 1620

<212> DNA

<213> Enterobacter cloacae

<400> 1280
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<210> 1281

<211> 375

<212> DNA

<213> Enterobacter cloacae

<400> 1281

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<210> 1282

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 1282

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<210> 1283

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 1283

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<210> 1284

<211> 2106

<212> DNA

<213> Enterobacter cloacae

<400> 1284

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<210> 1285

<211> 1053

<212> DNA

<213> Enterobacter cloacae

<400> 1285

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<210> 1286

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 1286

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gcgctcgggc	tggggctggc	gaccacgctg	gtgctgaacc	tgactaactt	ttccatttct	180

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<210> 1287

<211> 1548

<212> DNA

<213> Enterobacter cloacae

<400> 1287

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<210> 1288

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 1288

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gttgacttga	tgaaaaagcg	cctggaaaac	ggggatgact	tttttgcgat	taacccaaaa	180
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<210> 1289

<211> 345

<212> DNA

<213> *Enterobacter cloacae*

<400> 1289

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<210> 1290

<211> 780

<212> DNA

<213> *Enterobacter cloacae*

<400> 1290

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<210> 1291

<211> 468

<212> DNA

<213> *Enterobacter cloacae*

<400> 1291

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<210> 1292

<211> 597

<212> DNA

<213> *Enterobacter cloacae*

<400> 1292

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<210> 1293

<211> 672

<212> DNA

<213> Enterobacter cloacae

<400> 1293

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<210> 1294

<211> 1371

<212> DNA

<213> Enterobacter cloacae

<400> 1294

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<210> 1295

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 1295

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<210> 1296

<211> 1134

<212> DNA

<213> Enterobacter cloacae

<400> 1296

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<210> 1297

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 1297

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gatacgtctg	aatatcggtg	tgatgaaaaa	ccgtgacgg	tgaagctgaa	caaccgcgct	180
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<210> 1298

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 1298

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<210> 1299

<211> 1158

<212> DNA

<213> Enterobacter cloacae

<400> 1299

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agtgaataaca	tccgcgtcgg	tcttattggc	tacgggtacg	caagcaaaac	ctttcatgca	180
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<210> 1300

<211> 774

<212> DNA

<213> Enterobacter cloacae

<400> 1300

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<210> 1301

<211> 534

<212> DNA

<213> *Enterobacter cloacae*

<400> 1301

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gtggtggact	attactcgtc	aacgggaaac	aagccgaata	ccacggtgat	ggtggatatc	480
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<210> 1302

<211> 507

<212> DNA

<213> *Enterobacter cloacae*

<400> 1302

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gaaattcgtc	atgagtctat	agaatggaag	tacactgaag	gaaacataat	gtacaaagac	480
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<210> 1303

<211> 1035

<212> DNA

<213> *Enterobacter cloacae*

<400> 1303

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<210> 1304

<211> 1914

<212> DNA

<213> *Enterobacter cloacae*

<400> 1304

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<210> 1305

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 1305

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<210> 1306

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 1306

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<210> 1307

<211> 675

<212> DNA

<213> Enterobacter cloacae

<400> 1307

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<210> 1308

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 1308

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<210> 1309

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 1309

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cagcagggtt	tagactgtga	cgatctcttc	ccctcgcccg	tgctggccta	tatccttgcg	720
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<210> 1310

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 1310

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<210> 1311

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 1311

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<210> 1312

<211> 2712

<212> DNA

<213> Enterobacter cloacae

<400> 1312

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<210> 1313

<211> 405

<212> DNA

<213> *Enterobacter cloacae*

<400> 1313

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<210> 1314

<211> 471

<212> DNA

<213> *Enterobacter cloacae*

<400> 1314

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<211> 1149

<212> DNA

<213> *Enterobacter cloacae*

<400> 1315

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<210> 1316

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 1316

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<210> 1317

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 1317

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<210> 1318

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 1318

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<210> 1319

<211> 843

<212> DNA

<213> Enterobacter cloacae

<400> 1319

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<210> 1320

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 1320

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ttgaccacca	aagcgatgga	aacgggtggt	aaagcgctgg	cgggctaa		228

<210> 1321

<211> 1032

<212> DNA

<213> Enterobacter cloacae

<400> 1321

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<210> 1322

<211> 663

<212> DNA

<213> Enterobacter cloacae

<400> 1322

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<210> 1323

<211> 864

<212> DNA

<213> Enterobacter cloacae

<400> 1323

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<210> 1324

<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 1324

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<210> 1325

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 1325

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<210> 1326

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 1326

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<210> 1327

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 1327

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501

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<210> 1328

<211> 1602

<212> DNA

<213> Enterobacter cloacae

<400> 1328

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<210> 1329

<211> 1158

<212> DNA

<213> Enterobacter cloacae

<400> 1329

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<210> 1330

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 1330

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<210> 1331

<211> 363

<212> DNA

<213> Enterobacter cloacae

<400> 1331

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<210> 1332

<211> 1770

<212> DNA

<213> Enterobacter cloacae

<400> 1332

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<210> 1333

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 1333

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gtcaccacca	acgacggtac	gccgggcgct	gcgaagata	tcaaacctga	aacctcaat	840
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<210> 1334

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 1334

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<210> 1335

<211> 666

<212> DNA

<213> Enterobacter cloacae

<400> 1335

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ataagcacac	ctttaaggca	ggcgcacttc	ctcgacagc	ttgggcatga	atcatctggc		180
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aatcgaatca	gtcaggaaga	tgctttcaga	tatggtcgtg	ttgattctgg	ccaaaatcct		300
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gatcgcaaca	gtggtgatgg	atatcggtac	cgcgggcgcg	gcctgattca	ggtgacgggg		420
aaagcgaatt	acgcgcgcgt	ggtgaagcag	cttgccgttg	atattcgtgaa	gagcccgga		480
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accaacggac	tggaggacag	gaaagccgcg	ttgaccaaa	ctaagggggg	tttatgttcg		660
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<210> 1336

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 1336

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<210> 1337

<211> 486

<212> DNA

<213> Enterobacter cloacae

<400> 1337

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gatgctatcg	gtgtgatgtc	tcagctggac	gccagagccc	ttgagctgct	ggttgaggct	240
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gcctggaac gtctgcgcgc catgcttggg gagttcggca tgaagccagc cagccgcacg 420
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 gattaa 486

<210> 1338

<211> 1326

<212> DNA

<213> Enterobacter cloacae

<400> 1338

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 tttggtacca gcagcagcgg aaaggtggta acggccgata aagccatcca gctatcggct 180
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<210> 1339

<211> 471

<212> DNA

<213> Enterobacter cloacae

<400> 1339

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 tcggtaattt gtccaaacac gggaaatcgt tattcaagca tcttgggct caagttcttg 180
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 aaccagcaag aagagatatg cacatacgcg gtgcattgca acgcgcggaa atgcccgcac 420
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<210> 1340

<211> 1335

<212> DNA

<213> Enterobacter cloacae

<400> 1340

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<210> 1341

<211> 1419

<212> DNA

<213> Enterobacter cloacae

<400> 1341

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aacatggcgg	ccgtgcgcag	cccggccgca	ttactgattg	gctggggcat	taccgggtgtt	180
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<210> 1342

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 1342

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<210> 1343

<211> 765

<212> DNA

<213> Enterobacter cloacae

<400> 1343

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tcgcgtctgc	gtaaaaaact	gctagataac	gccacggaac	cttaccgcat	taaaaccgta	720
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<210> 1344

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 1344

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<210> 1345

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 1345

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ctgctgaact	acgatgctga	aaacgttcag	catcgatata	aaccccaggc	gcagccgcta	900
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<210> 1346

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 1346

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<210> 1347

<211> 1608

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1581)

<400> 1347

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<210> 1348

<211> 345

<212> DNA

<213> Enterobacter cloacae

<400> 1348

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<210> 1349

<211> 1398

<212> DNA

<213> Enterobacter cloacae

<400> 1349

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1398

<210> 1350

<211> 1716

<212> DNA

<213> Enterobacter cloacae

<400> 1350

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<210> 1351

<211> 939

<212> DNA

<213> Enterobacter cloacae

<400> 1351

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<210> 1352
 <211> 1290
 <212> DNA
 <213> Enterobacter cloacae

<400> 1352
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 ctgaccgaaa tcgatgaact gctgaagcag gactttgtca cccgcagcac caaaattctg 180
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 tttgctttcc cggcgccggt gaagcagggt gagcctgacg ttggctgtct ggagctgttc 300
 caaggcccca cgctggcggt caaagatttc ggcggtcggt ttatggcgca gatgctgacc 360
 cacatcagcg gcgacaaacc ggtgaccatt ctgaccgcca ctacaggcga taccggtgag 420
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<210> 1353
 <211> 969
 <212> DNA
 <213> Enterobacter cloacae

<400> 1353
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<210> 1354
 <211> 537
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1355

<211> 1350

<212> DNA

<213> Enterobacter cloacae

<400> 1355

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<210> 1356

<211> 2466

<212> DNA

<213> Enterobacter cloacae

<400> 1356

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<210> 1357

<211> 750

<212> DNA

<213> Enterobacter cloacae

<400> 1357

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<210> 1358

<211> 1500

<212> DNA

<213> Enterobacter cloacae

<400> 1358

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<210> 1359

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 1359

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<210> 1360

<211> 564

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(19)

<220>

<221>unsure

<222>(20)

<400> 1360

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564

<210> 1361

<211> 906

<212> DNA

<213> Enterobacter cloacae

<400> 1361

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<210> 1362

<211> 1008

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (982)

<400> 1362

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<210> 1363

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<400> 1363

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<210> 1364

<211> 1551

<212> DNA

<213> Enterobacter cloacae

<400> 1364

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<210> 1365

<211> 726

<212> DNA

<213> Enterobacter cloacae

<400> 1365

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agcaccagcc	ggatgaccat	tcagcaggcg	atgcgtcagc	tgattgtcga	agggctggtc	180
tatacccgac	aggggcaggg	cacgttcacc	cgcaaaaatt	tcctccagct	ttccagtggt	240

gatctctccg	gcagcgacta	cttcggggcg	acccaaaacct	gggaacattt	aggcacgggtg	300
agcagtcagg	ttgtgcactt	cgaactgcgc	ttcccgaaacg	agaaagagca	ggcatcgctg	360
atgataaatc	cggatacgcc	gatctatgac	tttatccgtc	tgcgtttact	aaacggtgag	420
ccgatgtctc	tggacgccac	ggtaatgccc	ctcaatctgg	tccccgggtc	gaacaaaacc	480
catcttgaaa	gttcgggtatt	ccggtatgtg	caggagacgc	tggggctgaa	gatcatggga	540
tcgtatcggg	tgggtgcgggc	gctgaagccc	agtgcgctgg	atatgcagca	ccttgtctgc	600
gagccaaccg	actcgggtgct	ggaggtagag	caggtgatct	atctggaaga	tggtacgccg	660
ctggagtacg	cccattgtca	ctatcgctat	gaccatggcg	gcacgttat	cgtgaataac	720
ggataa						726

<210> 1366

<211> 483

<212> DNA

<213> Enterobacter cloacae

<400> 1366

ggaagcacia	tgaaccgtcg	cgcaggtaag	ccaacaacaa	aaaaaacgac	gcaactgggtg	60
aacgttgaag	agcatgtgga	aggcttccgc	caggtgcgcg	aggcgcatcg	ccgggagctg	120
attgatgatt	atgtcgaact	gatctctgat	ctgattcgtg	agggttgaga	agcgcgccag	180
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gtgctgggcg	tcagcccggg	aattgcccgt	cgggatgcgc	aaggatatga	acaccacgtc	420
agcgaagaga	cgctgggtgaa	gttccgcgaa	tttaacgtca	aatacgggtc	ctccgctgaa	480
tga						483

<210> 1367

<211> 1590

<212> DNA

<213> Enterobacter cloacae

<400> 1367

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ccgtggggcg	tggcgattgt	ggtaaccctg	gcgggtgttta	tggaaattct	ggacaccacc	120
atcgtaacg	tggcgctgcc	ccacgtcgcg	gggtcgctct	cggccagcta	tgacgaatcc	180
acctgggtgc	tcaccagcta	cctgggtggcg	aacggcatcg	tgctgccgat	ttcggccttt	240
ctcagccgcg	tgtttggccg	caaacagttc	ttcctgatct	gtattgtgat	gttcaccatc	300
tgctcgttcc	tgtgcggtat	cgccaccgag	ctatggcaaa	tcatacctgt	ccgcgtgatg	360
caggggttct	ttggcgggcg	gttgcaacct	accagcagct	cggtgctact	cgactacttt	420
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ccgcctggg	agaaaaagtc	ggaagagaag	ctcaccgtcg	actggacggg	gatcggcctg	660
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aagagcgagg	ggagtgcagg	agcacactga				1590

<210> 1368

<211> 1398
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1368
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 teggtatcca gcatgcagac ggaaggggcc tggaatgagg gcgggaagg gatgtcgggtg 120
 tatgacattc gggaagccgg tgaaaacatc tctgactgga aagtggcgac cgactcctac 180
 caccggtacc gggaagattt cgacctgatg caggatctgg gcatgaactg ctaccgcttc 240
 cagatctcct ggagccgcac ctgcccgcag ggtgacggcg agttcaacga cgagggcate 300
 gccttttacg accgctttat tgacgatttg ctgcccgcg gtatcgagcc gatggtctgt 360
 ctctaccact tcgatatgcc gctggcgctg gcgcaagagt acaacggctt catcgatgc 420
 cgcgtgggtg acgcctttat ccgctacggc aaaaagatga tcgactgctt cgctgacgg 480
 gtgaagtact ggctgacctt caacgagcag aacattttcc atatgccgga agcttttgc 540
 atttccgggt acatgaaagg tgagcaaacc ctgcgcgagc tgtatgagct tcagcaccat 600
 gcgatgggtg cgcacatgac tctgaccgaa tacctgcacc agactaagcc gggcaagctg 660
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 cagggttaca gccggcggtt aatggcggtg gtggagcagg agggcttcgg cgatatctac 840
 cgcgcagacg atctcgcgct gtttgcgcgc acgaagaacg actttatggc cttcagctac 900
 tacgccagca aaacgctgga cagcgatgcc atcccggaa gcacgcgggt taactattac 960
 ctgctgcacg gcgagaaaaa caatccgtac ctgaaggcca ccgagtggaa ctggcagatc 1020
 gatccgctgg gctttcgcac catcatcacc cgctacgcca acgactggcg gatgcggta 1080
 ttcccgattg agaacgggat tggggtgatt gaggctctgg atggcgta tccggttgag 1140
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 gaggatgggg cagaggtgat gggctatctc ggctgggggt tgattgacat tctcagctcg 1260
 cagggtgaca tgcgcaagcg ctacggcggt gtctacgtca accgtgaaaa tcacgacctg 1320
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 aacggacgcg agatgtaa 1398

<210> 1369
 <211> 1338
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1369
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 gccttcgcca cggtaatgcc gattttcacc ctctgcggtc tggcggtgct ggtgaataac 180
 gtggtcttcc cgtggatttt tgccggcgac acgcttacgc actttaaggt gtggggcgag 240
 gcgattatca acggcacgct gaacatcgcc gcgctgctgc tggcccctat gatcgctgg 300
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 gtgctgattg ggtgctctc aacggaggtc ttcatcgcta tttcgcggct gaaggcgtg 540
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 ctgggggttca tgcgcgctg cgtggtgatg atcccgtgga ccacgcgcgc aattctcagc 1200
 gcctggctgg cgaaggcggg ggaactggcg gcggtagtgg tgcagttggc aatcatcgta 1260
 tttggtgtat tcttctacct gcctttcttc aaagttgccg agcaggtggc tttaaaaaac 1320
 agcgggacag aacactaa 1338

<210> 1370

<211> 1098
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1370
 actatggcag aagatcaaaa cccacctgct gacgagcagg atcaaaacaa taacgagcgc 60
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 gtggcgctgg tctggtggtt ttaaacccgt aacgaagaga ccaccgacga cgcctttacc 180
 gatggcgacg tagtgaccat tgccccaaaa acggcaggct acgtcacaga acttcgcgta 240
 cgggataacc agcgcgtgaa aaaaggggat gtgctggtgg tgatcgatcc gcgtgatacc 300
 accgcccagc gcgatcaggc tcaggcccag cttgggctgg cgtggcgca gctgcatcag 360
 gccaggcgcg agctggcgct ctogaagggtg caatatcccg ccagcgtga tgaagccaaa 420
 gccagggtac ttaaagccca ggccgatatg gccaacgcgc aggcggagta ccgcgctcag 480
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 cgcagcgcg agcggggct ggccagcgcc caggcgcgagc tggaggtggc ggagcaggtc 600
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 gccagagcgc agctggaaac cgcacaacctg aacctctctt ataccgaagt ccgcgccccg 720
 ttcgacggtt tcgtactaa acgcaacgtc cagcccggtg cgtggtgca ggccggcacg 780
 gcgtgttct cgtggtttc ccgaacgtg tgggtggtgg cgaatttcaa ggagtcgcag 840
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 gagctggaag gccatatcga cagcatccag caggcgagcg gctcgcgctt ctccgccttc 960
 ccgtcggaag acgccaccgg taactttgtg aagatcgttc agcgcgtacc ggtgaaaatc 1020
 gtgattgata aagggtgga tccgaacaag ccgtgcccgc tggggtgtgc ggttgaaccg 1080
 aaggtcaccg tggaatga 1098

<210> 1371
 <211> 1062
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1371
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 cgctggcagg acggatcaac accgtgcaca acgcctctca gacaaattat tgccgtgaag 180
 gatttttaacg atgtgaccag cgggactaaa ggcggttggg ttgaggatga acacgcgctc 240
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 ggcaacggct ggcttgacgc ggcagagggt agtcacgggg cggtaataag tgacaacgtc 420
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 cataatagcc tggtgattgc agccaaaggg ctgacaccgc accgtgagca gatcctgcaa 540
 atttatgacc gagccacggt cagccagtcg cgtattgtgc atcaggcgca aatctacggc 600
 gatgccatgg tgacctgggc ctttgtttgag caccgtgccg aggtgttcga tcgcgccatt 660
 cttgagggca acgcgctgaa taacgtctgg gtgtgcgact gcgcaaaagt gtacggcaac 720
 gccgctctgc tggccggtct ggaggatgat gccatcccga ccgtgcggtg cagttcacag 780
 gtcgcggaaa acgcccctcg tgaaggcaac tgcgtcatta aacaccacgt attaataggc 840
 ggcgaggcgt ggttacgcgg cgggcccaate ctgattgatg acaaagtggg tattcagggg 900
 cgggcgcgta tcagcggcga tgtcctgatt gagcatcagg tggaaataac ggacgatgcg 960
 gttatcgagg cgtgaggagg tgaagcatt cagctccggg gagccaaagt gatcaacggc 1020
 gacacgcgga tcaccgcgac gccgtgctg ggggcgctat ag 1062

<210> 1372
 <211> 1254
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1372
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 tttttccgct atctcgccat caccagccag agcgaccgga aagtcaaaac cctgccctcc 120
 accccggggc agcacgacat ggcgcgggag ctggcgaagg agctgaaaac gctgggggta 180
 gatgatattg tgatagatga gttcgccacc gttaccgcg tgaaaaaagg taatgttccc 240
 ggcgcgcgcg ggattggttt tattaccat atcgacaccg tcgacgtcgg tttatccccg 300

gatatttcac	cacaaatatt	aacctttacg	ggggatgac	tctgtctgaa	taaagagaaa	360
gatatttggc	tgcgcgtaaa	agagcaccgc	gaaattctgg	cttatcctga	tgaggagatt	420
attttccagc	acggaaccag	cgtattagcg	gcagataata	aagcggccgt	caccgtggtc	480
atgacggtgc	tggaaaacct	caccgctgag	cacaaccatg	gcgatattgt	ggtggcggtt	540
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gtcgattttg	cctggaccat	cgactgctgc	gagctgggcg	aaattgttta	cgagaacttt	660
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gggcagaacg	aagcgatact	gaaagccaat	attcgtgatt	ttgacaaaga	tggtttcgcc	900
gcccgcgaag	agcacattgc	cgatgtggcg	gcgcaaatag	ccgcgcagca	tcccacggca	960
aacgtggagt	atcgcatatg	ggatacctac	agcaatatca	gcaatgcgat	tggcgaagac	1020
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atccccatgc	gcggtggcac	ggatggggcg	gcctgtcag	ccaaaggcct	gctcaccccg	1140
aactttcttc	ccggcgccca	taacttccac	tcgaagtttg	agtttttacc	gctgtcgtcg	1200
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<210> 1373

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 1373

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cacctgaatc	ttacccatgc	cgcgaaggag	ctttgtctga	cgcagggggc	ggtaagccgt	120
aaaatcgcc	cgctggaaa	ctgggtccgc	ttcccgtgt	tcgagcgcca	tgcccgcggc	180
ctgcgtctct	cctcacagg	aagcgccctg	ctgccggagc	tgcaatctgc	ctttgagcac	240
ctgctgaacg	ttgctgaaca	ggcgcgaacg	caccagaccg	taatccgtct	gaaagcgcc	300
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gacgcggcga	ttgtgtttgg	gacgcacatg	agcgccggcg	atctgctgtt	cgaagaggcc	480
ttaaccccg	tgatgagccc	gctacggggc	ggctctgcgc	tggaaagcact	cactttcctt	540
cacccacgc	gggacaaaac	ggactggacg	ctgtggctgg	cgaacacagc	gggtccgccc	600
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cgcgacgcac	ccggccctga	aaacgggctg	gatgcgtttc	gcgcctgtct	gctcagtcga	840
ggctga						846

<210> 1374

<211> 1524

<212> DNA

<213> Enterobacter cloacae

<400> 1374

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gcactgattg	gttttactga	aggcgatacc	catgtgtggt	gtggcattcc	ctatgcagca	120
ccccctgttg	gcccgtggcg	ctggcgctcc	ccgcgtcccc	ctgcacgctg	ggatggcggt	180
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ggcggcgggc	accccggcca	gttctctgaa	gactgcctgt	atcttaacgt	ctggtcgcca	300
gtggctcgcg	ccgctccgct	tcgggtgatg	gtctggctgc	acggcgagg	atttaccctc	360
ggcgtggtgg	ggctgcctcc	gtataacggc	agggcgctgg	cgaagcgtgg	cacggtgggt	420
gtgacgatca	attacgctct	cggccacctc	ggcttttttg	ctcatccggc	gctggagggg	480
gaggaagagc	gogtggtgca	taacttcgca	ctgctcgatc	agatccaggc	cctggaatgg	540
gtgcgcgata	acattgcgcg	gtttggcggc	gatcctgaga	acatcaccgt	atttggcgag	600
tggcgcgggt	cgcgcagcgt	gctgtcgctg	atggcttccc	cgcttgccgg	aggactgttc	660
cataaagcca	ttgtgcaaa	cgggtacacg	ctgcccgaca	ccccgcgcga	gcaggccatg	720
cataaaggcg	aagcgattgc	cgcctatttc	ggcctgcaca	atgctaccgc	ggaacagctt	780
cgcgcgatcc	cgcctgaggc	gttctggccg	ctgacctcgc	cgttgaatat	cgcctctgcg	840
cccatcggtg	gggattgcgt	tttgccctgag	gccatgctcg	acgttttctt	cgcggcccg	900
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aaacaccacg	tcagcctcga	ctga				1524

<210> 1375

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 1375

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cataacgcca	tcaacctttc	tcaggggggcg	ccgaattttt	cctgcgaccc	aaaactttatc	180
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ccggcgagtg	agggtgctgt	gaccgccagc	gccagcgaag	ggctttactc	agccatcagc	360
gggctggttc	atcctggaga	cgagggtgatc	tatttcgagc	cctcctttga	cagctatgcg	420
ccgattgtcc	gtctgcaagg	agcgacgcgc	attgccatta	aactgacggg	accggatttt	480
gccgtgaact	gggatgaagt	acggggcggt	ataacccac	gcacgcggat	gatcatcgtc	540
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<210> 1376

<211> 1746

<212> DNA

<213> Enterobacter cloacae

<400> 1376

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<210> 1377

<211> 645

<212> DNA

<213> Enterobacter cloacae

<400> 1377

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<210> 1378

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 1378

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<210> 1379

<211> 861

<212> DNA

<213> Enterobacter cloacae

<400> 1379

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<210> 1380

<211> 1008

<212> DNA

<213> Enterobacter cloacae

<400> 1380

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<210> 1381

<211> 1599

<212> DNA

<213> Enterobacter cloacae

<400> 1381

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<210> 1382

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 1382

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<210> 1383

<211> 777

<212> DNA

<213> Enterobacter cloacae

<400> 1383

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<210> 1384

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 1384

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<210> 1385

<211> 1485

<212> DNA

<213> Enterobacter cloacae

<400> 1385

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<210> 1386

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 1386

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<210> 1387

<211> 1365

<212> DNA

<213> Enterobacter cloacae

<400> 1387

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<210> 1388

<211> 3918

<212> DNA

<213> Enterobacter cloacae

<400> 1388

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<210> 1389

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 1389

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<210> 1390

<211> 1293

<212> DNA

<213> Enterobacter cloacae

<400> 1390

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aaaaccgtca	cctatgactt	tgaacgtctg	atggaaggcg	ctaaactgct	gaaatgctca	1260
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<210> 1391

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 1391

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atagacgaag	cgcgcatitga	cgatatttga	aacttctctga	atcagtgggg	caatgaataa	300

<210> 1392

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 1392

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<210> 1393

<211> 282
 <212> DNA
 <213> Enterobacter cloacae

<400> 1393
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<210> 1394
 <211> 669
 <212> DNA
 <213> Enterobacter cloacae

<400> 1394
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 atgggcagct atacgctgga ctgctggca aacggggaat ggcgggatgt taccctaaag 660
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<210> 1395
 <211> 1287
 <212> DNA
 <213> Enterobacter cloacae

<400> 1395
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<210> 1396
 <211> 657

<212> DNA

<213> *Enterobacter cloacae*

<400> 1396

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<210> 1397

<211> 1143

<212> DNA

<213> *Enterobacter cloacae*

<400> 1397

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tga						1143

<210> 1398

<211> 1425

<212> DNA

<213> *Enterobacter cloacae*

<400> 1398

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<210> 1399

<211> 297

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(71)

<220>

<221>unsure

<222>(81)

<400> 1399

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<210> 1400

<211> 1548

<212> DNA

<213> Enterobacter cloacae

<400> 1400

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<210> 1401

<211> 483

<212> DNA

<213> Enterobacter cloacae

<400> 1401

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ctgcgctcgc	cactggttgc	ggaaagcatt	cgtctctggc	agtctacggc	gcgcctgccg	420
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tga						483

<210> 1402

<211> 720

<212> DNA

<213> Enterobacter cloacae

<400> 1402

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<210> 1403

<211> 1464

<212> DNA

<213> Enterobacter cloacae

<400> 1403

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<210> 1404

<211> 1431

<212> DNA

<213> Enterobacter cloacae

<400> 1404

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<210> 1405

<211> 2052

<212> DNA

<213> Enterobacter cloacae

<400> 1405

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tgctccccgg	cttttgagga	cgccttacag	gcactgttgc	ccgcgcggcc	ttgccaggct	180
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<210> 1406

<211> 411

<212> DNA

<213> Enterobacter cloacae

<400> 1406

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aaacgcctgg	cggccctcgc	ccgacagcag	accgtgacgc	tactctacgg	ggcgaaaaac	360
agggagcaga	atcacgcgcg	ggtactggcg	gactggctac	gtaaaactgtg	a	411

<210> 1407

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 1407

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ggcatgggtg	gcagtgttga	tatttcgtca	tcattatcag	acaaggcccc	ccagttagtg	240
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<210> 1408

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 1408

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<210> 1409

<211> 711

<212> DNA

<213> Enterobacter cloacae

<400> 1409

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<211> 1143

<212> DNA

<213> Enterobacter cloacae

<400> 1410

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<210> 1411

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 1411

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<210> 1412

<211> 1197

<212> DNA

<213> Enterobacter cloacae

<400> 1412

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<210> 1413

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 1413

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<210> 1414

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 1414

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<210> 1415

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 1415

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<210> 1416

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 1416

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<210> 1417

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 1417

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<210> 1418

<211> 882

<212> DNA

<213> Enterobacter cloacae

<400> 1418

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<210> 1419

<211> 1803

<212> DNA

<213> Enterobacter cloacae

<400> 1419

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<210> 1420

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 1420

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<210> 1421

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 1421

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<210> 1422

<211> 1086

<212> DNA

<213> Enterobacter cloacae

<400> 1422

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<210> 1423

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 1423

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tgccaggcgc	tgcattctgcc	tcacatgcaa	aatttcgacg	gcattttcga	tgccaaaaatc	180
gatctgatta	acgacgtgat	cctttttctcc	gcgctggctg	aagtaaagcc	gtccgcgctg	240
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<210> 1424

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 1424

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<210> 1425

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 1425

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gccattatta	tgatccgctg	tctggatgtg	ctgatgataa	tgaacacgct	gggtccgcgc	180
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attttccatt	cactgggtgat	gcaaaaaactg	ccggaatgct	tggttctgtt	cctgctattt	480
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<210> 1426

<211> 1542

<212> DNA

<213> Enterobacter cloacae

<400> 1426

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<210> 1427

<211> 1218

<212> DNA

<213> Enterobacter cloacae

<400> 1427

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<210> 1428

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 1428

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<210> 1429

<211> 1137

<212> DNA

<213> Enterobacter cloacae

<400> 1429

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<210> 1430

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 1430

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<210> 1431

<211> 1137

<212> DNA

<213> Enterobacter cloacae

<400> 1431

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<210> 1432

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 1432

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<210> 1433

<211> 2097

<212> DNA

<213> Enterobacter cloacae

<400> 1433

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<210> 1434

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 1434

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<210> 1435

<211> 2187

<212> DNA

<213> Enterobacter cloacae

<400> 1435

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<210> 1436

<211> 1818

<212> DNA

<213> Enterobacter cloacae

<400> 1436

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<210> 1437

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 1437

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<210> 1438

<211> 1134

<212> DNA

<213> Enterobacter cloacae

<400> 1438

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<210> 1439

<211> 678

<212> DNA

<213> Enterobacter cloacae

<400> 1439

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<210> 1440

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 1440

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gatgctcttt	ggtcactgga	cgggcacaaa	agagatcccc	gacccaccgc	taaaacccgc	180
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<210> 1441

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 1441

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<210> 1442

<211> 690

<212> DNA

<213> Enterobacter cloacae

<400> 1442

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<210> 1443

<211> 219

<212> DNA

<213> Enterobacter cloacae

<400> 1443

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aacctcgatt	taatttgcgc	gaacgacgta	tcgctgtcca	cgcaaggatt	taacagcgac	180
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<210> 1444
 <211> 684
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1445
 <211> 918
 <212> DNA
 <213> Enterobacter cloacae

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 gactttatga tgcaggagtt caatcgcgag tcgaacacgc tggcgtctaa gtctatcaat 840
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 atccagaata tcgagtaa 918

<210> 1446
 <211> 579
 <212> DNA
 <213> Enterobacter cloacae

<400> 1446
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<210> 1447
 <211> 645

<212> DNA

<213> *Enterobacter cloacae*

<400> 1447

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<210> 1448

<211> 570

<212> DNA

<213> *Enterobacter cloacae*

<400> 1448

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<210> 1449

<211> 1578

<212> DNA

<213> *Enterobacter cloacae*

<400> 1449

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<210> 1450

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 1450

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ctggtaacgg	cgctgctgga	aggaaaagca	atggatgacg	cgatccgctt	cgcgcgtgcc	180
gccgctgcga	tgcggtgac	gcgtaaaggc	gctcagcctt	ctgttccatg	gcgtaaagag	240
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<210> 1451

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 1451

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gccatcgatg	tggtgatcca	cgcgatggcc	cagcccacgc	tgcacacagc	acgtttgcag	960
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<210> 1452

<211> 1872

<212> DNA

<213> Enterobacter cloacae

<400> 1452

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<210> 1453

<211> 831

<212> DNA

<213> Enterobacter cloacae

<400> 1453

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atgagcccca	acttttttac	cgtaataaac	ctgttcaaca	ttcttcagca	gacctctgtc	180
aacgccatta	tggcggtggg	gatgacgctg	gtgattttga	cctcgggtat	cgatctgtcc	240
gtcggttccc	tgtggccct	caaccggcgcg	atcgcccgct	cgatttgtcg	tattgaggtc	300
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<210> 1454

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 1454

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accctgggac	aacacgactt	cagcgcgggc	gaagggtctt	acacgcatac	gaaagccctt	300
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<210> 1455

<211> 450

<212> DNA

<213> Enterobacter cloacae

<400> 1455

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<210> 1456

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 1456

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ggcgactga	tctcgggttt	cctgaataat	ggtttgaaat	tgtaggtgtg	ttctctctat	480
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cagtaa						546

<210> 1457

<211> 918

<212> DNA

<213> Enterobacter cloacae

<400> 1457

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<210> 1458

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 1458

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<210> 1459

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 1459

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<210> 1460

<211> 1464

<212> DNA

<213> Enterobacter cloacae

<400> 1460

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<210> 1461

<211> 1434

<212> DNA

<213> Enterobacter cloacae

<400> 1461

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<210> 1462

<211> 1587

<212> DNA

<213> Enterobacter cloacae

<400> 1462

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<210> 1463

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 1463

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gccctccagc	aggtaacttat	caacaagatc	caaacaatcg	atgaaattca	gtccactgaa	420
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<210> 1464

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 1464

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<210> 1465

<211> 978

<212> DNA

<213> Enterobacter cloacae

<400> 1465

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<210> 1466

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 1466

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<210> 1467

<211> 1260

<212> DNA

<213> Enterobacter cloacae

<400> 1467

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<210> 1468

<211> 957

<212> DNA

<213> Enterobacter cloacae

<400> 1468

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<210> 1469

<211> 381

<212> DNA

<213> Enterobacter cloacae

<400> 1469

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<210> 1470

<211> 1725

<212> DNA

<213> Enterobacter cloacae

<400> 1470

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<210> 1471

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 1471

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<210> 1472

<211> 1254

<212> DNA

<213> Enterobacter cloacae

<400> 1472

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<210> 1473

<211> 981
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1474
 <211> 1416
 <212> DNA
 <213> Enterobacter cloacae

<400> 1474
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<210> 1475
 <211> 888
 <212> DNA
 <213> Enterobacter cloacae

<400> 1475
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<210> 1476

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 1476

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cagcacctgg	cacggctggg	acggaagtcg	ctgtcgtttc	caaaatcggt	ggagctgcat	480
gacaaagtca	tcgggcatta	tctgaacata	aaacactatc	aataa		525

<210> 1477

<211> 234

<212> DNA

<213> Enterobacter cloacae

<400> 1477

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ctgccggaca	tcagcgctat	ctctgctctc	actgccgtaa	aacatggcag	ttacagttca	180
catacacagc	ctctcaaccc	ggtacgcacc	agaaaatcat	tgatatggcc	atga	234

<210> 1478

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 1478

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<210> 1479

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 1479

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gatatggcca	tgaatggcgt	tggatgccgg	gcaaccgccc	gcattatggg	cgttggcctc	240
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<210> 1480

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 1480

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<210> 1481

<211> 234

<212> DNA

<213> Enterobacter cloacae

<400> 1481

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ctgccggaca	tcagcgctat	ctctgctctc	actgccgtaa	aacatggcaa	ctgcagttca	180
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<210> 1482

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 1482

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gatatggcca	tgaatggcgt	tggatgccgg	gcaaccgccc	gcattatggg	cgttggcctc	240
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<210> 1483

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 1483

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ccggcctttg	aatgggttca	tgtgcagctc	catcagcaaa	aggggatgat	aagtttatca	660
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<210> 1484

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 1484

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<210> 1485

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 1485

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<210> 1486

<211> 1413

<212> DNA

<213> Enterobacter cloacae

<400> 1486

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<210> 1487

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 1487

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<210> 1488

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 1488

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atccatatca	ccacgtcaaa	gggtgacagc	aggctcataa	gacgccccag	cgtcgccata	240
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<210> 1489

<211> 1386

<212> DNA

<213> Enterobacter cloacae

<400> 1489

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<210> 1490

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 1490

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<210> 1491

<211> 1041

<212> DNA

<213> Enterobacter cloacae

<400> 1491

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<210> 1492

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 1492

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<210> 1493

<211> 381

<212> DNA

<213> Enterobacter cloacae

<400> 1493

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<210> 1494

<211> 2184

<212> DNA

<213> Enterobacter cloacae

<400> 1494

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<210> 1495

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 1495

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<210> 1496

<211> 2571

<212> DNA

<213> Enterobacter cloacae

<400> 1496

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<210> 1497

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 1497

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tcggatccgg	tgcttttcag	tctgctgttt	acccagtgc	caacgggaac	gcagagtgtg	420
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acaggctcca	gcatgacca	gaccattgac	gcggacagaa	ccgcgacatt	agctatgctg	600
gcctcggtaa	aatccatgac	ggggggcgcc	acgcgggaa	gcacccgcgc	ggttgtggtg	660
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<210> 1498

<211> 1284

<212> DNA

<213> Enterobacter cloacae

<400> 1498

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1284

<210> 1499

<211> 852

<212> DNA

<213> Enterobacter cloacae

<400> 1499

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ttaatggcct	attacagtat	cggcgaagtg	gcogaacgat	gcggtatcaa	ccccgttacg	180
ttgcgtgcct	ggcagcgccg	ttatggattg	ttgaagccgc	agcgaagcga	agggggccat	240
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<210> 1500

<211> 378

<212> DNA

<213> Enterobacter cloacae

<400> 1500

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ggtttaaacc	agttattcaa	atttcataac	ccgaaagccc	agaacgaatg	cggctgcggc	360
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<210> 1501

<211> 1317

<212> DNA

<213> Enterobacter cloacae

<400> 1501

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cgtattgacg	atgagcagat	gttctacttg	cgctcgcgcg	ggatagacca	gcaggccgcg	1200
caaaagatga	ttattttacgc	ctttgcggtc	gagctgacgg	aagcgctgcc	cgatggcgga	1260
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<210> 1502

<211> 1065

<212> DNA

<213> Enterobacter cloacae

<400> 1502

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<210> 1503

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 1503

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gcagatttgc	cggacagaga	taaattgctg	cgcaactttg	ggcgttgccg	gaactgggaa	180
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gttcgcccgt	ggtttgaaaa	aatggcctta	acccaacacc	tcaccccgtc	ccgatcccag	480
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<210> 1504

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 1504

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aaagagggtt	tccttcacgca	gctgcaaacc	gatgaactgg	cgaaaggcat	caacgaagag	180
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aaagagggtg	aagaggcggt	caatcagctc	ggcgtgcccg	tgccggaagg	caaagagggtg	480

gcggttagatg	ccatttttga	ctccgtctcg	gtggcaacca	cctaccgtga	aaaactggcg	540
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<210> 1505

<211> 702

<212> DNA

<213> *Enterobacter cloacae*

<400> 1505

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gttaacggct	tctgtaagga	cgtgttctct	gaactgcgc	tggaatttgc	cgttgaagcc	660
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<210> 1506

<211> 756

<212> DNA

<213> *Enterobacter cloacae*

<400> 1506

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<210> 1507

<211> 1269

<212> DNA

<213> *Enterobacter cloacae*

<400> 1507

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gcctatctcg	acagtgcggc	cagcgcgcaa	aaaccgaatc	aggtgggtgga	tgccggaagcc	180
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<210> 1508

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 1508

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ccaaaatag						609

<210> 1509

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 1509

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<210> 1510

<211> 990

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(91)

<220>

<221>unsure

<222>(124)

<400> 1510

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<210> 1511

<211> 810

<212> DNA

<213> Enterobacter cloacae

<400> 1511

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aatcgctctc	agagtgtgaa	caccatagta	ggcatccgct	ggaacttccc	tggtaaccaa	780
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<210> 1512

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 1512

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ggcagcgaat	gccagctgtt	aggcacccgc	actggcgagc	aaagcaactg	gatgtcgggg	360
cagcacggcg	aagaggggcg	ctctatgcgc	ggtgcggcca	atgccctgcg	taatcaggct	420
gcggcaatgg	gcggcaacgt	gattttacgg	gtgagcagcc	cgacgcaggg	gatgctgtcc	480
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<210> 1513

<211> 843

<212> DNA

<213> Enterobacter cloacae

<400> 1513

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cagatcgggtg	aagtgatcaa	agtggatacc	cgctccggcg	aatacgtatc	ccgcgtgaag	840
ttaa						843

<210> 1514

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 1514

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cagggttaagt	acaagcactc	cgagaccgcc	agcaaaaccg	atgccgatct	cccgagtgct	1140
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<210> 1515

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 1515

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ctttatgttt	acattgaaat	ttcgattttc	atccaggttg	cccatgtgct	gggcgtcctg	180
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aaagacgatac ggtga

555

<210> 1516

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 1516

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gatggctacg	gcgtgaaatc	cgagaagatc	gacaatgaag	aagtgttgat	catgtccgag	360
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<210> 1517

<211> 219

<212> DNA

<213> Enterobacter cloacae

<400> 1517

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cagatgctgg	cgtgtgggga	actgcctgtt	gatgttgcca	cggcagtggg	ttttgccgat	120
caaagccatc	ttggtcgtcg	gttccagcgt	gcataccgta	tttctccggc	acactaccgc	180
cggttgtgca	caaaccttcc	agacgtttcc	agaaaataa			219

<210> 1518

<211> 1659

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1141)

<400> 1518

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<210> 1519

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 1519

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ctgctgctgg	gggagtctgc	gagcctggcg	cgcacgcgca	gcctcgcggt	aatcgctcgcg	300
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<210> 1520

<211> 1248

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (217)

<400> 1520

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<210> 1521

<211> 1518

<212> DNA

<213> Enterobacter cloacae

<400> 1521

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<210> 1522

<211> 1722

<212> DNA

<213> Enterobacter cloacae

<400> 1522

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<210> 1523

<211> 1041

<212> DNA

<213> Enterobacter cloacae

<400> 1523

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<210> 1524

<211> 627

<212> DNA

<213> Enterobacter cloacae

<400> 1524

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cgtaaaaaata	tcattggactt	gtttatcgat	ggcgcccgcc	gcggctttac	catcgccacc	240
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<210> 1525

<211> 1674

<212> DNA

<213> Enterobacter cloacae

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<221> unsure

<222> (465)

<400> 1525

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<210> 1526

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 1526

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gtccagatgt	tgctcaaaac	caacctgaca	aaccagcagg	cgtctctcga	ctgcctcaag	240
tctcatcatc	cataccaaac	cccgagctg	ctggtgctgc	cagtggtcca	cggcgataac	300
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<210> 1527

<211> 681

<212> DNA

<213> Enterobacter cloacae

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<210> 1528

<211> 966

<212> DNA

<213> Enterobacter cloacae

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<211> 639

<212> DNA

<213> Enterobacter cloacae

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<210> 1530

<211> 711

<212> DNA

<213> Enterobacter cloacae

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<210> 1531

<211> 1191

<212> DNA

<213> Enterobacter cloacae

<400> 1531

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<210> 1532

<211> 474

<212> DNA

<213> Enterobacter cloacae

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<211> 1317

<212> DNA

<213> Enterobacter cloacae

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<210> 1534

<211> 1734

<212> DNA

<213> Enterobacter cloacae

<400> 1534

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<210> 1535

<211> 525

<212> DNA

<213> *Enterobacter cloacae*

<400> 1535

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<210> 1536

<211> 768

<212> DNA

<213> *Enterobacter cloacae*

<400> 1536

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<210> 1537

<211> 1470

<212> DNA

<213> *Enterobacter cloacae*

<400> 1537

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<210> 1538

<211> 1719

<212> DNA

<213> Enterobacter cloacae

<400> 1538

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<210> 1539

<211> 1347

<212> DNA

<213> Enterobacter cloacae

<400> 1539

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<210> 1540

<211> 999

<212> DNA

<213> Enterobacter cloacae

<400> 1540

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<210> 1541

<211> 1296

<212> DNA

<213> Enterobacter cloacae

<400> 1541

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1296

<210> 1542

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 1542

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<210> 1543

<211> 1230

<212> DNA

<213> Enterobacter cloacae

<400> 1543

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<210> 1544

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 1544

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<210> 1545

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 1545

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gccatggagg	atgtccagcc	gctcaaaccg	tgcgcggata	ttcaactggca	gcagagccgc	180
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<210> 1546

<211> 1410

<212> DNA

<213> Enterobacter cloacae

<400> 1546

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1410

<210> 1547

<211> 1602

<212> DNA

<213> Enterobacter cloacae

<400> 1547

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<210> 1548

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 1548

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<210> 1549

<211> 1437

<212> DNA

<213> Enterobacter cloacae

<400> 1549

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<210> 1550

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 1550

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<210> 1551

<211> 837

<212> DNA

<213> Enterobacter cloacae

<400> 1551

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<210> 1552

<211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 1552

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<210> 1553

<211> 894

<212> DNA

<213> Enterobacter cloacae

<400> 1553

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<210> 1554

<211> 1548

<212> DNA

<213> Enterobacter cloacae

<400> 1554

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gaaggtcaat	accttgaaac	cagccatccg	gtcgatcctg	acgcggagct	ggcgggtgtg	180

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<210> 1555

<211> 1107

<212> DNA

<213> Enterobacter cloacae

<400> 1555

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<210> 1556

<211> 369

<212> DNA

<213> Enterobacter cloacae

<400> 1556

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gatacgcccc	tgggcagacc	gggcccagcc	gttgaaatcg	caccgcgtga	tgtattgttt	300

gcctccgata cctgctcata cgcctccggg caagtgtggt gctctgacgg cggtaaccggc 360
gtgctgtaa 369

<210> 1557

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 1557

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aggccgcagg	tcgcgacggt	tttgacagg	atatcgcgga	tgcttgaacc	caccacgttt	300
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<210> 1558

<211> 1434

<212> DNA

<213> Enterobacter cloacae

<400> 1558

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accgtctccc	gtctcgactg	gcctcccggt	tcactggtga	atggccgtag	cgcggaccag	360
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<210> 1559

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 1559

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cggcctgctg	ggtcagggcc	gaagcctgtt	gctcggtaacg	ggaggccagg	tcgatattgc	180
cggaggcaat	ttcctgcgct	gcacgcgtca	cggtttggct	ggcatcgcgc	acctgagaaa	240
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<210> 1560

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 1560

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<210> 1561

<211> 1572

<212> DNA

<213> Enterobacter cloacae

<400> 1561

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<210> 1562
 <211> 1206
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1562
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<210> 1563
 <211> 195
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1563
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 gtcgcggaag aacttcgcgc caccataacc ggcgagcgga tcgtggcgcg ctttgaggat 180
 gaagatgaag aataa 195

<210> 1564
 <211> 1920
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1564
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gacaaccgcc	tggtgatgcg	tccctacggc	gcgaccttcc	tcgccagcct	gccgcccgcg	1860
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<210> 1565

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 1565

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ctggtctgcg	ttgatggccg	catgggggaa	gtctactggg	cggagtacac	ccgtgactga	420
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<210> 1566

<211> 1755

<212> DNA

<213> Enterobacter cloacae

<400> 1566

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<210> 1567

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 1567

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ccgcagctgc	gcaaaagacat	tctggaagtg	atctgcaaat	acgtgcagat	tgaccagaaa	180
atggtcaccg	ttcagctgga	gcaaaaagac	ggggatatatt	cgattctgga	gctaaacgtg	240
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<210> 1568

<211> 966

<212> DNA

<213> Enterobacter cloacae

<400> 1568

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gaaaatgccg	agacgctgat	tgaaaaatac	actgctcagc	ttgagaagct	ggataccagc	180
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gcccgtaaag	tttccacgga	tcagaaactg	aaaatgatgg	atttgatcgg	caaagtgggg	960
aaataa						966

<210> 1569

<211> 615

<212> DNA

<213> Enterobacter cloacae

<400> 1569

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gtcgatgaag	tttcagcggg	gttcgaaatg	ccgctggaag	aggcccttcg	tctgggccgc	480
tatcaccac	tggatattca	ccgcgcgga	cacgatcatc	gggtctggct	gtcgtgggat	540
cagcattatt	ttgtctgggg	catgacggca	ggcatcattc	gtgagctggc	cctgcaaate	600
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<210> 1570

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 1570

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tcttgccgcc	tgacgacgaa	agataacgag	gatacgttta	tgacaattac	gcgcattgat	180
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<210> 1571

<211> 1380

<212> DNA

<213> Enterobacter cloacae

<400> 1571

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<210> 1572

<211> 1407

<212> DNA

<213> Enterobacter cloacae

<400> 1572

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<210> 1573

<211> 1728

<212> DNA

<213> Enterobacter cloacae

<400> 1573

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<210> 1574

<211> 573

<212> DNA

<213> *Enterobacter cloacae*

<400> 1574

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ccgcatttgc	acaaaaccga	ttattacacg	ggcctcaccg	aatctgacct	tgacgctctt	540
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<210> 1575

<211> 792

<212> DNA

<213> *Enterobacter cloacae*

<400> 1575

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<210> 1576

<211> 495

<212> DNA

<213> *Enterobacter cloacae*

<400> 1576

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<210> 1577

<211> 297

<212> DNA

<213> *Enterobacter cloacae*

<400> 1577

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<210> 1578

<211> 1272

<212> DNA

<213> Enterobacter cloacae

<400> 1578

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<210> 1579

<211> 570

<212> DNA

<213> Enterobacter cloacae

<400> 1579

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<210> 1580

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 1580

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<210> 1581

<211> 516

<212> DNA

<213> Enterobacter cloacae

<400> 1581

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<210> 1582

<211> 1500

<212> DNA

<213> Enterobacter cloacae

<400> 1582

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<210> 1583

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 1583

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<210> 1584

<211> 1959

<212> DNA

<213> Enterobacter cloacae

<400> 1584

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<210> 1585

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 1585

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<211> 759

<212> DNA

<213> Enterobacter cloacae

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<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 1587

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<210> 1588

<211> 234

<212> DNA

<213> Enterobacter cloacae

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<210> 1589

<211> 3963

<212> DNA

<213> Enterobacter cloacae

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<210> 1590

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 1590

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<210> 1591

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 1591

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<210> 1592

<211> 213

<212> DNA

<213> Enterobacter cloacae

<400> 1592

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<210> 1593

<211> 1506

<212> DNA

<213> Enterobacter cloacae

<400> 1593

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<210> 1594

<211> 462

<212> DNA

<213> Enterobacter cloacae

<400> 1594

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<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 1595

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<210> 1596

<211> 672

<212> DNA

<213> Enterobacter cloacae

<400> 1596

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<210> 1597

<211> 3141

<212> DNA

<213> Enterobacter cloacae

<400> 1597

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<211> 1164

<212> DNA

<213> Enterobacter cloacae

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<210> 1599

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 1599

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<210> 1600

<211> 576

<212> DNA

<213> Enterobacter cloacae

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<210> 1601
 <211> 1155
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1602
 <211> 1386
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1603
 <211> 1284

<212> DNA

<213> Enterobacter cloacae

<400> 1603

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<210> 1604

<211> 1062

<212> DNA

<213> Enterobacter cloacae

<400> 1604

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<210> 1605

<211> 666

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (596)

<400> 1605

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<210> 1606

<211> 1209

<212> DNA

<213> Enterobacter cloacae

<400> 1606

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<210> 1607

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 1607

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816

<210> 1608

<211> 1326

<212> DNA

<213> Enterobacter cloacae

<400> 1608

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<210> 1609

<211> 4464

<212> DNA

<213> Enterobacter cloacae

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<210> 1610

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 1610

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<210> 1611

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 1611

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<210> 1612

<211> 225

<212> DNA

<213> Enterobacter cloacae

<400> 1612

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tggccgagca	gtataagcat	gtcgaaatgg	cgcgcgaact	gggcgagcac	aatggtgctg	180
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<210> 1613

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 1613

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acgtcggtgg	cctgcgtggg	ttcgccccgc	agccaccgga	gtcattaccg	ggcacggctg	300
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<210> 1614

<211> 1908

<212> DNA

<213> Enterobacter cloacae

<400> 1614

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<210> 1615

<211> 693

<212> DNA

<213> Enterobacter cloacae

<400> 1615

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<210> 1616

<211> 1218

<212> DNA

<213> Enterobacter cloacae

<400> 1616

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<210> 1617

<211> 1392

<212> DNA

<213> Enterobacter cloacae

<400> 1617

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<210> 1618

<211> 1586

<212> DNA

<213> Enterobacter cloacae

<400> 1618

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<210> 1619

<211> 1275

<212> DNA

<213> Enterobacter cloacae

<400> 1619

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<210> 1620

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 1620

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cgcgccaaact	ccagcgttac	gcgcttaaa	ctttccgcgc	cggtgcgcag	gatcgccctg	180
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tcgcccaccg	tctcgccgcg	tccggtgacg	atgttaaaca	cgcccggcgg	cagcgcgggc	300
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ctgttccacg	gcgtaatcag	cccggccacg	ccgagcggcg	tcattctgcac	cgttgcgcca	480
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<210> 1621

<211> 906

<212> DNA

<213> Enterobacter cloacae

<400> 1621

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<210> 1622

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 1622

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aacgcctgga	accgcctggg	cattacctcc	cgcattggagc	cgggctcgct	ggatgcggcg	1020
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<210> 1623

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 1623

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<210> 1624

<211> 744

<212> DNA

<213> Enterobacter cloacae

<400> 1624

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cggtttcac	ttggcggtga	ggcgggcgct	gcgctgctta	tccacatgga	aagcaaaggc	660
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<210> 1625

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 1625

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cgcgtattc	tgagccagat	gagcgacgag	cagctcaagg	acgtcgggtt	atcgcgatat	180
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<210> 1626

<211> 1449

<212> DNA

<213> Enterobacter cloacae

<400> 1626

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<210> 1627

<211> 399

<212> DNA

<213> Enterobacter cloacae

<400> 1627

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atcgatatcg	aacggttcca	gagcctgacg	accgaaggca	aaatcctctc	cctttcctgg	240
tggcgggatg	aagaggccgt	ccgcgcgtgg	aagcagaacg	tctttcatca	ggcggcgacg	300
gccgaaggac	gggcgttgat	tttctctttc	taccgtattc	gcgtggcgca	gctggtgcgg	360
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<210> 1628

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<400> 1628

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gactccaccg	tgatgcgcgt	ggtgaccccg	gtgtctgccc	gcgtctccgg	gtatgtggcg	180
gcggtacatg	tccataacaa	tagccagggt	aagaaaggcg	atctgctgtt	tgagctcgac	240
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<210> 1629

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 1629

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<210> 1630

<211> 1170

<212> DNA

<213> Enterobacter cloacae

<400> 1630

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<210> 1631

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 1631

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gcggacgggc	aggggacgcc	atgcgggacg	atccattttc	gcgatctgct	ggcgggggag	1080
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<210> 1632

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 1632

gccagaccgc	tatacccgaa	ttaccctaacg	attgcgcgtg	gaggagaacg	catgttaaga	60
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cagagtata	tcgaggttgt	gggggaatgt	gccaatgcca	ttgaaggcat	cggcgcggtg	180
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gagatccgcc	tggaaataaa	cggccaggcc	gagctgggtg	tacgtgccgg	gcaaaccgtt	720
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<210> 1633

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 1633

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gtggcgctgg	tggtgatgga	cgccttcggc	aaatataccc	acttcgcgga	tgccagccgc	180
ctgcgtacct	ggattgaaac	cgggaaagtg	catccggctg	cggcttcagc	gctggcgat	240
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<210> 1634

<211> 2391

<212> DNA

<213> Enterobacter cloacae

<400> 1634

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cgcaagatgc	aggatcagg	gatggagctg	agccgcctga	aaatccact	gttcttcgct	420
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<210> 1635

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 1635

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<210> 1636

<211> 1704

<212> DNA

<213> Enterobacter cloacae

<400> 1636

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<210> 1637

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 1637

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cgcattcttg	cgctctccga	catggaatcc	acgtccgcgc	ggttcgacac	ctggatgact	180
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cgggtgaata	acaacacggt	gctgaaaaaa	ctgcgtattg	ctttctgcct	gaaaactgac	360
gacattcttg	cgatcatgac	cgagcagaaa	tttcgctgtg	cgatgccgga	aatcacccgc	420
atgatgcgcg	cgccggatca	taagaattac	cgcgagtgtg	gggatcaatt	tctgcgttat	480
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<210> 1638

<211> 1182

<212> DNA

<213> Enterobacter cloacae

<400> 1638

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<210> 1639

<211> 825

<212> DNA

<213> *Enterobacter cloacae*

<400> 1639

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<210> 1640

<211> 1923

<212> DNA

<213> *Enterobacter cloacae*

<400> 1640

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<210> 1641

<211> 636
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1642
 <211> 900
 <212> DNA
 <213> Enterobacter cloacae

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 <211> 417
 <212> DNA
 <213> Enterobacter cloacae

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 <212> DNA
 <213> Enterobacter cloacae

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<210> 1645

<211> 1044

<212> DNA

<213> Enterobacter cloacae

<400> 1645

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<210> 1646

<211> 1842

<212> DNA

<213> Enterobacter cloacae

<400> 1646

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<210> 1647

<211> 417

<212> DNA

<213> Enterobacter cloacae

<400> 1647

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<210> 1648

<211> 3483

<212> DNA

<213> Enterobacter cloacae

<400> 1648

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<211> 810

<212> DNA

<213> Enterobacter cloacae

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<210> 1650
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 <212> DNA
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<210> 1651
 <211> 981
 <212> DNA
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 gacaccaacc tgcctggaagc gcttaaggcc ggtttgcgcg actgctccgc cgtggcgctg 900
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<210> 1652
 <211> 1563
 <212> DNA
 <213> Enterobacter cloacae

<400> 1652
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 ccgttttata tcgtttccgc tctgtttctc tttatcccggt ttgcgctgat gatggcggag 240
 atgggctcgg cgtaccggaa agaagagggt ggcattctatt cgtggatgaa caacagcgtc 300
 ggtccgcgtt atgcgtttat cggtaagctt atgtggtttt catcctacgt cgtctggatg 360
 gtcagcacgg cggccaaggt ctgggtgccc ttctcaacgt ttctcttcgc tgcggataaa 420

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<210> 1653

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 1653

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tgtcataggg	gtgaccaact	ggatttaatt	aggcgggcta	ttagtaccgg	gttggtatta	180
aataatttat	ttcctgactt	ggcaaatatt	ataaatggtt	taaacgaaaag	attaacactt	240
gcagatctta	ataggtttct	gaatgatgga	aatactatag	atactgaacc	taagcctcct	300
attaatgtat	tgctagagaa	tgtcttagat	caaaagttta	aggagtattt	aacacctcta	360
caattagata	attcaaagca	ggattctgtt	tctgtaaaag	aaaccttcct	tgtacaaaag	420
gaacatgcct	gcttttggtg	gaagattgaa	aatgagggaa	gcgataacct	tataccatct	480
gaaagcccac	tttcttcagg	tgcatccaaa	atttcaaaaag	aaaagtccat	ttcctctgtg	540
gtgccagtgc	tagaaaaagt	atcggatgaa	aatcaaaccg	cctccataag	cataaaatct	600
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<210> 1654

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 1654

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gatgaacctc	acgaatgtgc	cgtgttactg	caacaaatag	ccgccatacg	tggtgccgtg	180
aatggtttat	tgctggaagt	gattaaagga	catttgactg	aacatattgt	tcatgaaagt	240
gaagaacaga	aacgagaaga	agacctggac	gttgtgctga	aggttcttga	ttcttacatc	300
aagtga						306

<210> 1655

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 1655

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gataaagaaa	aaagcctgaa	cgatgctacc	tcgccagagg	tgcagaatga	catccgcagc	180

gaatccacag	aaaaatcaaa	ggaaatgggt	cgttcaagg	actcatctat	tgcgatgac	240
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gatctgagct	tcaaagttca	ctggctcaga	aacgctgttg	gcggctcggt	tgcaaggcca	360
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<210> 1656

<211> 765

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (59)

<400> 1656

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gctttaggg	aaacgaatat	tgaataatatt	cagagaaaaa	aagataatct	gatgaaacca	180
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tcaagtttg	taattgatct	tgggtggtact	actcttgatg	ttgcaagtat	tactgggcaa	360
ttagaacaga	tttcgaaagt	aaaagggttt	gaccgtattg	gttggttctat	tgtttacgat	420
gagatcagca	ggtatcttga	atctgagaaa	ctgaatacga	gtaatgctta	cattcatcat	480
cttggttgata	atcgtcattga	taaaacagct	ttgaagggtg	cagaggacaa	gcgtgacgg	540
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gaaacagcta	ttcgtaaaaca	ttttgaaacg	gctaaagtta	tcatggtaga	caatccgcag	720
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<210> 1657

<211> 1416

<212> DNA

<213> Enterobacter cloacae

<400> 1657

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gccgcgggtg	tgettacgg	atggtggtta	tcaagtttta	tcctgattag	cacccttaat	120
ggctattttc	ataatcagga	ccgcgatttt	ctgacaggta	aacttcagct	caccgaagag	180
tttcttaaaa	cagagacgtt	ccggaacaaa	acggatatta	agtcattatc	agaaaaata	240
aacgatgcga	tggttagggc	caatggttta	ttcatttcta	taaaaaacat	ggaaaatgaa	300
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gccacggata	ctgggtatca	caccctgttt	atggataagc	tcagtacctg	gctgttctgg	540
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attacaaggt	cgatcattca	tgctcatggc	ggcgaactgt	cagcagaaca	gcaggggcgg	1380
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<210> 1658

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 1658

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gcgtcggaac	tgtgcggtct	ctctctcttc	accagcagaa	ttatgcagcc	caacgcattt	180
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acgtggaaaa	ggctctttga	agaaataggt	atggaccggt	actggaacca	taagcaaaaa	300
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ggaaacgttc	atatttgtat	cgacagtatc	tcgcttctga	atgctctgaa	cgatcttata	780
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<210> 1659

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 1659

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ctcatcgagc	gttttctatga	tgatgttaaa	ggtattaccc	ttatcgtagc	tcttcagatt	180
ttttacgttt	tccagaacaa	aaattgcagg	ttgttttgcc	cggatgatcc	tggccacatc	240
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tttactgaca	cggcgatgc	tgaatggctg	gcatggaaat	cccgaagaa	gaacatcatg	360
atccgggata	gaggcatcga	taaatttgta	tgctcgtca	tcagtaacct	cgggcccgtt	420
gctaagagtg	atgtcacgga	tgtctga				447

<210> 1660

<211> 255

<212> DNA

<213> Enterobacter cloacae

<400> 1660

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ctgccttca	ccgaagacct	tcagcccgggt	ggaatcaatt	accagggtgtg	cgattttcacc	180
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<210> 1661
 <211> 468
 <212> DNA
 <213> Enterobacter cloacae

<400> 1661
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 gtaaataatg cccaggcacc cgcccatcag atgcagtcaa cctctgaaaa aagcgtgtgt 180
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 gagcatgaaa aagccgctgt tgtgcacgag aaggcgaata atggtcagtc ttccgttatt 420
 catcagcagc aggctgaaaa gcacgcgagc cagatcacc cagaattaa 468

<210> 1662
 <211> 585
 <212> DNA
 <213> Enterobacter cloacae

<400> 1662
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 gtggcgctct gggggaactc aacaactttt gaggcaaagg tggtaagat tgttgacggt 180
 gacaccataa ctgcgttgga tgcacaaaac acaaccatca aaatacggat gtatggtata 240
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 tgggttttatc ggttcgaaga taacgccatt gtccctggct atatcaaata tgaatccgca 480
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<210> 1663
 <211> 1536
 <212> DNA
 <213> Enterobacter cloacae

<400> 1663
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 ggtatctctg tocgatctgg tcgccggatc gagaaagatc agtggtcgaa agccggtgaa 180
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 cgtggtctgt ctgactttac tgagctgaaa ggcgtagtgt tcaccatcgc cggtaagtgt 480
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 gtgctgggtg gggagagctt ccttgccctg gctgaagggt tgcaggaggc gctcggtcag 600
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<210> 1664

<211> 1101

<212> DNA

<213> Enterobacter cloacae

<400> 1664

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caagccgtat	tggaacttca	ccggagtcgt	cagagcttca	tcaaacagcg	aaccgcacaa	480
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<210> 1665

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 1665

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gatggtcagg	ttgcggaggc	tatggccctg	gtacgagcgc	tgaacaaaat	gacgaaagca	960
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<210> 1666

<211> 1482

<212> DNA

<213> Enterobacter cloacae

<400> 1666

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<210> 1667

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 1667

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<210> 1668

<211> 1131

<212> DNA

<213> Enterobacter cloacae

<400> 1668

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acaatgatgg	cagcattcat	cattgctata	aaaggcaccg	tacgtcaggc	cgtgatgctg	180
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<210> 1669

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 1669

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gccgcatcca	ttctctgtcg	actcattggc	atgccgccca	tcattatcgg	catgacgggtg	180
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gggtaa						1026

<210> 1670

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 1670

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<210> 1671

<211> 576

<212> DNA

<213> Enterobacter cloacae

<400> 1671

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<210> 1672

<211> 732

<212> DNA

<213> Enterobacter cloacae

<400> 1672

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<210> 1673

<211> 417

<212> DNA

<213> Enterobacter cloacae

<400> 1673

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gaagacacta	tgcagctcaa	tatcaccgga	cataacgtcg	agattactga	ggctttacgc	180
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ggaggggaac	tccatgccag	tgcggaagg	caagacatgt	acgcggctat	cgacggcttg	360
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<210> 1674

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 1674

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gaaatcacca	ataagctggg	tatgcatgcg	cgccggcgca	tgaagctgtt	tgagctgatg	180
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<210> 1675

<211> 891

<212> DNA

<213> Enterobacter cloacae

<400> 1675

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<210> 1676

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 1676

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<210> 1677

<211> 1062

<212> DNA

<213> Enterobacter cloacae

<400> 1677

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<210> 1678

<211> 507

<212> DNA

<213> Enterobacter cloacae

<400> 1678

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<210> 1679

<211> 900

<212> DNA

<213> Enterobacter cloacae

<400> 1679

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<210> 1680

<211> 594

<212> DNA

<213> Enterobacter cloacae

<400> 1680

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cagatcaacc	tggtcaccca	ggatgtcacc	tcgcaggatt	tagtcacct	gtatggcaca	480
acatttaatt	ccagcggttt	aagaatgcgc	gggaacttac	gcagcaaaaa	cgccgagctg	540
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<210> 1681

<211> 1473

<212> DNA

<213> Enterobacter cloacae

<400> 1681

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gatcagggtg	ttatggtggc	acgtcgtaet	gtcgcgaagt	atcgagagtc	tttatccatt	1440
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<210> 1682

<211> 833

<212> DNA

<213> Enterobacter cloacae

<400> 1682

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ggcggttatc	ccaggttgat	gaatctgacc	tgacgaaccc	gaaacagatc	accggttcgc	420
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cgatgggggt	ccgcgtggta	actggtatca	gctttgggtt	cgtgttctac	gtcctcgatc	720
agattttcgg	tccgctgaca	ctggtgtatg	gcattccgcc	aattatcggc	gcgctgttgc	780
cgagcgccag	tttcttccgt	atcagcctct	ggatgctgct	aaaacgctcc	tga	833

<210> 1683

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 1683

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tacctgcccc	tgacggcgat	gatcaagaag	ttctgggata	cctgtgatga	agaggagagc	120
accatgacgt	ctgttgatag	cgccaaagcc	caaacgatac	tggataccgc	catgctggag	180
cagtatatcg	atctggtagg	accaaaactg	atcacccgatg	gcctggccgt	gttcgaaaaa	240
atgatgcggg	gctatctgaa	cgtgctcgaa	tccaacctga	cggcgcgtga	ccagaagggc	300
atcgtcgaag	agggacataa	aatcaaaggc	gcggcaggat	cggtcggggt	acgtcatctc	360
cagcaactgg	gccaacagat	tcagtgcct	gatttacctg	cctgggaaga	taatgtaggt	420
gattgggtcg	aagagatgaa	acaggagtgg	caaaacgatg	tggcagtgct	gaaagcctgg	480
gtagatgcca	gaaaaaaatg	a				501

<210> 1684

<211> 759
 <212> DNA
 <213> Enterobacter cloacae

<400> 1684
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 attgcgctgt tcagcatcct gcccgctccg ttctccgcgc tgatggcaga gggcgagatt 180
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 gaaatctccc cgtggatggg gctggcggtc attgcggcag aagatcagaa attcccgag 300
 cactgggggt ttgacgtggc ggctattgag aaggcgctgg atcataatga acgtcatgaa 360
 aaccgcgtcc cggcgcgctc gacgctttct cagcagacgg taaaaaacct gttcttatgg 420
 gacggctgca gctgggtgag aaaagggtc gaggcgggc tgacgctggg cgtcgagacg 480
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<210> 1685
 <211> 798
 <212> DNA
 <213> Enterobacter cloacae

<400> 1685
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 gagttccgca agcatgcgcc gttactggtg cggcagctct ataacgtcgg cgtgctgtcg 180
 atgcttatca tcacgtgtgc gggtttgttt attggcatgg tgctgggggt gcagggggtat 240
 ctggtactga caacctacag cgcggaaaacc agccttgga tgctgggtgg gctctcgtcg 300
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 acgcgtactg togtacattc gtcgctggcc gtttttaggtc tggattttgt gctcaccgca 780
 ctgatgtttg ggaattga 798

<210> 1686
 <211> 357
 <212> DNA
 <213> Enterobacter cloacae

<400> 1686
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 ctggatcagg atctgcttaa ccgcgtgtgg gacgctcgcc ataacgcgat gcaggcgctg 180
 acgctgattg atctccatgg cgtcaacggg gtagataacc ccggtatcgc cctgctggcg 240
 cacctggtgg ccacgggcaa aaagcagggg agtagcgtca ccctgacggg ggtaagcgat 300
 aacgtgatta cocttgcaca gctttacaat ttgccgaag acgtattacc tcgctaa 357

<210> 1687
 <211> 381
 <212> DNA
 <213> Enterobacter cloacae

<400> 1687
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gaccccatgg	aaaataatga	aatccagact	gtgctgatga	atgcactctc	ccttcaggaa	180
gccacgtct	ctggcgatgg	cagtcacttc	caggttattg	ctgtgggtga	gatgttcgac	240
ggaatgagtc	gcgtgaagaa	acagcaggct	gtgtacgcgc	cgctgatgga	atacattgcg	300
gataaccgca	tccacgcct	gtcgattaaa	gcgttcaccc	cacaggagtg	ggcacgcgat	360
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<210> 1688

<211> 702

<212> DNA

<213> Enterobacter cloacae

<400> 1688

tcagaatttt	taatgtgctt	cagcgagttg	cttagaagga	tcgtcagaat	gaagaaagtg	60
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acgctgctgg	cattatcgcg	gcagggggca	gacgttatct	gcttcgcgcc	ggataaaaact	180
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gaacttgatg	cgctcatcgt	gccggggcgc	tttggcgccg	caaaaaacct	gagcacgttt	360
gcaacagaag	gocggcgctg	ccatgtcgat	cccgatttga	aagcgctatc	gctggcgatg	420
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aaaatcatca	ccacgccggc	gtatatgtcg	gocgagaata	tcgctgaggc	tgccgcaggc	660
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<210> 1689

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 1689

tgtttgggaa	ttgagttcat	gcaaacgaga	aaaaatgaaa	tttgggttgg	cgtgtttctg	60
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cgcgcgcgag	cgacgtaccg	tatctacgct	actttcgata	acatcggcgc	cctgaaagcg	180
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aaagggggatg	ataaaaagtc	tgacgatgcc	cctgcgcaga	gtgaagacca	caccaacgct	540
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<210> 1690

<211> 654

<212> DNA

<213> Enterobacter cloacae

<400> 1690

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gcgaagaaaa	ccttcgaccg	tcttaaaaac	gaacagccaa	aaatccgttc	taaccctgat	180
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<210> 1691

<211> 1977
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1691

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aacgtgctga	aagataaaaa	agagtacctc	gaggccggaa	tggacgatgt	gctcagcaag	1920
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<210> 1692
 <211> 813
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1692

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<210> 1693

<211> 1305

<212> DNA

<213> *Enterobacter cloacae*

<400> 1693

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ctgcccattc	ttttcgctgc	gctgctcgca	gaagagccgg	tagagatoca	gaacgtaccg	180
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<210> 1694

<211> 1020

<212> DNA

<213> *Enterobacter cloacae*

<400> 1694

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cgttcacgcg	catatgcctg	gggcgcgtgc	cattatttca	ttatcgaaca	tgaccaatg	180
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gatattgaca	gcgtgggaag	cttcaaggct	gactacaaac	gtcttaagg	tgagattagt	360
goccatatcg	cctcaaaggc	ggcagagggtg	gagatccgcg	tactggactc	gatgtccgac	420
aaagaatgta	aagatgttgc	ctcgggtggca	tgtactgttc	gccgtgactt	acgtacgcag	480
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catatccagg	caatcaacga	agacgtcacc	cgttcacagg	cggaaccacg	ctgccctgga	960
aagcttcttc	tgaaaatgac	cagtcattgag	gaagtgcggg	actcactgag	cacctgttag	1020

<210> 1695

<211> 201

<212> DNA

<213> *Enterobacter cloacae*

<400> 1695

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cagaaagtag	tcgtaagaac	ggtgatcact	gtccgctttg	tgccagaagc	ggacttttta	120
aaaatattgc	gtgcccacaa	attgggcgca	ggtcacatca	agtaccctca	gaattataga	180

gaataacctga aattttttgta g

201

<210> 1696

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 1696

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cgagctgggt	gcctcaatga	tgggtggcat	gaccaagggt	ccttgagtca	tcatgacgcc	180
tgtctcggcc	agccagcgat	tgatgggtct	gaacaattgg	cgggccagtt	gatgctgctc	240
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<210> 1697

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 1697

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tctggtctga	cggcgcttac	tgtgtgaatt	actgtcggcg	aaggtaagtt	gatgactcat	180
gatgaaccct	gttccatggc	tccagatgac	aaacatgac	tcatatcagg	gacttggttc	240
caccttcctt	ag					252

<210> 1698

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 1698

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gaacaagctg	cggcaccgat	tggcattttc	attcggcagg	ttaaactgtc	ggtgcaacgg	180
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gcccgaattt	atcagcgccg	gatgcggcgc	ccatcctacg	gtgaactcat	ccagattgat	480
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cacacgtgcg	ataaagacac	tgggcatcga	gccaatccat	gccaacagcc	cgcaggcaaa	780
agggcgggta	gagcgtgcc	atcagacact	gcaggacagg	ctggtcaaag	aaatgcggct	840
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<210> 1699

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 1699

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gcggcgcccc	atctgacctg	gtcgatggat	ttcgtcatgg	acgcactttc	caccgggtcg	180
aggatcaagt	gtcttacctg	cgtcgatgat	ttcacaaagg	aatgcctgac	ggtcactggt	240
gccttttggg	tttcaggcgt	tcagggtcag	cgtattcttg	acagcattgc	actgttttca	300
ggctatccgg	cgacgataag	aactgaccag	gggcgggagt	tcacttgccg	tgcactggat	360
caatgggcct	ttgagcatgg	tgttgagttg	cgcttaatcc	agccgggcaa	gccaacgcag	420

aacggatttta	ttgagagctt	taacggacga	tttcgcgatg	aatgtttgaa	tgagcaactgg	480
ttcagcgata	tcgttcacgc	caggaaaatt	attaatgact	ggcggcagga	ttataacgaa	540
tgccgcccgc	actccacgct	gaattatcag	acaccgtctg	aatttgacgc	gggctggaga	600
aagggtcatt	ctgagaatga	agattccgac	gttactaact	ga		642

<210> 1700

<211> 1053

<212> DNA

<213> Enterobacter cloacae

<400> 1700

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ggtggggaaa	tccttaatcg	agttcaacaa	tgtaccagtt	acactttggc	attaacaggg	120
accccatgga	gaacggataa	taatccata	gtgctttcaa	attacactga	tccgcaaggg	180
aagatctgtt	gtgactatgt	atatggtcta	cacgaggcta	ttgtcgatgg	ggtttgtcgt	240
aaacctaata	ttgctcttat	aaatagtaat	aattttacttt	attcatcagg	ggaagttggt	300
cagcattttg	attccatagc	aggtttcctg	agtgaaccca	tcacttcgta	tcaatcaata	360
atttggcatc	cagatgcaat	gaagtattta	ctcaaatctg	gatgtaaaaa	actttgtgaa	420
atacgtaaag	ttaattctga	cgcgggtggg	ttagtgtgctg	cttcttctgt	cgaacatgca	480
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gttagcgttg	gtatgattag	tgagggcaca	gatatcccta	gactacaggt	gtgctgccac	660
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aatggatatgt	caaaaatcgg	agagtttaat	ttgaaaatga	atttcagtga	aataactata	960
tcgccacctg	ctgtttttaga	caaaaacaaa	caactaaaca	tgggttctct	atatcaacag	1020
gtgatcgacg	cattttttatt	ttcagttatt	tga			1053

<210> 1701

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 1701

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gcgcgaggag	ctggccgagg	tggatgtgga	ctggctgacg	gccgagcgcc	ccggcaaggt	120
aagaaccttg	aaacagcatc	cacgcaagaa	caaaacggcc	atcaacatcg	aatacatgaa	180
agccagcatc	cgggccaagg	tggagcacc	atttcgcatc	atcaagcgac	agttcggctt	240
cgtgaaagcc	agatacaagg	ggttgctgaa	aaacgataa			279

<210> 1702

<211> 690

<212> DNA

<213> Enterobacter cloacae

<400> 1702

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atcgagccaa	tccatgccaa	cagcccgcag	gcaaaagggc	gggtagagcg	tgccaatcag	120
acactgcagg	acaggctggt	caaagaaatg	cggcttcagg	gtatcagtga	tattgaaaca	180
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ccttggtctca	cgcgccgcac	gcaaagtaat	cagcaagtga	agccccctaa	attaccagaa	660
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<210> 1703

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 1703

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tggaaaatga	ccggttcggt	cggctctgcta	tctgatgcc	tccaatccgt	agttaacctc	180
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catgcatatg	ggcacggcaa	agccgaatat	ttctcgagt	ctttcgaagg	atttctgac	300
ctattggcgg	cagccagtat	gcctataacc	gcagttgagc	ggatgttaac	tccacagccg	360
cttgaggaga	ttgggtctcg	attactgggt	tcaacagtcg	catcaatcct	taattttgtg	420
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aatgatatcc	gcaccgcact	gccttttata	catatcacca	ctcatgtgga	accgttgga	900
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<210> 1704

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 1704

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attgaagcaa	acaagctcgg	tggtatgcct	gattgttaca	agattaagct	ccggtcttca	180
ggctatcgcc	ttgtatacca	ggttatagac	gagaaagttg	tcgttttcgt	gattttctgt	240
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<210> 1705

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 1705

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accttcgcgg	acagtgaatt	cagcagtaag	cgccgtcaga	ccagaaaaga	gattttcttg	120
tcccgatagg	agcagattct	gccatggcaa	aacatgggtg	aagtcacga	gcggttttac	180
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ttcggcttcg	tgaaagccag	atacaagggg	ttgctgaaaa	acgataacca	actggcgatg	960
ttattcacgc	tgccaacct	gtttcggggc	gaccaaata	tacgtcagtg	ggagagatct	1020
cactaa						1026

<210> 1706

<211> 1374

<212> DNA

<213> Enterobacter cloacae

<400> 1706

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aaaaaggagt	tggatgatgac	tgtgactaat	caattttgctg	cgacacgttg	tctggactgg	180
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<210> 1707

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 1707

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gacaatgaac	gcttgccgtt	caaacagaca	ctcctgagtg	atgaagatgc	tgaacttgtg	180
gagatagtga	aagaacgact	tcgtaatcct	aagccagtag	gtgtgacgct	ggatgaactc	240
tga						243

<210> 1708

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 1708

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atccggtaa						189

<210> 1709

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<400> 1709

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cattcgcgtg	tgatccgcga	tctggatgcg	tttaagaaag	aagcggatgt	aattatctcc	1140
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<210> 1710

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 1710

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tccacgccag	ccaccagtgt	tttaagcagc	gggatttggc	gcttcgcgcg	atctttcgcg	420
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<210> 1711

<211> 351

<212> DNA

<213> Enterobacter cloacae

<400> 1711

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<210> 1712

<211> 1143

<212> DNA

<213> Enterobacter cloacae

<400> 1712

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agcaatactc	gggatagcgt	tgtaaacgtt	gataaattga	cctatgcgcg	taactctgaa	180
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tcgaatgtga	aaagcggcgc	ctataagagc	tggattgagc	agaattatgg	ggagcgtaag	1140
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<210> 1713

<211> 882

<212> DNA

<213> Enterobacter cloacae

<400> 1713

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<210> 1714

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 1714

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<210> 1715

<211> 1449

<212> DNA

<213> Enterobacter cloacae

<400> 1715

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<210> 1716

<211> 1143

<212> DNA

<213> Enterobacter cloacae

<400> 1716

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aaacaagatt	atttttgccc	tttttcatct	gttagggatt	gtatgacgca	aaacaacaat	180
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<210> 1717

<211> 984

<212> DNA

<213> Enterobacter cloacae

<400> 1717

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aaatcaggcc	gtttaagcga	cgattcacgc	gaactgctgg	cccgctgcgg	gattaaaatc	180
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<210> 1718

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 1718

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<210> 1719

<211> 933

<212> DNA

<213> Enterobacter cloacae

<400> 1719

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<210> 1720

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 1720

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acgccctatc	agtctgcgcg	tcgtcttggc	ggcaacggcg	atgtctggct	gaatgccaac	180
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<210> 1721

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 1721

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<210> 1722

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 1722

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caccaaacag	cgctgtgga	cgaaagggga	aacctcggtt	cacttcctga	atgtgggtcag	180
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ctgccacaaa	ggcaccagca	gctgcttcgg	cgagacgagc	caccagtggc	tgcttcctcta	300
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<210> 1723

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<400> 1723

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cacaagctgg	acttagcgga	ccgcaagggc	atggccgtgc	tcttcgcca	tgaaaaattt	240
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<210> 1724

<211> 1326

<212> DNA

<213> Enterobacter cloacae

<400> 1724

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<210> 1725

<211> 621

<212> DNA

<213> *Enterobacter cloacae*

<400> 1725

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acctacacca tcgccagtg caattacggc gaggcgttca ccgccgccgt gcagaaagat 540
aacttttacg gcgtgcagtt tcacccggaa cgctccgggtg ccgccgggtg gcaactgctg 600
aaaaatttcc tggagatgtg a

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<210> 1726

<211> 654

<212> DNA

<213> *Enterobacter cloacae*

<400> 1726

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gaggagctga cgaacgaagc gtcggattta atgtatcacc tgctggtact gcttcaggat 600
caggagctgg atttaacgac ggtgattgag aatttgcgga aacggcataa ataa 654

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<210> 1727

<211> 531

<212> DNA

<213> *Enterobacter cloacae*

<400> 1727

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gtatcagtc tttggtacct tttgaacagc gccagcactt tagagcggtt gtactttcca 60
aaggttcaac acgccactga caagatgtct aaagctgaat ctgaatatca ggatgctgta 120
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caccagcgaa acaagattgt aactgaagcc cgtaaagctc tggattcaat caaatccttt 480
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<210> 1728

<211> 2559

<212> DNA

<213> *Enterobacter cloacae*

<400> 1728

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gaacgggtatt cttcaggagg aagcatgatt gcccgctggt tctggcgcgga gtggcgctcg 180
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ggtagcgtea gcgatcgtat ggagaaaggg cttagccagc agagtcggga atttatggcc 300

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<210> 1729

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 1729

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aacaccatcc ttcagcacgt cgatttttgt ctctctccgg gcgaatttaa actgataacc 180
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735

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<210> 1730

<211> 741

<212> DNA

<213> *Enterobacter cloacae*

<400> 1730

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<210> 1731

<211> 642

<212> DNA

<213> *Enterobacter cloacae*

<400> 1731

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<210> 1732

<211> 864

<212> DNA

<213> *Enterobacter cloacae*

<400> 1732

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<210> 1733

<211> 1167

<212> DNA

<213> Enterobacter cloacae

<400> 1733

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<210> 1734

<211> 1581

<212> DNA

<213> Enterobacter cloacae

<400> 1734

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<210> 1735

<211> 1554

<212> DNA

<213> *Enterobacter cloacae*

<400> 1735

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<210> 1736

<211> 564

<212> DNA

<213> *Enterobacter cloacae*

<400> 1736

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<210> 1737

<211> 645

<212> DNA

<213> *Enterobacter cloacae*

<400> 1737

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ggagttttaa	gacgcagtgc	ttcccgcgaat	aatccggcgc	gtgtcgccat	cgtgatgggg	180
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gaaagcgccg	aagagaacgg	ttacgaggtg	atcattgccg	gtgcgggcgg	cgcagcacat	360
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gtcggtagcg	tggcgattgg	taaagcgggt	gcggaacatg	cgcgcctgct	ggcgcgcgag	540
atcctggcga	cgcatgataa	agagttacat	cagcgtctgg	cggagtggcg	taaagcccag	600
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<210> 1738

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 1738

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ttgtccccgg	ttttacgggtc	gagattgccc	gttggtctcat	cggcaaacag	cacttccggg	180
cgcgcgttaa	acgccttggc	cagcgcacag	cgtctgtgct	caccgcggga	aagctgtgcc	240
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<210> 1739

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 1739

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<210> 1740

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 1740

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tctcaggaag	tcattctccaa	ggataacgcc	aacgtcacca	tcgatgcggg	gtgctttatt	420
cagggtgattg	atgcgcacaa	agcggcctat	gaggtgagca	acctggagct	ggcgcgctc	480
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<210> 1741

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 1741

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ggtagcaaca	ctgattcaga	ataccttgca	ggcgtgcgag	gagtatcacg	acgtagagga	120

cgcgtaatca	tggcaacttt	ttcttttaggt	aaacacccgc	acgttgagct	gtgcgatctg	180
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<210> 1742

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 1742

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<210> 1743

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 1743

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gtcgtggacg	tgggtattaa	ccgcctggaa	aacggcaaa	tgggtggcga	cggtgtgtat	120
gaagatgccg	cagcgcgcgc	atcctatatt	actccggtec	cgggcggcgt	tggcccgatg	180
acggtagcaa	cactgattca	gaataccttg	caggcgtgcg	aggagtatca	cgacgtagag	240
gacgcgttaa						249

<210> 1744

<211> 1173

<212> DNA

<213> Enterobacter cloacae

<400> 1744

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<210> 1745

<211> 558

<212> DNA

<213> Enterobacter cloacae

<400> 1745

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<210> 1746

<211> 726

<212> DNA

<213> Enterobacter cloacae

<400> 1746

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ggcgacctgt	ttgaggcctg	gattggcgac	gaogatccga	acccgctgca	ccgtgagatg	180
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<210> 1747

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 1747

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gccgagccgg	aagccgtgcc	gttccaccag	agcgtgatca	ccgccgaaat	tgaacgctgg	180
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<210> 1748

<211> 1155

<212> DNA

<213> Enterobacter cloacae

<400> 1748

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<210> 1749

<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 1749

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<210> 1750

<211> 630

<212> DNA

<213> Enterobacter cloacae

<400> 1750

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ggaaaaccag	caccgcttcc	gggggtaatg	atgttttttaa	gtcaggaaga	ttttgccacg	180
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<210> 1751

<211> 1422

<212> DNA

<213> Enterobacter cloacae

<400> 1751

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<210> 1752

<211> 1497

<212> DNA

<213> Enterobacter cloacae

<400> 1752

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gatacgctgt	cggactttgg	tatcgccaac	tccattatcc	agcgcgaaga	gatcagccat	240
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<210> 1753

<211> 1296

<212> DNA

<213> Enterobacter cloacae

<400> 1753

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<210> 1754

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 1754

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gcgattgttc	gccagctgga	acagcgcggg	gacgtggagg	tgattgttcg	caccgcgcac	180
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<210> 1755

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 1755

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<210> 1756

<211> 1134

<212> DNA

<213> Enterobacter cloacae

<400> 1756

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<210> 1757

<211> 1275

<212> DNA

<213> Enterobacter cloacae

<400> 1757

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<210> 1758

<211> 1440

<212> DNA

<213> Enterobacter cloacae

<400> 1758

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<210> 1759

<211> 1467

<212> DNA

<213> Enterobacter cloacae

<400> 1759

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<210> 1760

<211> 1392

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (197)

<400> 1760

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<210> 1761
 <211> 1398
 <212> DNA
 <213> Enterobacter cloacae

<400> 1761
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<210> 1762
 <211> 1011
 <212> DNA
 <213> Enterobacter cloacae

<400> 1762
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<210> 1763
 <211> 438
 <212> DNA
 <213> Enterobacter cloacae

<400> 1763

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<210> 1764

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 1764

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cactgtacct	ttgtctgcga	cgatgaaacc	ttgcaggcgc	aggctcgtca	ctacaaacaa	660
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<210> 1765

<211> 288

<212> DNA

<213> Enterobacter cloacae

<400> 1765

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tcgtccaatc	aggccgtaaa	aaccacggat	ggcaaaacga	ttgttactga	cgggaaaccg	180
cagggtggatg	acgataccgg	tctgggtatcg	tacaaaaacg	ccgaaaccgg	tcaaactgaa	240
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<210> 1766

<211> 1977

<212> DNA

<213> Enterobacter cloacae

<400> 1766

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<210> 1767

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 1767

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ctgtatctga	cgcacattga	tcgggaagtg	gaaggggata	cccatctccc	ggattacgat	420
ccggacgagt	gggagtctgt	attcagtgag	tttcacgatg	cggatgagca	aaactcgcac	480
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<210> 1768

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 1768

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ctgttcgatc	acttcacoga	acttattgag	caataccgta	agatcgctaa	ataa	834

<210> 1769

<211> 3243

<212> DNA

<213> Enterobacter cloacae

<400> 1769

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<210> 1770

<211> 1299

<212> DNA

<213> Enterobacter cloacae

<400> 1770

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<210> 1771

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 1771

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<210> 1772

<211> 1437

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (29)

<400> 1772

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<210> 1773

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 1773

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<210> 1774

<211> 381

<212> DNA

<213> Enterobacter cloacae

<400> 1774

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<210> 1775

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 1775

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<210> 1776

<211> 969

<212> DNA

<213> Enterobacter cloacae

<400> 1776

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<210> 1777

<211> 471

<212> DNA

<213> Enterobacter cloacae

<400> 1777

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<210> 1778

<211> 3102

<212> DNA

<213> Enterobacter cloacae

<400> 1778

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<210> 1779

<211> 1221

<212> DNA

<213> *Enterobacter cloacae*

<400> 1779

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<210> 1780

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 1780

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<210> 1781

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 1781

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<210> 1782

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 1782

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<210> 1783

<211> 1239

<212> DNA

<213> Enterobacter cloacae

<400> 1783

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<210> 1784

<211> 2145

<212> DNA

<213> Enterobacter cloacae

<400> 1784

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<210> 1785

<211> 636

<212> DNA

<213> Enterobacter cloacae

<400> 1785

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<210> 1786

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 1786

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<210> 1787

<211> 1404

<212> DNA

<213> Enterobacter cloacae

<400> 1787

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<210> 1788

<211> 1008

<212> DNA

<213> Enterobacter cloacae

<400> 1788

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<210> 1789

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 1789

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<210> 1790

<211> 678

<212> DNA

<213> *Enterobacter cloacae*

<400> 1790

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<210> 1791

<211> 1845

<212> DNA

<213> *Enterobacter cloacae*

<400> 1791

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<210> 1792

<211> 894

<212> DNA

<213> *Enterobacter cloacae*

<400> 1792

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<210> 1793

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 1793

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cacttttaacc	ccgggtctgt	cagcattcct	aaaggcggca	acccggcaag	ctacggcatg	480
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<210> 1794

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 1794

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gaattatttt	ccagcgacga	agatatggct	gaattacatc	gggcgaatac	gctggaggag	420
ataaaaaacca	tcacgatcg	cttctga				447

<210> 1795

<211> 858

<212> DNA

<213> Enterobacter cloacae

<400> 1795

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<210> 1796

<211> 549

<212> DNA

<213> Enterobacter cloacae

<400> 1796

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<210> 1797

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 1797

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<210> 1798

<211> 1383

<212> DNA

<213> Enterobacter cloacae

<400> 1798

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<210> 1799

<211> 264

<212> DNA

<213> Enterobacter cloacae

<400> 1799

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<210> 1800

<211> 3363

<212> DNA

<213> Enterobacter cloacae

<400> 1800

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<210> 1801

<211> 4020

<212> DNA

<213> Enterobacter cloacae

<400> 1801

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<210> 1802

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 1802

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aaatcgacca	gtggcagcaa	tgcgacgcca	tactgacggg	tcgcgaacat	cgaaagctct	300
atttctgccc	tgtgtcttgc	gtatgacgat	ttgctacagg	ctaagggtcac	cattcacgac	360
acaaaggcaa	aatatctcga	tgcgaaaaac	ttcgcaggcg	gtaaccctac	agcagatccg	420
actcaggaga	aaacttcagg	ctggtatata	gacgggaaaa	cgaccgagct	tgctggcgaa	480
accattgagt	ttgtactgtc	cagtcoccat	gatcttcagg	gacaaatgat	ccccacgcgg	540
cagcttcatt	coctgtgcac	atggtgcatt	cgtaataagt	accgcaccgg	cgacggttgc	600
gactatgccg	gtacgcgcta	tttcgacaaa	aacaacaacc	cggtaaagcg	tccgtcactg	660
gatgaatgca	acggcacgct	gacggcctgc	aaacttcgat	tcggtgaaag	caacgaactc	720
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<210> 1803

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 1803

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gttcagatgc	tttcgcctca	gcctacaggg	ttagccagca	aacaaagcgc	agataaccgt	480
gcacgtatg	cgtttggcgg	ggtgacaaat	accgcgcgac	agggttaccc	ggttccgctc	540
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<210> 1804

<211> 672

<212> DNA

<213> Enterobacter cloacae

<400> 1804

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gcaaaaacttg	agggaaagca	tacgcgggata	ttcgccaggc	cgcagacaac	ccccggcggc	600
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aattatgatt	ga					672

<210> 1805

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 1805

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aggggtgctt	aaacagatgt	tgggtttgca	gtcattgagc	cagccacgaa	aaaaaggcca	180
ggagatgtat	tgttaatttt	gtgcgacggc	cacacgcagt	ttgcaaaact	gatgggtaag	240
tcattgatca	cggatgatgg	cgaggcaata	gagggaaccg	ctctggaaga	ggtggaagtg	300
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<210> 1806

<211> 1122

<212> DNA

<213> Enterobacter cloacae

<400> 1806

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ctggagcaac	atgttgccca	gatgccgctg	gcaaacgcaa	aacaggttat	cgagtccgtt	180
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aagcgcacat	gcattcccggt	caaggccgcc	ctgacttcgg	tggatgtgcc	tgatggtgtc	300
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aagaacatga	tcaccatccg	ttgcgaagaa	cgtcttgccg	tggctgtgaa	acgccctgag	1080
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<210> 1807

<211> 387

<212> DNA

<213> Enterobacter cloacae

<400> 1807

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gcgcagttcg	gagatgggta	cacccagaca	tcgggtgacg	gacttaacct	tcgctcacia	180
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gatcgtcatg	agggaaacaa	agcatttgca	tgggaagccg	cgctagagga	cttgggtctc	300
tatcgatgca	aacagtacaa	gcctcccca	atggggggag	gcaactgggtc	tttgactgca	360
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<210> 1808

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 1808

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taa						723

<210> 1809

<211> 1398

<212> DNA

<213> Enterobacter cloacae

<400> 1809

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<210> 1810

<211> 195

<212> DNA

<213> Enterobacter cloacae

<400> 1810

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<210> 1811

<211> 666

<212> DNA

<213> Enterobacter cloacae

<400> 1811

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tcgcagtttg	gtattcacgg	tacgcgcctt	gagcaggtag	cggagcaggc	cggggtgtcc	180
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<210> 1812

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 1812

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<210> 1813
 <211> 534
 <212> DNA
 <213> Enterobacter cloacae

<400> 1813
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<210> 1814
 <211> 1509
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1815
 <211> 975
 <212> DNA
 <213> Enterobacter cloacae

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<210> 1816

<211> 1092

<212> DNA

<213> Enterobacter cloacae

<400> 1816

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<210> 1817

<211> 324

<212> DNA

<213> Enterobacter cloacae

<400> 1817

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gattttatccg	cagttcgcca	cccacaacgc	ccacaccctg	gcggcgatct	acagcctggc	240
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<210> 1818

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 1818

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ctcgccgacg	gcgtgggtga	tgtctcgggc	acgctgcgct	ttgataaaga	caacaacgtg	180
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tggaaaaaact	acgcgcgcgat	taacgaaatc	tacgcggagt	ttttccccgg	cgataaaccg	360
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<210> 1819

<211> 1116

<212> DNA

<213> Enterobacter cloacae

<400> 1819

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<210> 1820

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 1820

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<210> 1821

<211> 4092

<212> DNA

<213> Enterobacter cloacae

<400> 1821

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 gggttcaggaa ccgaaggtgg cactattcag ccgatgatta tcaaccagtg cctgacggag 360
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<210> 1823
 <211> 783
 <212> DNA
 <213> Enterobacter cloacae

<400> 1823
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 caggccgggc cggatttttg ccagaaagcc gccctgttca atatcgaaac cttttttggc 720
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<210> 1824
 <211> 858
 <212> DNA
 <213> Enterobacter cloacae

<400> 1824
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 gccgcactcc cgcacgcccg caaaacggc atgcgccag gcgggcatgc ctgcaacgtg 780
 accgcgcccg acatctttta cactctgctg ctgaacgggc ttgccagcct gctgcacagc 840
 ccagaaccgg ctttgtaa 858

<210> 1825
 <211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 1825

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ggcacgctgc	ttaaaagcaa	tctgctgata	aacatcggtc	acggcgatac	gaccgaactg	540
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<210> 1826

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 1826

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gtaccggaaa	ccatgcaggc	ggaagccttc	gccaaagccg	gggggaaaac	acaaaacgcc	180
ccggtcgcga	ccccgcagga	gctogcggac	tatgatgcc	ttatcttcgg	caccccgacc	240
cgcttcggca	atatgtccgg	ccagatgcgc	accttcctcg	accagacggg	cgggctctgg	300
gcctccggcg	cgttatacgg	caagctggcc	agcgtgttca	gctctaccgg	cacggggcgg	360
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ccctatggcg	caacaacgat	tgcgggtggg	gatggttcac	gtcagccaag	caatgaagaa	540
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<210> 1827

<211> 246

<212> DNA

<213> Enterobacter cloacae

<400> 1827

cctaacagga	ggacaagtat	gccaaactcaa	gaatccaaag	ctcaccacgt	gggcgaatgg	60
gcaagtttac	gcaatacctc	tccggagatt	gccgaagcca	tctttgaagt	cgccaattat	120
gacgaaaagc	tggctgaaca	gatttgggaa	gaaggcaacg	atgaagtgct	ggttcgcgcc	180
ttcaaaaaaa	ccgacaaaaga	ctcgtctgtc	tggggcgagc	aaaccatcga	acgtaaaaac	240
gtctga						246

<210> 1828

<211> 183

<212> DNA

<213> Enterobacter cloacae

<400> 1828

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tggagatctc	cctcgatctg	ctggaaaaac	tgtgcttcga	gccggagctg	gcgggctgga	120
acgggattgg	tttcgttata	caggcctacc	agaaacgctg	cccgttcgtc	attgactacc	180
tga						183

<210> 1829

<211> 1179

<212> DNA

<213> Enterobacter cloacae

<400> 1829

caccctaata	acaaagtgat	tttcaaaact	ggcactgcct	ttgcaaaaac	accgttacac	60
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aacggctggc	ttatctcgac	cactgcaccg	caatacatgc	cgaccttga	gctgaataaa	180
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gccagaatgc	tcgacgaagt	ggctgcctg	ccggcgccg	aaggcggtg	gctgaccttc	1080
gatgattttc	tcaccggcgt	ggaaaccttc	ggcgagcgca	ttcagccgct	gatgcagtgc	1140
cgcgccaca	tccttgccgt	gacgaaggag	gtggcgtaa			1179

<210> 1830

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 1830

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gcggtatgca	gcgtaaccga	taccccgccc	actctgctgg	tgtgcctcaa	ccgcggcgcg	180
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gcccgctggc	agacggggga	gacgggctgc	ccgcgtctgg	aggcgggccct	ggcctcattc	360
gactgccgca	tcagccaggt	ggtgagcgtc	ggcaccacag	acattctgtt	ttgcgacatt	420
gtatcgatta	tcgcgccccc	ggcgccgcaa	gggctggtgt	ggttcgaccg	cggtatcac	480
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<210> 1831

<211> 1344

<212> DNA

<213> Enterobacter cloacae

<400> 1831

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ggcggtcagc	atgcggctgc	gatgtttggt	gcgacggtgc	tgatgcccat	gctgatgggg	180
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cgctggatcg	agcggtatgat	gccccccgct	gtcaccgggg	cggtggtgat	ggcgataggc	480
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<210> 1832

<211> 2682

<212> DNA

<213> *Enterobacter cloacae*

<400> 1832

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gaaacgcagt	tctggctggg	cacgcctaaa	gcctccctgg	cggcggtttc	cgggctggat	420
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<210> 1833

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 1833

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cgaacgttaa	gtattccctg	caaatccgat	ccggatttgt	gcatgcagct	ggacgcctgg	180
gatgcagata	ccagcgtccc	ggcaatcctt	gatggggaac	attccgttct	gtaccgtgag	240
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<210> 1834

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 1834

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<210> 1835

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 1835

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catctgcgcg	actgggtttc	cgaacgtctc	attgcgcata	gcctcgcctc	cgtcaatctc	240
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<210> 1836

<211> 684

<212> DNA

<213> Enterobacter cloacae

<400> 1836

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gccgaagctg	cctggcatgg	gtgcgatttg	atcgtctttc	cggagctttc	gcttacgggc	180
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gccgcccagt	cacgtttcat	cacgggtgatt	gctggtatta	cgctccagca	acacggccag	300
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gtacgtgccg	ataagggaga	actgctgcta	accggttctt	taggccaaca	gggttgga	660
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<210> 1837

<211> 678

<212> DNA

<213> Enterobacter cloacae

<400> 1837

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ctggtgcgcc	cggatcgccc	catcagtgcg	caggcgatgg	ctatacatcg	cattacggaa	180
tcgatgggtg	cggataagcc	gtggattgaa	gagatcatcc	ctctttacca	cggtagccag	240
tggatatgtc	cccataacgc	cagctttgac	cgcgcgctgc	tgccggagat	gcccggcgaa	300
tggatttgca	ccatgaagct	ggcgcgcgct	ctgtggccag	ggatcaaata	cagcaatatg	360
gcgctgtata	agtcgcgcaa	actcagcgtg	cgaacgcgcg	aagggctgca	tcacaccgct	420
gccctctatg	actgctacat	caccgcagcg	ctcctgattg	atatcatgaa	tacttccggc	480
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ttcggtaaat	atcgcgggaa	gccagtatcg	gaagtggcgg	acaaagatcc	gggctatctg	600
cgctggctgt	acaacaacct	cgacagaatg	agcccggaa	tgccgctgac	gctgaagcat	660
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<210> 1838

<211> 1314

<212> DNA

<213> Enterobacter cloacae

<400> 1838

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<210> 1839

<211> 1464

<212> DNA

<213> Enterobacter cloacae

<400> 1839

atgtttccct	gtgggtgtgcc	cgtgggtcaa	aactccgtat	ttcttcccga	acaattccctc	60
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<210> 1840

<211> 1275

<212> DNA

<213> Enterobacter cloacae

<400> 1840

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cgccctgccg	cgacgcgcgt	catgctggtg	ggatcgggtg	aactgggtaa	agaagtggcc	180
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gccatgcacg	ttgcgcacgc	ctgcacgcgc	atcgatatgc	ttgacggcaa	tgcctgcggt	300
gcgttaattg	ccgaggaaaa	accggatttc	gtggtgcctg	aaattgaggc	cattgccact	360
gagatgctgg	ttgcccttga	gcaggaaggc	cagcgcgtag	tgccttgccg	cactgcggca	420
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gcaaccgggg	aaaacgtgga	cgaagccgtc	gcgagagcga	aaatagcggc	cactgcggta	1260
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<210> 1841

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 1841

tgcacgggta	gccaatctct	tcgacggcct	ggagaaacgc	agcttttatcc	ccggcaaaac	60
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ggtagctgga	ggtcgggagc	tgtaattctt	ctgccgccag	gcgacgaatg	ccttcccggg	120
tcatggtcag	ttttgccgca	gtggcgcaag	gcactacgcg	ctggccttcc	tgctcaaggg	180
caaccagcat	ctcagtgcca	atggcctcaa	tttcaggcac	cacgaaatcc	ggtttttcc	240
cggcaattaa	cgcccgccag	gcattgccgt	caagcatatc	gatga		285

<210> 1842

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 1842

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caacagattt	ttatcaggat	gacacaggca	gaggtggtgc	tgggcgcgct	ggtactggcg	840
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<210> 1843

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 1843

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ttcttgagct	gtgccgccat	cgatatcgat	cactttatgg	agcgcagcta	cctgaacgcc	600
ctgggcgatg	cgctgaagat	ccccaggac	gttcgcgagg	gaattgagca	ggatattcag	660
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<210> 1844

<211> 2103

<212> DNA

<213> Enterobacter cloacae

<400> 1844

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tcccggccag	agggtgctga	ctatctgcac	gaggaaaacg	actatggccg	ccaggtcatg	180
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cgtgatgtct	ctgccccgtg	gtgcaaaaac	ggttatcgct	atcgccatat	ttatgagccg	300
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gagatcctgc	tggatgccaa	caaacgtgct	gccacagtg	agttttatac	gctggcgggc	420
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cagtacgggt	tgcgtttccg	caatcttgaa	acgggaaact	ggtatcccga	aatgctggat	540

aatgtctccc	ccgatttctgt	ctgggggtaac	gattcagaaa	cggtctacta	cgttaaaaag	600
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taa						2103

<210> 1845

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 1845

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cgtgaagagg	tcattgtcac	ctgcgcgtccc	ggtaacgcgc	tgtatgtcat	taatccagct	180
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aacggacagc	ctgtcacgct	gatccagggtg	gatgaccggg	caaaccggcg	gcagaagaaa	300
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<210> 1846

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 1846

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<210> 1847

<211> 516

<212> DNA

<213> Enterobacter cloacae

<400> 1847
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 gagcgtaaac cgcgcccggc accgcgtcgt actgaaaata acgatcgcaa accgcgtgct 480
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<210> 1848

<211> 390

<212> DNA

<213> *Enterobacter cloacae*

<400> 1848
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 ccgcaggaaa ataccgttgc ggtggcacca gaggtcatta ccctgaactt ctcggaaggc 180
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 aaaggcagct atcactttag cgtgaaatag 390

<210> 1849

<211> 777

<212> DNA

<213> *Enterobacter cloacae*

<400> 1849
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<210> 1850

<211> 216

<212> DNA

<213> *Enterobacter cloacae*

<400> 1850
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<210> 1851

<211> 1587

<212> DNA

<213> *Enterobacter cloacae*

<400> 1851

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<210> 1852

<211> 1713

<212> DNA

<213> *Enterobacter cloacae*

<400> 1852

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<210> 1853

<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 1853

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<210> 1854

<211> 2643

<212> DNA

<213> Enterobacter cloacae

<400> 1854

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<210> 1855

<211> 3507

<212> DNA

<213> Enterobacter cloacae

<400> 1855

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<210> 1856

<211> 2100

<212> DNA

<213> Enterobacter cloacae

<400> 1856

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<210> 1857

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 1857

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<210> 1858

<211> 1176

<212> DNA

<213> Enterobacter cloacae

<400> 1858

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<210> 1859

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 1859

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<210> 1860

<211> 2541

<212> DNA

<213> Enterobacter cloacae

<400> 1860

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<210> 1861

<211> 1113
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1861
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<210> 1862
 <211> 249
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1862
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 caacaataa 249

<210> 1863
 <211> 348
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1863
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 tatcgggtaca acgcgatgg gcttcgacgt ggtcgtatgt gtgggcagcc tgagctacag 180
 caacgattta gggccgattg gctacaccct gaacgcccat cgcgctccga tttccagctc 240
 ggtgctggcc ttgcgcgggc aaaaagatcc caataccgac accacctggg gcggcgtgcg 300
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<210> 1864
 <211> 1020
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1864
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<210> 1865

<211> 807

<212> DNA

<213> Enterobacter cloacae

<400> 1865

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<210> 1866

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 1866

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<210> 1867

<211> 838

<212> DNA

<213> Enterobacter cloacae

<400> 1867

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<210> 1868

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<400> 1868

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<210> 1869

<211> 765

<212> DNA

<213> Enterobacter cloacae

<400> 1869

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<210> 1870

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 1870

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<210> 1871

<211> 1032

<212> DNA

<213> Enterobacter cloacae

<400> 1871

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<210> 1872

<211> 858

<212> DNA

<213> Enterobacter cloacae

<400> 1872

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<210> 1873

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 1873

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<210> 1874

<211> 1059

<212> DNA

<213> Enterobacter cloacae

<400> 1874

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<210> 1875

<211> 1638

<212> DNA

<213> Enterobacter cloacae

<400> 1875

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<210> 1876

<211> 2310

<212> DNA

<213> Enterobacter cloacae

<400> 1876

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<210> 1877

<211> 1407

<212> DNA

<213> Enterobacter cloacae

<400> 1877

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<210> 1878

<211> 1626

<212> DNA

<213> Enterobacter cloacae

<400> 1878

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<210> 1879

<211> 1098

<212> DNA

<213> Enterobacter cloacae

<400> 1879

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<210> 1880

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 1880

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<210> 1881

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 1881

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<210> 1882

<211> 957

<212> DNA

<213> Enterobacter cloacae

<400> 1882

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<210> 1883

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 1883

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<210> 1884

<211> 1350

<212> DNA

<213> Enterobacter cloacae

<400> 1884

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<210> 1885

<211> 1119

<212> DNA

<213> Enterobacter cloacae

<400> 1885

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<210> 1886

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 1886

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<210> 1887

<211> 1425

<212> DNA

<213> Enterobacter cloacae

<400> 1887

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<210> 1888

<211> 1494

<212> DNA

<213> Enterobacter cloacae

<400> 1888

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<210> 1889

<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 1889

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<210> 1890

<211> 2322

<212> DNA

<213> Enterobacter cloacae

<400> 1890

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<210> 1891

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (468)

<400> 1891

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<210> 1892

<211> 1185

<212> DNA

<213> Enterobacter cloacae

<400> 1892

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<210> 1893

<211> 1365

<212> DNA

<213> Enterobacter cloacae

<400> 1893

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<210> 1894
 <211> 930
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1894
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<210> 1895
 <211> 540
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1895
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<210> 1896
 <211> 363
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1896
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 taa 363

<210> 1897
 <211> 609
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1897
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<210> 1898

<211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 1898

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<210> 1899

<211> 1209

<212> DNA

<213> Enterobacter cloacae

<400> 1899

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<210> 1900

<211> 1074

<212> DNA

<213> Enterobacter cloacae

<400> 1900

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<210> 1901

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 1901

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<210> 1902

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 1902

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gaaaagaccg	acattaaaa	gctcgttatc	gtctctcacc	cttatccgga	acgctcagtt	180
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<210> 1903

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 1903

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<210> 1904

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 1904

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<210> 1905

<211> 1491

<212> DNA

<213> Enterobacter cloacae

<400> 1905

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<210> 1906

<211> 549

<212> DNA

<213> Enterobacter cloacae

<400> 1906

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<210> 1907

<211> 2484

<212> DNA

<213> Enterobacter cloacae

<400> 1907

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<210> 1908

<211> 2091

<212> DNA

<213> Enterobacter cloacae

<400> 1908

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<210> 1909

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 1909

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<210> 1910

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 1910

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gacttcattc	tggagatggc	ctgtcaggca	cccgagaatg	tgatcctcga	tgcacgtgta	180
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<210> 1911

<211> 1788

<212> DNA

<213> Enterobacter cloacae

<400> 1911

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<210> 1912

<211> 663

<212> DNA

<213> Enterobacter cloacae

<400> 1912

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gaagcaaacc	gcgttactca	ggttaaagat	ctggctaacc	atggctaccg	cgctattcag	180
gttaccactg	gtgctaaaaa	agctaaccgt	gtaaccaaac	cagaagcggg	tcacttcgct	240
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<210> 1913

<211> 368

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (301)

<400> 1913

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<210> 1914

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 1914

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<210> 1915

<211> 1374

<212> DNA

<213> Enterobacter cloacae

<400> 1915

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<210> 1916

<211> 615

<212> DNA

<213> Enterobacter cloacae

<400> 1916

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<210> 1917

<211> 2031

<212> DNA

<213> Enterobacter cloacae

<400> 1917

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<210> 1918

<211> 423

<212> DNA

<213> Enterobacter cloacae

<400> 1918

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taa						423

<210> 1919

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 1919

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<210> 1920

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 1920

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<210> 1921

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 1921

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ctgatgttcc	agatctcccg	tcgcggcctg	acaagtacta	accgtaccgc	tattatgtgc	540
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<210> 1922

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 1922

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agccaggggc	cgggcaccgc	cattgatttt	ggcctgaaga	ttattgacct	gctggttggg	540
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<210> 1923

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 1923

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tttgaacgcg	gtgtgcagct	tgcgcgccag	gggcaggtaa	agcttcagca	ggccgagcag	180
cgtgtgcaga	tcctgctttc	cgacagcgaa	gacgctaaaa	ccacgccatt	cacaccggac	240
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<210> 1924

<211> 900

<212> DNA

<213> Enterobacter cloacae

<400> 1924

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gttcaggatg	acattctgga	tgtggtgggc	gatactgcaa	cattgggaaa	acgtcagggt	720
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<210> 1925

<211> 1887

<212> DNA

<213> Enterobacter cloacae

<400> 1925

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<210> 1926

<211> 1209

<212> DNA

<213> Enterobacter cloacae

<400> 1926

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ttaggtaacg	acgcgcgcgg	cctgtttgtg	ctgcccggcc	ttgaaaaact	ggccgatgcg	1140
ccgcaactct	cattcagtga	gattcgtccg	gtaggcccgg	atgtctgcct	ccatttaacg	1200
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<210> 1927

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 1927

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ctgaaacgta	tcggccagggt	taaagatgac	aacattaccg	tcgtttgggt	accagggtgc	180
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accaccgaaa	gtattgaaca	agccatcgaa	cgtgctggca	ccaaagccgg	taacaaaggt	420
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<210> 1928
 <211> 441
 <212> DNA
 <213> Enterobacter cloacae

<400> 1928
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 aaacgtgatg atgtgccgta caaagtggcc atcaacgaag cgatcgaact ggcgaaaacc 360
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<210> 1929
 <211> 555
 <212> DNA
 <213> Enterobacter cloacae

<400> 1929
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<210> 1930
 <211> 462
 <212> DNA
 <213> Enterobacter cloacae

<400> 1930
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 gggttaggtg agcgcgaagt gccgagcaaa atgatcgga atctggtgat ggaacagctg 360
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<210> 1931
 <211> 975
 <212> DNA
 <213> Enterobacter cloacae

<400> 1931
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<210> 1932

<211> 1473

<212> DNA

<213> Enterobacter cloacae

<400> 1932

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<210> 1933

<211> 2160

<212> DNA

<213> Enterobacter cloacae

<400> 1933

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<210> 1934

<211> 969

<212> DNA

<213> Enterobacter cloacae

<400> 1934

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<210> 1935

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 1935

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<210> 1936

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<400> 1936

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<210> 1937

<211> 1224

<212> DNA

<213> Enterobacter cloacae

<400> 1937

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<210> 1938

<211> 486

<212> DNA

<213> Enterobacter cloacae

<400> 1938

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<210> 1939

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 1939

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<210> 1940

<211> 1083

<212> DNA

<213> Enterobacter cloacae

<400> 1940

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<210> 1941

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 1941

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<210> 1942

<211> 1581

<212> DNA

<213> Enterobacter cloacae

<400> 1942

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<210> 1943

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 1943

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tgcgacatgg	ccagctgcgc	caccaccttc	gtacgtgaaa	aaccgctttg	tacgctggga	300
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<210> 1944

<211> 255

<212> DNA

<213> Enterobacter cloacae

<400> 1944

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gtgcccagac	cggcagacac	cctgcggggc	cagggtttcc	gtcagcttcc	ggttggtggt	180
gccggcgaca	ccagctggtc	tggttccgc	ccggacatga	tcaaccgcct	tgcgcgtcag	240
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<210> 1945

<211> 627

<212> DNA

<213> Enterobacter cloacae

<400> 1945

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gaacaaatgc	ttaagttccg	cgccagtcgt	catgaggact	tcccgatatca	ggaaattctg	180
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gatcgccgct	gcctgcatct	gcaactgacc	gagaaaaggtc	acgaattctt	gcgcgaagtg	480
ctgccaccgc	agcacaactg	cctgcaccag	ctctgggtctg	ccctcagcac	cgccgagcgc	540
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<210> 1946

<211> 1695

<212> DNA

<213> Enterobacter cloacae

<400> 1946

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acctgcgccc	cgcgttggct	ctcgaccgac	ttacgcgacg	gtaaccaggc	gctggccgag	180
ccgatggaca	gcgcgcgcaa	gctgcaattc	tgggatctgc	tgctgacctg	cgggtttaaa	240
gaaatagaag	tcgccttccc	gtccgcctcg	cagacggact	ttatttttgt	acgtcagctg	300
attgaggaga	atcgcatccc	ggatgaagtc	accattcagg	tggttaacgca	ggcgcgggac	360

gatcttattcc	atcgcacttt	cgactccctg	cgcgggcgga	agcaggccac	cgttcacctg	420
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<210> 1947

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 1947

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ggtatgcgtt	tcgatttaca	ggcgatgatt	gccctcaacg	gatcgcccac	ctggcgctatc	180
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gtcgtcaagg	agtggcacgg	ccgtcgtcct	atgtctgtcg	gtacgggcag	cgagagcgcg	360
attgctgaag	cgctactcaa	tcaccttggg	cctgcgccac	tatttttctg	ccgtcgtttgc	420
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<210> 1948

<211> 462

<212> DNA

<213> Enterobacter cloacae

<400> 1948

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gtggcgatgc	tgttgtccgg	cgtaagtcag	ccctgggttg	tggctttaat	agcaacaatg	180
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ttattaagct	gtagcctgt	aataggcgat	ttactgtgtc	tgttggcggg	atggatgcgc	360
atctcctggg	gacgggtgct	cttttttttg	tgccttggca	aggcgttacg	ctatgtttta	420
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<210> 1949

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 1949

tgttcgtgta	aacagcaacg	acgagctggc	cctgcacaaa	gaaaaacttc	aggaactgca	60
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ttacgcgtgg	cgtggtatct	gggttatggc	agccacagcg	cctttacggc	aatgtttcgc	840
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<210> 1950

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 1950

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gtcaaccgtg	aagcaagaat	ggggcgact	gctctcatta	ttcacccgac	actcaaagac	180
agaagcctgt	catttgctga	gcccgcctcg	gatattaaaa	cctgcgatca	ttatcagcaa	240
tttccgctct	atttaggcgg	cgagacgcac	gaacattatg	gtattccgca	cggtttcagc	300
tcgcgtatgg	cgtgagcg	attcctgaaa	gggctgtttg	gcgacgtaca	ataa	354

<210> 1951

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 1951

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ctgcgcact	atttttctgc	cgtcgttgcc	gccgatcatg	ttaaacatca	taaaccgcga	180
cggataacct	tctgctctg	tgcagaatta	atgggtgttc	cacctgcaaa	atgcgtgggtg	240
tttgaagatg	ctgattttgg	tattcagccc	gcgcgtgatg	ccggaatggc	ggcgggtggac	300
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<210> 1952

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 1952

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cgcgtggcga	agaccatgaa	cacgcgcgac	ggcgacacga	tcaccgtttt	cgacctgcgc	120
ttctgcgtgc	cgaataaaga	agtgatgcca	gagaaaggca	ttcacacgct	ggaacacctg	180
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atccctgagc	tgaacgttta	ccagtgcggc	acttaccaga	tgcactctct	ggaagaagct	420
caggagattg	cccgatcat	catcgaacgt	gatgttcgtg	taaacagcaa	cgacgagctg	480
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<210> 1953

<211> 1572

<212> DNA

<213> Enterobacter cloacae

<400> 1953

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cgcgtaaattg	cggatggtag	cttagcgact	acgggacacc	cgaaggcgTt	aggctcgGcg	180
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gttGtGcgTc	agaaagaggt	cgaagcGgGc	gatactgagT	cGtttgagGc	gtttctGggG	1560
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<210> 1954

<211> 357

<212> DNA

<213> Enterobacter cloacae

<400> 1954

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gaagccGagc	agcGcgaact	taaaaGcgTt	ctGacGcgG	ccGcatGcg	gcatggccGc	180
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caacgtgagG	ctGcgGcGaa	aaaagccGcg	aagctGaaaa	aagagcagGc	ttataagccG	300
gatGcagagG	cGaccttttc	ctggTccGcc	aatacatcaa	ccGtggaag	gGgctaa	357

<210> 1955

<211> 1362

<212> DNA

<213> Enterobacter cloacae

<400> 1955

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gtactttccg	cctcagccGg	cgtgacGaac	ctGcTggtTt	ctctgtctga	aggactggaa	180
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<210> 1956

<211> 1020

<212> DNA

<213> Enterobacter cloacae

<400> 1956

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<210> 1957

<211> 933

<212> DNA

<213> Enterobacter cloacae

<400> 1957

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tcacgcctga	ccgacgacgg	cgtcacccag	ctgggcgcga	tggtgattaa	ggccgcgaaa	900
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<210> 1958

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 1958

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ggcttagcgg	gcgacattag	acccgtgggg	gaaggtatca	gtgaactgag	gatccacttt	180
ggcccgggct	acagagtcta	ttttaaggac	cagggcaatt	gcatcatcgt	gctgttatgt	240
ggtggtgaca	aaagcagcca	ggccagagac	atacttatgg	caaaaatgct	gagcaatgta	300
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<210> 1959

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 1959

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ctgggctgca	tcgcccgcgc	gaaagggtatg	tcgaccattt	cccagcaaac	gggcctgtca	180
cgagaacaac	tgtatcgatc	attcagtgat	aagggggaacc	caacgctcaa	aaccacgctg	240
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<210> 1960

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 1960

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aaggtgctga	tccttaattt	gatgccaaag	aagatcgaaa	cagagaacca	gttcttgctg	180
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tcacgcaaca	cgctgctga	gcatctgaat	aactctctact	gtaattttga	agatattcgc	300
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gacgttgcc	actggccaca	gatcaggcag	gtgctggagt	gggcaaaaaga	tcacgtcacg	420
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<210> 1961

<211> 1365

<212> DNA

<213> Enterobacter cloacae

<400> 1961

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<210> 1962

<211> 1803

<212> DNA

<213> Enterobacter cloacae

<400> 1962

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<210> 1963

<211> 3702

<212> DNA

<213> Enterobacter cloacae

<400> 1963

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<210> 1964
 <211> 954
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1964
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<210> 1965
 <211> 225
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1965
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<210> 1966
 <211> 1629
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 1966
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<210> 1967

<211> 1647

<212> DNA

<213> Enterobacter cloacae

<400> 1967

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<210> 1968

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 1968

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gtgggtatga	tgaccaccgt	gtctggcggtg	gaaatgtccc	gcgacctggc	gtacgccaaa	180
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<210> 1969

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 1969

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attaaccacc	tgcaaggtca	ctttgcagag	cacaaaaaag	atcaccacag	cgcgtcgtgt	420
ctgctgcgta	tggtttctca	gcgtcgtaaa	ctgctcgact	acctgaagcg	taaagatgtt	480
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<210> 1970

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 1970

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cagggtgctg	aacaggtact	gagctggcag	ttccgccagg	cgtacagga	cggtagctg	180
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ttaatggat	ccattgagct	ggagcagatg	ccgaaagcgc	tgcgtatgat	gttgatgcaa	480
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<210> 1971

<211> 492

<212> DNA

<213> Enterobacter cloacae

<400> 1971

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<210> 1972

<211> 1011

<212> DNA

<213> Enterobacter cloacae

<400> 1972

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cagcaggaag	tcattctggc	acgcattgaa	caaatacttg	ccagtcgggc	tttaaccgat	300
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<210> 1973

<211> 1935

<212> DNA

<213> Enterobacter cloacae

<400> 1973

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<210> 1974

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 1974

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cgggaagcgg	gcagtaaaga	agcttttgtc	catgcggatt	acacgctggg	ggtggatacc	360

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taa						723

<210> 1975

<211> 1518

<212> DNA

<213> Enterobacter cloacae

<400> 1975

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aagaaaaaat	acgaacaaga	gatcgatggt	cgcgtagaaa	tcgatcgtaa	aagcggtgac	180
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<210> 1976

<211> 2709

<212> DNA

<213> Enterobacter cloacae

<400> 1976

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<210> 1977

<211> 978

<212> DNA

<213> Enterobacter cloacae

<400> 1977

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<210> 1978

<211> 2220

<212> DNA

<213> Enterobacter cloacae

<400> 1978

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<210> 1979

<211> 1251

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(1159)

<400> 1979

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<210> 1980

<211> 507

<212> DNA

<213> Enterobacter cloacae

<400> 1980

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<210> 1981

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 1981

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caacgtaaac gctatacgcg ccgcttcccg gtggctgcgg cgctaaaagc cccggtgtgg 360
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<210> 1982

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 1982

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ctatatcctg gcttttga 738

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<210> 1983
 <211> 363
 <212> DNA
 <213> Enterobacter cloacae

<400> 1983
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<210> 1984
 <211> 1038
 <212> DNA
 <213> Enterobacter cloacae

<400> 1984
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<210> 1985
 <211> 1014
 <212> DNA
 <213> Enterobacter cloacae

<400> 1985
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<210> 1986

<211> 456

<212> DNA

<213> *Enterobacter cloacae*

<400> 1986

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<210> 1987

<211> 540

<212> DNA

<213> *Enterobacter cloacae*

<400> 1987

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<210> 1988

<211> 1125

<212> DNA

<213> *Enterobacter cloacae*

<400> 1988

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<210> 1989

<211> 999

<212> DNA

<213> *Enterobacter cloacae*

<400> 1989

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caaaccacgc	tcggcgcgta	tcaccgtaaa	tggcagtgta			999

<210> 1990

<211> 321

<212> DNA

<213> *Enterobacter cloacae*

<400> 1990

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caacgtattg	gcatcgcttt	ttctggcggc	ctggatacca	gcgctgcact	gctgtggatg	120
cgcagaagg	gagcgggtcc	ttatgcatat	actgcgaacc	tgggtcagcc	ggacgaggaa	180
gattatgacg	cgatccctcg	tcgtgccatg	gaatatggcg	cagagaacgc	acgtctgata	240
gactgccgta	agcagctggg	ccccggaagg	gattgccgcg	atcccagtg	ggtgctttcc	300
ataacactac	cggcggcctg	a				321

<210> 1991

<211> 474

<212> DNA

<213> *Enterobacter cloacae*

<400> 1991

actgtaatcg	ccatggcggc	caggaagtct	atcatattca	tatgcatctg	ctgggtggac	60
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gcgctgatcg	tgacgctggg	aatgggtggg	tgcagcgcgc	gtcccgccat	cccggtcagt	180
gaagaacaga	cgctggatgat	ggagtcctca	gtgcttgctg	cgggcatacc	ggcggagaag	240
ccttcgctga	ccataagcga	aatccagctc	tcagcctctt	ctacgctcta	taacgaaagg	300
caagagccag	tgacgggtgca	ttatcgcttc	tactggatg	acgtgagagg	tcttgagatg	360
caccgccttg	aggcgccgcg	cagcgtgacc	atcccagcaa	gatcgctcgg	cacgctctac	420
ggcagcgcca	gctatctggg	tgcacataag	gtgagacttt	atctttattt	gtaa	474

<210> 1992

<211> 270

<212> DNA

<213> *Enterobacter cloacae*

<400> 1992

aggtataaaa	tcattgaaaa	cgttaaaaac	ctcatogetg	ccgccgttct	gagttcactc	60
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ggtaccatct	ctgccactgc	cgggactaac	ctgggctctc	tgggaagatc	gctggcgcaa	180
aaagctgacg	aaatgggtgc	gaaatcattc	cgcatacct	ctgtgaccgg	tcctaacc	240

ctgcacggta ccgcagttat ctacaaataa

270

<210> 1993

<211> 1269

<212> DNA

<213> Enterobacter cloacae

<400> 1993

actgacgctg	atgggagcgg	agtaatggct	tcaccgttat	cgttactcat	cggggttacgc	60
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ggtatcgccc	tgggcgtggc	ggtgctgatt	gtgggcttaa	gcgccatgaa	cggcctttgag	180
cgtgaactga	ataaccgcat	tctggccgtt	gtccctcacg	gtgaaatcga	gccgggttaac	240
cagccgtggt	ccaactggca	ggattccctg	aacaaagtgg	aaaagggtgc	cggatttgcg	300
gcggctgcac	cttacattaa	ctttaccggg	ctggtagaga	gcggggtaaa	cctgcgcgcc	360
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gccagcgctg	atcacaaatt	gcagcagcct	aagcgcgtac	gtctgcacgt	caccgggtatt	600
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tgcggcgctg	cgatcggcgt	ggtgggttcc	cttcagctga	cgcgattat	caacgggatt	1080
gaagcgctta	ttggccatca	gttcctgtca	ggcgatatct	atcttattga	cttcctgccg	1140
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ctggcaagct	ggtatccggc	gcgtcgcgct	agccgaattg	atccggcgag	ggtattaagt	1260
ggccagtaa						1269

<210> 1994

<211> 966

<212> DNA

<213> Enterobacter cloacae

<400> 1994

tttcgtcatg	gttttagcgg	cttttggccg	ctgaatcaaa	cagaggaatg	catcatgtat	60
tacggatttg	atattggcgg	caccaagatt	gcgctcggcg	tgttcgataa	agatcttaag	120
ctacaatggg	aaaccgcgct	ccccacgcgc	cgcgaaagct	acgatgaatt	tttaaccgcc	180
attgccgcac	tgggtggcga	agcggatgaa	cgtcttggcg	tcaaaggcag	cgttggcatt	240
ggtattccgg	gtatgcccg	aaccgacgat	ggcacgctgt	acgcggccaa	cgtgcctgcc	300
gccagcggca	aaccgctgcg	ggcgcgatct	tcgcgcctcc	ttgaacgcga	cgtgcgctta	360
gataacgatg	ccaactgctt	cgcgctctct	gaagcctggg	atgatgaatt	ccgtcgcttc	420
ccgctggtga	tggggctgat	cctcggaacg	ggcgtcgggtg	gcgggattgt	cattaacggt	480
aagcccatta	ccgggcgcag	ctatattacc	ggcgaatttg	gccatatccg	cctgccgggtg	540
gatgctctgg	aggctgctgg	acgtgatttc	ccgctgaccc	gctgcggctg	tgggcagcac	600
ggctgtattg	agaactacct	atcaggccgc	gggtttgcat	ggctttacga	acacttctat	660
catcagaaaac	ttgaggcccc	tcaaatacatt	accctgtggg	agcaggggga	tgcgcaggcg	720
cgtgagcacg	tcgagcgcta	tctggatctg	ctggcgggtg	gtctggggaa	tatcctgact	780
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gaacagttgt	ccgggcgtct	gaccgcacat	ttattgccgg	tcgcccgcgt	gccgcgcatt	900
gagcgtgcgc	gacacgggga	cgcaggaggc	atgcgcggag	ccgcattcct	tcatctcacc	960
gattag						966

<210> 1995

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 1995

accttgatta	aaacaatgag	ccgttatgcg	ctcctgagtg	cctttgcaact	ctttctggcg	60
ggttgtgtga	cgcgaacgga	agaacctgca	ccggtggatc	aggcgaagcc	gggaacggaa	120
cagccaacaa	cgccagcgca	gcctgttcca	accgtgccgt	ctgtaccgac	cattccggcg	180
cagcctggcc	cgatcgaaca	tccggacgac	accgcacagc	ctgcgcgcgc	agtacgccac	240
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gcgggagaag	cgacggaaac	cctgcgcaac	gcgctggcaa	acaacggtaa	atttacgctg	420
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ctgggttcgc	gcagtaaagc	gattggtatt	gcccgcacacg	ttggcgcgca	gtatgtcctt	540
tattctaacg	cgacaggcaa	cgtgaacacg	ccgtcgttgc	agatgcagtt	aatgctgggt	600
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<210> 1996

<211> 1068

<212> DNA

<213> Enterobacter cloacae

<400> 1996

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ggggggctga	ttcttttcac	ccgcaattat	catgatccgg	agcagttgcg	tgagctgggt	180
cgccagatcc	gtgcggcgctc	gcgcaatcac	ctgggtggtg	ccgtagacca	ggaagggtggg	240
cgtgtgcagc	gtttccgcga	aggggtttacc	cgttttaccg	ccgcgcgaatc	ttttgctgcg	300
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gagatgatcg	ccatggatat	cgacatcagc	ttcgccccgg	tgctggacgt	aggacacatt	420
agcgcggcaa	ttggtgagcg	ttcgatatcat	gacgatccgc	gtattgctgt	ggcaatggcg	480
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gcagacattc	gcgctaaaga	tatgtcgggt	ttccgctcgc	tgatcgtctga	taacaagctg	660
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agcgtgctgg	ataacctgtc	gcgatcaat	gctgaacgtg	ttacacaatt	gtatcataaa	960
ggttcattta	gtcgtcagga	gctgatggac	tcggcgcgct	ggaaaacggt	aaacgcccgg	1020
cttgaagccc	tgaacgagcg	ctggcaggca	cataaagcag	ccotttaa		1068

<210> 1997

<211> 1320

<212> DNA

<213> Enterobacter cloacae

<400> 1997

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atcacgctgg	tggatcgtaa	ccacagccat	ctgtggaagc	cgttactgca	cgaagtggcg	180
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cacttccagt	tccagctggg	ttcgggtggtg	gatatcaatc	gtgaaaacaa	aaccatcacg	300
ctggctgagc	tgcgtgatga	taaaggcgag	ttgctggttc	ctgagcgcaa	gctggcctat	360
gacacgctgg	tgatggccct	gggcagtacc	tccaatgatt	tcaacacccc	aggcgtaaaa	420
gagcactgca	tcttctctgga	taaccgcgat	caggcgcgtc	gtttccatca	ggagatgctt	480
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gtgtacattt	ctctgtaccg	tatgcaccag	attgcgttgc	acggctactt	caaaaccggc	1260
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<210> 1998

<211> 1944

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1064)

<400> 1998

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cgttttgtct	cctggctttc	gactattggc	attacgcttg	gcgtgatggc	actggtgacg	180
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cctggcgggc	tgccgccact	caaccgcgtg	aggctttacg	ttatgaataa	gacccgtgtg	1260
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caactggcta	agcggatggg	gcgtcagctg	gaaatgcgcg	acggtcgtct	gaatgctgaa	1920
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<210> 1999

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 1999

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ccgacgcaca	tcottattat	tcccaatatt	ctgatcccg	ccgttaatga	cgtaaaaacc	180
gagcatgaag	tggcgctggg	ccgtatgctg	acgggtggccg	cgaaaatcgc	tgagcaggaa	240
gggattgctg	aagacggata	ccgtttgatc	atgaactgta	atcgccatgg	cggccaggaa	300
gtctatcata	ttcatatgca	tctgctgggt	ggacgtccac	tgggaccgat	gctggcacat	360

aaaggtcttt aa

372

<210> 2000

<211> 864

<212> DNA

<213> Enterobacter cloacae

<400> 2000

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gcccccgccg	ggcttggcgg	cgcgagttgc	attattgagc	atggcgacca	tgggttggtt	180
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gcggtggcgt	ttatagcggg	tgagatcaaa	agcgagcttc	ccgatacgcc	tgcgctgaca	360
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gaaatgcgcc	ttcagcagac	aggtgacaaa	caattttattg	cgctggcaaa	tgatgcctgg	840
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<210> 2001

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2001

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cgatcatccga	agcatgacat	gcagcatctg	cttaaagaag	tggataaaat	gttgcagctc	180
aatatcgacg	atcgcccgct	gatctgcggc	gtggggttag	gaggatactg	ggcagagcgc	240
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gcgctgaaca	gctcccgcgc	cgccgagctt	ctgcaccatt	actacgaaat	tgtctgggac	480
gaagagcaga	cccacaagtt	caaaaacatt	tcccgcact	tgcagcgtat	taaagccttt	540
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<210> 2002

<211> 612

<212> DNA

<213> Enterobacter cloacae

<400> 2002

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gcgacggttg	ttggtgcgct	gggtggcggt	tatgcgggta	accaggtgca	gggcgcgatg	420
caggaaaatg	atacctacac	cacaacgcag	cagcgctgta	aaaccgtgta	tgacaagtct	480
gaaaaaatgt	tgggctacga	cgtaacctac	aaaattggcg	atcagcaggg	caaaatccgc	540
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aacaaagtgt	aa					612

<210> 2003

<211> 900

<212> DNA

<213> *Enterobacter cloacae*

<400> 2003

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<210> 2004

<211> 279

<212> DNA

<213> *Enterobacter cloacae*

<400> 2004

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<210> 2005

<211> 1059

<212> DNA

<213> *Enterobacter cloacae*

<400> 2005

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<210> 2006

<211> 1155

<212> DNA

<213> *Enterobacter cloacae*

<400> 2006
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<210> 2007

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<400> 2007
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<210> 2008

<211> 807

<212> DNA

<213> Enterobacter cloacae

<400> 2008
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<210> 2009

<211> 3513

<212> DNA

<213> Enterobacter cloacae

<400> 2009

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<210> 2010

<211> 1020

<212> DNA

<213> Enterobacter cloacae

<400> 2010

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<210> 2011

<211> 882

<212> DNA

<213> Enterobacter cloacae

<400> 2011

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<210> 2012
 <211> 669
 <212> DNA
 <213> Enterobacter cloacae

<400> 2012
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<210> 2013
 <211> 846
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2014
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<400> 2014
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<210> 2015

<211> 1437

<212> DNA

<213> Enterobacter cloacae

<400> 2015

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<210> 2016

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 2016

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<210> 2017

<211> 1194

<212> DNA

<213> Enterobacter cloacae

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<210> 2018

<211> 1797

<212> DNA

<213> Enterobacter cloacae

<400> 2018

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<210> 2019

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 2019

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<210> 2020

<211> 1164

<212> DNA

<213> Enterobacter cloacae

<400> 2020

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<210> 2021

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 2021

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<210> 2022

<211> 1725

<212> DNA

<213> Enterobacter cloacae

<400> 2022

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<210> 2023

<211> 1725

<212> DNA

<213> Enterobacter cloacae

<400> 2023

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<212> DNA

<213> Enterobacter cloacae

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<211> 270

<212> DNA

<213> Enterobacter cloacae

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<211> 1032

<212> DNA

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<211> 660

<212> DNA

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<210> 2029

<211> 282

<212> DNA

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<210> 2030

<211> 546

<212> DNA

<213> Enterobacter cloacae

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<211> 520

<212> DNA

<213> Enterobacter cloacae

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<210> 2032
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 <212> DNA
 <213> Enterobacter cloacae

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<210> 2033
 <211> 2289
 <212> DNA
 <213> Enterobacter cloacae

<400> 2033
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<210> 2034

<211> 810

<212> DNA

<213> Enterobacter cloacae

<400> 2034

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caacaggaga	tcccgaacgc	tgaaacatg	aagcagactg	aaagccatgc	ggtgaaaatc	780
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<210> 2035

<211> 831

<212> DNA

<213> Enterobacter cloacae

<400> 2035

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<210> 2036

<211> 1515

<212> DNA

<213> Enterobacter cloacae

<400> 2036

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<210> 2037

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 2037

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<210> 2038

<211> 1638

<212> DNA

<213> Enterobacter cloacae

<400> 2038

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<210> 2039

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 2039

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aaaccgctgg	tcatcaacgg	tgcgtaccat	gagatccttt	ttgaaaagga	cgctatgcgc	180
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<210> 2040

<211> 1602

<212> DNA

<213> Enterobacter cloacae

<400> 2040

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<210> 2041
 <211> 771
 <212> DNA
 <213> Enterobacter cloacae

<400> 2041
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<210> 2042
 <211> 1677
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2043
 <211> 780
 <212> DNA
 <213> Enterobacter cloacae

<400> 2043

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gccaacgata	tctatcaggt	ggtttccgca	ccgctgatta	aacagatgcc	gctgggcgcg	180
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gcgctgtaca	ggcatgaacg	caagctgggt	attccgctgc	tggtgtccag	ttcgctgctg	360
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<210> 2044

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 2044

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aagtccaatc	cttttagtga	atttgagcgt	ttacgcaaag	gatcgggcct	gaaaacagat	180
gaattcgcaa	gagcgatggg	tgtcagcgta	gcaatggtgc	tggagtggga	gtcaaaacgt	240
gaaaaaccta	ccccagccga	gctaaagctg	atgcgcctga	tcagggcaaa	cctgacctt	300
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<210> 2045

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 2045

cgatcccgcg	agggttttgg	tatgcttgcg	ccccgaacaa	tgggaagagt	gattatgcag	60
gcctgggtatt	tactgtattg	caaacgcggg	caacttcagc	gcgcgcagga	acatcttgaa	120
cgtcagtctg	ttaactgcct	gacacccgtg	atcacgcttg	aaaaaatgca	gcgtggaaga	180
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gcctttgaag	gcttacaggc	catcttcgct	gagccggacg	gtgaagcgcg	ctccatgctg	480
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<210> 2046

<211> 861

<212> DNA

<213> Enterobacter cloacae

<400> 2046

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gaagaagcca	ttaccgcagg	cgagacctcc	attccctccc	agggagagaa	catgccagcg	180
taccacgcgc	ggccaaaatc	tgcgatggc	ccgctgccca	tcgtgatcgt	ggtgcaggaa	240
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ctggccggtg	cgcgggaact	ctatttccgt	cagggcgatc	cgaatgatta	cagcgacatc	360
ccgacgctgt	tcagcaacct	ggtcagcaaa	gtgcgggacg	cgcaggtact	ggccgatctc	420
gaccacgttg	ccagctgggc	ggcgcgcaac	ggtggcgacc	cgcaccgtct	gatggtgacc	480
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<210> 2047

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 2047

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ttaatgccga	ttatcgccg	agctatcacg	cggaatccgc	gaaagatggc	tggcagagaa	180
tgctggcgtg	gttcagccag	tacggcggga	agaaagcgta	ataccaaaag	cccgggtggcg	240
gctacgccaa	ccgggcaatc	cagccccact	acgcctgacg	caaattctgc	gcgcctgca	300
ccatgttcgc	cagcgccgcg	cggttttcag	gccagccgcg	agttttcagg	ccgcagtcog	360
ggtttaccca	cagacgttcc	gcggggatgc	gctgggccgc	tttttgccgc	agcgattcaa	420
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<210> 2048

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 2048

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agcgatctgg	aacaacgcct	cggctttcgt	ctttttgtgc	gtaagagcca	gcctttgcgc	180
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gtggagatgg	acttcaaatt	cggcgtaacg	tttgatccgc	agcgcctcgt	tcagcagggc	420
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taa						963

<210> 2049

<211> 1506

<212> DNA

<213> Enterobacter cloacae

<400> 2049

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catttgcccg	gttcacgaac	gctggcgcgt	cagatctcgg	tgccccgaaa	taccgtcaac	240
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gtggggcaat	tcgctcctcg	tacgattgcc	cggacattac	cggacccgga	cgtcaggctg	360
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cagtttgccg	cgggtatccg	acgtcttcag	gcgttaatta	cgcagcagtg	gggcgggaaa	1500
gggtaa						1506

<210> 2050

<211> 666

<212> DNA

<213> Enterobacter cloacae

<400> 2050

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atctttcttg	agatgtgcca	gctctgtccg	acccttcaaa	gtaagcatca	ccccgcttct	660
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<210> 2051

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 2051

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ttcgatctcg	gcggcgagca	gcgtctggaa	aaacagggtta	ttaccagcta	cagcctgggtg	600
ccattcccg	gacattaa					618

<210> 2052

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 2052

cgtgaaagaa	gagagaagcc	tatgtttggt	ggaaaaggcg	gtctgggtgg	cctgatgaag	60
caggctcagc	agatgcagga	aaaaatgcag	aagatgcagg	aagagatcgc	tcagctggaa	120

gtcacgggtg	aatccgggtgc	cggtctggtc	aaggtgacca	tcaacgggtgc	gcataactgc	180
cgtcgcgtgg	aaatcgaccc	gagcctgctc	gaagacgaca	aagagatgct	ggaagatctg	240
gttgcagccg	cgtttaacga	tgccgctcgc	cgtatcgacg	aaacccagaa	agagaaaatg	300
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<210> 2053

<211> 1974

<212> DNA

<213> Enterobacter cloacae

<400> 2053

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tatgaagaga	agctcgcaca	ggcgcgcgag	gcgataattg	cggataacaa	catccagacc	1920
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<210> 2054

<211> 1875

<212> DNA

<213> Enterobacter cloacae

<400> 2054

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tccgaccaca	tgcgctgccc	ggttgagatt	gaaaaacagg	aagagaaaga	cggcgaaaacc	660
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<210> 2055

<211> 678

<212> DNA

<213> Enterobacter cloacae

<400> 2055

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<210> 2056

<211> 1410

<212> DNA

<213> Enterobacter cloacae

<400> 2056

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<210> 2057

<211> 3483

<212> DNA

<213> Enterobacter cloacae

<400> 2057

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<210> 2058

<211> 405

<212> DNA

<213> Enterobacter cloacae

<400> 2058

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<210> 2059

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 2059

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cgcagcggcg	ggatgcgcct	ggcgcaggct	ctgacccgcg	ccatgtcaga	aattggccac	180
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<210> 2060

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 2060

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agctacggta	agccgtccct	ggaaaagcgc	gttgactctc	tgctggcgca	ggcgcttgaa	360

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<210> 2061

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 2061

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gtaaaaccca	gcaccgctg	ctgcggggcg	caatcgccga	atttaaccag	tatgagttca	180
gccgcgctat	gcgtcataaa	gactgcatca	acccgctgcg	tatcttctct	cacatcgcac	240
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<210> 2062

<211> 792

<212> DNA

<213> Enterobacter cloacae

<400> 2062

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tcccgacgcg	gcagggtatc	gtgcgcggcg	cggtggctca	gctcggactc	gttcagcacc	120
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<210> 2063

<211> 312

<212> DNA

<213> Enterobacter cloacae

<400> 2063

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tcggcagaat	ga					312

<210> 2064

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 2064

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<210> 2065

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2065

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<210> 2066

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 2066

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gtgcggcggg	attttgaggg	gaaacttccc	cctcaccctg	ccctctcccc	agaggggaga	180
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<210> 2067

<211> 1266

<212> DNA

<213> Enterobacter cloacae

<400> 2067

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<211> 201

<212> DNA

<213> Enterobacter cloacae

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<210> 2069

<211> 573

<212> DNA

<213> Enterobacter cloacae

<400> 2069

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<211> 278

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<213> Enterobacter cloacae

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<210> 2071

<211> 3114

<212> DNA

<213> Enterobacter cloacae

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<210> 2072

<211> 1740

<212> DNA

<213> Enterobacter cloacae

<400> 2072

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<211> 414

<212> DNA

<213> Enterobacter cloacae

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<210> 2074

<211> 228

<212> DNA

<213> Enterobacter cloacae

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<210> 2075

<211> 477

<212> DNA

<213> Enterobacter cloacae

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<210> 2076

<211> 744

<212> DNA

<213> Enterobacter cloacae

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<211> 798

<212> DNA

<213> Enterobacter cloacae

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<211> 1008

<212> DNA

<213> Enterobacter cloacae

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<210> 2079

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<212> DNA

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<210> 2080

<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 2080

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<210> 2081

<211> 1581

<212> DNA

<213> *Enterobacter cloacae*

<400> 2081

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<210> 2082

<211> 1194

<212> DNA

<213> *Enterobacter cloacae*

<400> 2082

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<210> 2083

<211> 1077

<212> DNA

<213> *Enterobacter cloacae*

<400> 2083

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<210> 2084

<211> 354

<212> DNA

<213> *Enterobacter cloacae*

<400> 2084

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<210> 2085

<211> 1761

<212> DNA

<213> *Enterobacter cloacae*

<400> 2085

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<210> 2086

<211> 1080

<212> DNA

<213> Enterobacter cloacae

<400> 2086

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<210> 2087

<211> 810

<212> DNA

<213> Enterobacter cloacae

<400> 2087

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<210> 2088

<211> 717

<212> DNA

<213> *Enterobacter cloacae*

<400> 2088

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<210> 2089

<211> 270

<212> DNA

<213> *Enterobacter cloacae*

<400> 2089

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<210> 2090

<211> 999

<212> DNA

<213> *Enterobacter cloacae*

<400> 2090

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<210> 2091

<211> 837

<212> DNA

<213> *Enterobacter cloacae*

<400> 2091

gcgcgacgca	cctgcacgcc	ggacggggaga	agaaaccctt	taccgcgggt	caactccagc	60
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atgggattat	tgaacgtgac	tgaacgttat	tttgttaccg	gcacggacac	tgaagtcggt	180

aaaacggttg	ccagcgccgc	gctgttgca	gcggcgcgc	tgctggggaa	aacaactgcc	240
gggtataagc	ccgtagcctc	cggcagcgag	atgacgcggg	aaggcttacg	caataccgat	300
gcgctggcgc	tacagcgtaa	tagcagcctt	gcgctggcct	attctgcggt	gaacccttat	360
accttttctg	aaccacaccc	gcgcacacac	gtcagcgccg	atgaagatcg	tccgattgat	420
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gccatgctga	ccgctcaggc	cgtgcagcag	gccggggttg	gtctggcagg	gtggattgcc	660
aatgacgtgg	ttgcgcgggg	taaaogtcat	gctgagtacc	tggcgacgct	gaagcggggg	720
ctgcctgcgc	cgttttctcg	cgagatcccg	tggtttgcgc	acggcgacga	gcaggcgga	780
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<210> 2092

<211> 351

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (56)

<220>

<221> unsure

<222> (129)

<220>

<221> unsure

<222> (130)

<400> 2092

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gggctggann	gacggctggc	gcaccaaact	ctgctggggg	ttaccgggtc	gggcaaaacc	180
ttcaccattg	ccaacgtcat	tgcgcgtctc	cagcgtccga	cgaatgtcct	cgcgccgaaa	240
aaaacgctgg	cggggccact	gtatggtgag	atgaaagagt	tcttccccga	aaaaccgggg	300
ggaatatctc	gtcttccact	tacgactact	accaaccccc	gaagcctacc	t	351

<210> 2093

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 2093

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acatcactct	gtgcataccc	cccacacatt	tttaaggaga	gaaagatggt	gagctcgcgt	120
gctgtaaatc	agttttacgg	aagccaacat	acgctatgga	acgtgaatat	cgatttcccg	180
caaggcatct	gtacgggcat	tgttggcctg	cctggcatgg	gtaaatccac	gctcatgaac	240
tgcattaccg	gaaaggtgcc	cgttgagagc	ggcaccatca	tctggcatga	ggctggcgcg	300
cgcgcgcgta	atttgctcag	ccctgcgtca	gcattcacgg	cgcgcgcgac	gataggctac	360
gtcccgagc	atcggcggat	attttcccag	ctgaccgtcg	atgaaaatct	gcatactcgt	420
atgcgggcga	cagggaaaacc	tgacccgaca	tcaaaaagtg	acgtgtatgc	cctgtttccg	480
gagctctatc	cgctgcgaca	gagccgtgcc	tcttcgctgt	cccctgacga	ccagtatcag	540
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catggcgagc	ggcacgggtt	cgcgcgcagg	ctggggcagc	tgctggtgcg	gctgaatcgg	660
gagctgggaa	tgacgggtgt	gttagctgag	caacagctgt	cgttttatcc	ccgggtagcg	720
gatcgtttct	gcattgctcta	tgcggggcgt	aacgtggcac	agggccacgt	taacgagctg	780
gatgacgacc	ttattgcgca	ctggatggcg	cgggacataa	ggcgctaa		828

<210> 2094

<211> 498

<212> DNA

<213> Enterobacter cloacae

<400> 2094

gtgagtaacg	aggaaaatcg	gatgaaaatc	atcagtaaag	atttgcgcgga	cggcgaaaag	60
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ctggcggtgg	acgatgtgcc	agcgggaacc	aaaagttttg	ttgtgacctg	ctacgatccg	180
gatgcgcca	cgggtcggg	ctggtggcac	tggatcggtg	caaacctgcc	cgccgacacg	240
cgcgtattac	cgcagggctc	cggttccgat	ctggttgctc	tgcctgacgg	tgcgattcag	300
acgcgcactg	actttggcaa	agcgggctac	ggcggcgcg	cgccgcaaaa	aggggaaacg	360
caccgctata	tcttcaccgt	gcacgcgctg	gatgttgaca	agattgaggt	cgacgaagg	420
gcgagcgcg	cgatggtagg	ctttaacgtg	catttccatt	cgctgggtag	cgctcgatt	480
acggcgatgt	attcgtaa					498

<210> 2095

<211> 1137

<212> DNA

<213> Enterobacter cloacae

<400> 2095

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cagggcgtta	cacacacctc	tattcaggca	gccgttgatg	cgcgaatcac	caaacacagc	180
gcatctcgtc	agtacattgc	catcctgccg	ggtgaatacg	aaggaaaccgt	ttatgttccg	240
gcggcaccgg	gaagcattac	actttacggc	ctgggcgaaa	aagcggtcga	cgtaaagatt	300
ggcctggcga	ttgattcaga	gategacagc	accacctggc	gccatctggt	aaaccggcc	360
ggtaaaataca	tgccaggtaa	accggcggtg	tatatgtttg	ataactgcca	gcgcaagcgt	420
gccgccacca	ttggcggtga	gtgttcggcg	gtattctggt	cacaaaacaa	tggcctgcaa	480
ttgcaaaacc	tgaccattca	gaacaccctg	ggcgacagcg	ttgacgcagg	taatcatcag	540
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cgccagaaca	ccttcttctg	gaccaacagc	ggcgtgcaga	atacccttca	gaacaaccgt	660
ctgacgcgta	ctctggteac	caacagctac	attgaaggcg	acgtggatat	ggtctctggc	720
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gactccgcca	ctaacggcca	ggtagtgate	cgcgacagcg	tgattaacga	aggctttaac	960
atggcgaaac	cgtgggcgga	tgcggcgatc	tcgaaacgctc	ctttctccgg	caacaccggc	1020
acggtggatg	ataaagacaa	cgtgcagcgt	aacctgaacg	acgctaactt	caaccgcatg	1080
tgggaataca	acaaccgcgg	tctgggtagc	aaagtgggtg	ctgagccgaa	gcagtaa	1137

<210> 2096

<211> 1350

<212> DNA

<213> Enterobacter cloacae

<400> 2096

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atgaccagag	acgatctcgc	cttcgacaag	cagcatatct	ggcaccctta	cacctccacg	120
acccgcccc	ttcccgctca	tcgggtagcc	tctgcccacg	gctgcgagct	gcatctcgcc	180
agcggcgagc	ggcttggtga	cgggatgtcc	tcttggtggg	cggcgatcca	tggctacaac	240
caccgcgctc	tgaacgcggc	gatgaaagcg	cagattgacc	agatgtcaca	cgtgatgttt	300
ggcgggatca	cacatcagcc	cgcgggtggat	ttatgcgcgc	gcctggtagc	gatgacgcct	360
gaatcgctgg	agtgtgtttt	cctggccgac	tcgggctcgg	tggccgtgga	agtggcgatg	420
aaaatggcgt	tgcagtactg	gcatgcgaag	ggcgaaacgc	gccagcggtt	cctcaccttc	480
cgcaacggct	atcacggcga	caccttcggg	gcgatgtcgg	tgtgcgatcc	ggacaactcc	540
atgcacagcc	tgtggaaagg	ctacctgccc	gaaaacctgt	ttgcgccagc	cccgcagagc	600
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gcgggctgct	ttatgcacgg	cccgacgttt	atgggcaacc	cgctggcctg	cgccgtggca	1020
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gcgcagctga	agcagcagtt	aagcgcgggc	gcggaggcgg	aatacgtcgc	ggacgtccgc	1140
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cgcttcttcg	ttgaccaggg	cgtgtgggtg	cgacctttcg	gtaagctgat	ttacctcatg	1260
ccgccgtaca	gcattttctg	ggatcagctc	cgcaagctga	ccggggcagt	ggttgaagcc	1320
gttaacactt	cagcgcattt	cgcgatttaa				1350

<210> 2097

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 2097

tataaaaaag	caggctatatt	cgtctatcca	gataagactt	gcatacccag	gagcattacc	60
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gcttgcagtt	caacaccacc	ggatcagcaa	ccttctgagc	aggttgctcc	gggcaccgct	180
tcccgctccga	tctgttcagc	ggctgaagcg	agaacttca	cccgtgcgca	ctattttctcg	240
gcgatggatc	ccaatgcagc	accgtggacg	ctttttttat	taacctgccg	aaacagccag	300
acttcgttgt	cggcccgcc	ggggcgcagg	gcgttacaca	cacctctatt	caggcagccg	360
ttgatgccgc	aatcaccaaa	cacagcgcct	ctcgtcagta	cattgccatc	ctgccgggtg	420
aatacgaagg	aaccgtttat	gttcggcgcg	caccgggaag	cattacactt	tacggcctgg	480
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<210> 2098

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 2098

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acactgctta	cccctcagaa	aacctgtctc	ccctcttctc	ttgaggccct	caaacgagcc	180
caggaagcgg	ggtatcaact	tctcatcgta	acgggtcgac	atcacgtagc	cattcatcct	240
ttttatcagg	cactgggctt	agatacacct	gcaatttggt	gtaatggcac	ctattttgtat	300
gattatcagg	caaaaaaggt	tttagccctc	gacccgcttc	ccgttacgca	ggcgctgcaa	360
ttgattgatt	tactggatga	gcacgccatt	caaggcctga	tgtatgtgga	taacgccatg	420
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gaagcgcagc	gtccggtggt	tactcagggt	tctccctgc	gccaggcggc	ggaagacgtc	540
gaagcaatct	ggaaatttgc	cctgaccgat	gaagacaccg	ccaaactgaa	taccttcgca	600
aaacttgctg	agcatacgtc	gggtctggaa	tgtgaatggt	cctggcacga	tcagggtggat	660
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gcggccggaa	cgggcgtggc	gatgggtaat	gcgatgacg	cggtgaaagc	gcgcgctgac	840
gtggtgattg	gtgataaacac	caccgacagc	atcgcgagct	atatctatac	ccacctgctg	900
tga						903

<210> 2099

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2099

tgggaggctt	gctctaccgc	tggtgaaaaa	ctgggtgtcg	catggctggc	gtcgccggca	60
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gaaccgaacg	atgtcgtcgt	cacgggttcg	cgcattccgc	agccgaacct	tgagggcgcc	180
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gcggacggaa	ccgcgaccgt	cgatcttcgc	ggcctcgggc	cgacgcgtac	gctggtgctg	360
gtcaacggcc	gtcgctgat	gccgggcgac	ccgaccacgt	cggcggcgga	tctgaactcc	420
atccccgcgg	cgtcgatcaa	gcgggttgaa	gtgcttaacc	gcggtgcata	gtccacctat	480

ggcgcggacg cgggtggccgg cgtcgtggac ctcatgtctt cactccgagg gaggccgac 540
ccccatata cgccc 555

<210> 2100

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 2100

tttgattttt ggagaataga catgtcccga gtctgccaa ttactggcaa gcgtccggtg 60
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cactctcacc gtttctgggt tgagagcgag aagcgttttg tcacctgcg cgtatctgct 180
aaaggtatgc gtgtaatcga taagaaaggc atcgatacag ttctgtccga actgcgtgcc 240
cgtggcgaaa agtactaa 258

<210> 2101

<211> 775

<212> DNA

<213> Enterobacter cloacae

<400> 2101

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ttgcacgatg ttattcctcc tcttttaaaa atagcggatg aattcgttgt agttgattcc 120
ggaagtacag acgcaacgat atatatattgc cagagttatg gattgtcggc catattcaaa 180
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ttaaaaaatgg gcgatgaacc cgaacccgat atggcgtggc ggatatgtcg tcaactggtt 360
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agtgggtgct ggcgtcaggg caaagtgggt gtgggtgacag ggttttatgc caccgctac 720
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<210> 2102

<211> 183

<212> DNA

<213> Enterobacter cloacae

<400> 2102

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ggtacaggct acttctacac caccacgaag aacaaacgta ctaagccgga aaaactggaa 120
ctgaaaaaat tcgatccagt tgtacgccag cactactgt acaaagaagc taaaatcaaa 180
taa 183

<210> 2103

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 2103

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ggaaccatgc ctgaattacc tgaggtagag accagccgcc ggggcattga gccccatctg 120
gttggcgcga ctattcttca tgctgtcgtt cgcaacgggc gtctgcgctg gccggtgtcc 180
gatgagatcc acgcgttaag tgacaaaccc gtctgagcg tgcagcccg cgcgaaatac 240
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cgtattctta ccgaagagtt gcctgcggaa aagcacgacc acgttgatct ggtgatgagt 360
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aacgcagatt atctcaaaaga gaagtgcgcg aaaaagaaaa ccccgattaa accctggctg 540

atggataaca	agctggtggt	gggcgtgggg	aataatctacg	ccagcgaatc	gttgtttgcc	600
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<210> 2104

<211> 1395

<212> DNA

<213> Enterobacter cloacae

<400> 2104

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agagatactg	cgatcatctg	tcatagaacta	ttgggttggg	taatatgtgc	caaaattttgc	180
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<210> 2105

<211> 1038

<212> DNA

<213> Enterobacter cloacae

<400> 2105

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tgcggtactg	acgttcacat	ctacaactgg	gaccagtggg	cgcaaaaaac	tattcccgtg	180
ccaatggtag	tcggccacga	atatgtcggc	gaagtagtcg	gcacgcggca	ggaagtgaag	240
ggcttcaaca	ttggcgacccg	cgtctccggg	gaaggccaca	ttacctgtgg	tcactgccgc	300
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ccgggctgct	tcgcggaata	cctgggtgatc	ccggcgttta	acgcgttcaa	aatcccggac	420
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1038

<210> 2106

<211> 1137

<212> DNA

<213> Enterobacter cloacae

<400> 2106

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<210> 2107

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 2107

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<210> 2108

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 2108

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<210> 2109

<211> 1086

<212> DNA

<213> Enterobacter cloacae

<400> 2109

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<210> 2110

<211> 1047

<212> DNA

<213> Enterobacter cloacae

<400> 2110

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<210> 2111

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 2111

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<210> 2112

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 2112

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<210> 2113

<211> 975

<212> DNA

<213> Enterobacter cloacae

<400> 2113

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<210> 2114

<211> 1218

<212> DNA

<213> Enterobacter cloacae

<400> 2114

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<210> 2115

<211> 1152

<212> DNA

<213> Enterobacter cloacae

<400> 2115

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cctggcggtc	ctgctgagat	ccttactggc	ccctggcg	gaggtctgac	agcgttaacc	1020
gacgaatcac	tggcgaaaac	actggcagaa	ttgtatgcct	ctccgccagt	tggtgatcgc	1080
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<210> 2116

<211> 576

<212> DNA

<213> Enterobacter cloacae

<400> 2116

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atggaggcca	gatcgtcaga	gatattgtcc	gggaatttga	acgcgttaaa	cgccgggatc	480
accaggtatt	ccgcgaagca	gcccggacgg	ttcaogccca	cgccgacggg	gttgccggc	540
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<210> 2117

<211> 930

<212> DNA

<213> Enterobacter cloacae

<400> 2117

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aaccctattc	ctccgatgtt	atgttatgag	gatttctcgt	tcttccctgg	aatgctgatg	600
caatcgaaca	aaatagtcta	tcaacgccag	gggcattatt	attacatcaa	gcgtcgcgac	660
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<210> 2118
 <211> 1161
 <212> DNA
 <213> Enterobacter cloacae

<400> 2118
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<210> 2119
 <211> 849
 <212> DNA
 <213> Enterobacter cloacae

<400> 2119
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 gccgacctgc ttccggattg cctggcctct gttgcctggg ctgacgaaat cgtcattctc 180
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 aaaacgtga 849

<210> 2120
 <211> 483
 <212> DNA
 <213> Enterobacter cloacae

<400> 2120
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 ccgagcaaaa agccgatgtt cgacctgaac gaacgcgtgc agcttgccac cgatgcgatt 180
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 gaccggcatg ccaatatcct gatccgcggg cttcgcgcgg tagcagactt cgaatatgag 300
 atgcagctgg cacacatgaa ccgcatctg atgccggagc tggagagcgt attcctgatg 360

cctccaaaag	agtggtcctt	catctcttct	tcgctggtga	aagaggtggc	gcgccatcat	420
ggggacgtta	cccacttcct	gccggttaac	gtccaccagg	cgttgatgga	aaagctaaag	480
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<210> 2121

<211> 402

<212> DNA

<213> Enterobacter cloacae

<400> 2121

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tggcaaggcg	gggacatcgc	ggaagggcag	atacgctttt	ccgcccacgg	ctggagtgat	360
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<210> 2122

<211> 2907

<212> DNA

<213> Enterobacter cloacae

<400> 2122

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acaatccgta	agagcgataa	ggacacccgt	cagtatcagg	cgattcgtct	tgataacggg	180
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<210> 2123

<211> 1338

<212> DNA

<213> Enterobacter cloacae

<400> 2123

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ctgttaaaaag	gggccggggc	gatgtgggtg	cttagcgtea	gccagggtgg	tcttgccgcc	180
acaagccagg	tagtcgcggt	gcgcgtctgg	ccgtcgtcga	cctatacgcg	cgtgacggtc	240
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gttgatctcg	aaggtgtgaa	cctcaactcc	gtgcttaaaag	gcatggcagc	acaaatccgt	360
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<210> 2124

<211> 879

<212> DNA

<213> Enterobacter cloacae

<400> 2124

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cttgctggcc	gtcgcgccag	tcgtccgggc	agtggatgga	cgaagaacga	agtggaaaac	180
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atcagcatgg	ggcagatcct	ctccatcccc	atgattgtcg	cggttgccat	tatgatgatt	840
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<210> 2125

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 2125

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<210> 2126

<211> 579

<212> DNA

<213> Enterobacter cloacae

<400> 2126

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tttgcgcccg	tcattcagtat	cgagctgcgt	gcccgcgcta	aagggtgaact	gaccgcccc	540
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<210> 2127

<211> 1851

<212> DNA

<213> Enterobacter cloacae

<400> 2127

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<210> 2128

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 2128

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<210> 2129

<211> 2259

<212> DNA

<213> Enterobacter cloacae

<400> 2129

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<210> 2130

<211> 516

<212> DNA

<213> Enterobacter cloacae

<400> 2130

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<210> 2131

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 2131

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<210> 2132

<211> 3387

<212> DNA

<213> Enterobacter cloacae

<400> 2132

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<210> 2133

<211> 3549

<212> DNA

<213> Enterobacter cloacae

<400> 2133

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<210> 2134

<211> 1353

<212> DNA

<213> Enterobacter cloacae

<400> 2134

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<210> 2135

<211> 726

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (53)

<400> 2135

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<210> 2136

<211> 1752

<212> DNA

<213> Enterobacter cloacae

<400> 2136

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1752

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<210> 2137

<211> 750

<212> DNA

<213> *Enterobacter cloacae*

<400> 2137

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750

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<210> 2138

<211> 375

<212> DNA

<213> *Enterobacter cloacae*

<400> 2138

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375

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<210> 2139

<211> 558

<212> DNA

<213> *Enterobacter cloacae*

<400> 2139
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<210> 2140

<211> 843

<212> DNA

<213> Enterobacter cloacae

<400> 2140
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<210> 2141

<211> 199

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (86)

<220>

<221> unsure

<222> (157)

<400> 2141
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 cgcgctgcc tgaaacagct cgatttacat aagtttngtc ttcaaccgcc cagggcattg 180
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<210> 2142

<211> 642

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (611)

<400> 2142

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<210> 2143

<211> 1812

<212> DNA

<213> Enterobacter cloacae

<400> 2143

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<210> 2144

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 2144

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<210> 2145

<211> 810

<212> DNA

<213> Enterobacter cloacae

<400> 2145

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<210> 2146

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 2146

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cgcggcgtca	tcgtgcgcgg	taacgggggt	caggtcattct	atggcccgca	cgtcaccatt	240
atcaaaaacg	aagtggaaga	gatcttatcg	ttaa			273

<210> 2147

<211> 2397

<212> DNA

<213> Enterobacter cloacae

<400> 2147

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<210> 2148

<211> 1443

<212> DNA

<213> Enterobacter cloacae

<400> 2148

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<210> 2149

<211> 918

<212> DNA

<213> Enterobacter cloacae

<400> 2149

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<210> 2150

<211> 1434

<212> DNA

<213> Enterobacter cloacae

<400> 2150

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<210> 2151

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 2151

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<210> 2152

<211> 1080

<212> DNA

<213> Enterobacter cloacae

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<210> 2153

<211> 363

<212> DNA

<213> Enterobacter cloacae

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<221>unsure

<222>(348)

<400> 2153

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<210> 2154

<211> 1053

<212> DNA

<213> Enterobacter cloacae

<400> 2154

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<210> 2155

<211> 1293

<212> DNA

<213> Enterobacter cloacae

<400> 2155

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<210> 2156

<211> 1425

<212> DNA

<213> Enterobacter cloacae

<400> 2156

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<210> 2157

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 2157

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tgtgctttcc	ggtactatgc	ggcgggtttt	tccgcattcc	tgagagctat	gatgtccacc	180
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cacaaatgtg	gccgcctgca	tggacactcg	tttatgggtg	gtcttgaaat	caccggtgaa	300
gtcgatcccc	atacgggctg	gatcatggac	tttgccgaac	tgaaggccgc	gtttaagccg	360
acctacgatc	gtctcgatca	ctactatctg	aatgatattc	cgggccttga	aaacccgacc	420
agcgagggtg	tggcgaaatg	gatttgggat	cagatgaaac	cgctgggtgc	gctgctgagt	480
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<210> 2158

<211> 324

<212> DNA

<213> Enterobacter cloacae

<400> 2158

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gtcaccattc	atgtgccgga	tcaaccgccc	attgagaccc	gcctgaccga	aggatgaaaac	180
cgctgcacat	tgtgcgccat	tgccagactc	gtaaacgaaa	acggcgcaat	taaagtgcag	240
cgaattaaacc	agtacttcaa	aggccaggac	gaaatggacc	gggcatttgg	ctggggattt	300
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<210> 2159

<211> 306

<212> DNA

<213> Enterobacter cloacae

<400> 2159

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gtcactcaac	agacatactc	tcgtctggaa	gccaaacctg	ccagtgcgag	cattgaacgg	180
ctattttaagg	tgtttaccgt	cctgggtgta	aaaatcagtt	tctcctcggc	aaccacttct	240
tcagagagga	agcagacgga	agacatatat	aaattaaatt	cacctgcacc	acaggaggat	300
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<210> 2160

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 2160

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aagctggaag	cagaaggtta	tgacacctcg	gtcatcgagc	aaatgaccac	aggcgcagca	360
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atgcggaaac	ctgacgtaga	tatocagggt	gagcactcgg	agcgcgtagt	gacgcaacgt	480
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ggcgagctgt	ttgaaggcgg	taaaatcaca	ccgctggtgt	acgatctgga	cttagagcgg	780
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<210> 2161

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 2161

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ggcagtgacg	tcatcgctct	cgcggaatg	gacgaacagt	ggggatacgt	cggggctaaa	180
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ctgcacgtaa	tcagcaagcg	atatacgcag	cgaattgagc	ggcataacct	gaatctgagg	420
cagcacctgg	cacggctggg	acggaagtcg	ctgtcgtttc	caaaatcggg	ggagctgcat	480
gacaaagtca	tcgggcatta	tctgaacata	aaacactatc	aataa		525

<210> 2162

<211> 588

<212> DNA

<213> Enterobacter cloacae

<400> 2162

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aaggaaaacag	gtatgagctt	tttcgacaaa	gttaaagggtg	ccattaactc	aggccgtgac	180
gaactgaccc	gccaggttgg	ccgtttcaaa	aacaaaaaat	tcatgcaggg	caccgttgct	240
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atgaaataca	tcctggcgct	gaaagatcag	cctgaggccg	ctcagctggc	cttacgtgtt	480
ggtattgccc	ttgcgaaaag	tgacggtaac	ttcgatcagg	acgagaaact	ggcctcccgc	540
gagatcgcta	tcgcgttggg	cttcgacccg	gctgaatttg	gcctctga		588

<210> 2163

<211> 633

<212> DNA

<213> Enterobacter cloacae

<400> 2163

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gttgctatgg	ttggcctagg	ctgggatgcc	cgtgtaaccg	atggtcaggg	ttttgacctg	180
gacgcttccg	tgtttcgagt	aggcgaagac	ggtaaagtgt	tgtcagatgc	gcatttcatt	240
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ggtgaaggcg	acggcgacga	tgagcaggtc	aaaatcgatc	tgaccaaagt	ctcagcagat	360
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cgtttcgata	tgtctgaaga	tgcctcaacc	gaaaccgcta	tggctcttcgg	tgaactgtat	540
cgatcatggc	ctgagtgga	gttttaaagct	gtcgggtcagg	gctttgccc	tggcctggcg	600
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<210> 2164

<211> 1263

<212> DNA

<213> Enterobacter cloacae

<400> 2164

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acctgcctgt	tcctgcttaa	tgtcaggga	aagggtcagg	gcgattctga	ctttatcttt	180
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gttgcatctt	tacttgacgc	atccggctca	atgagtggcc	agttcagtaa	gggtaacgtt	720
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gataacaccc	acttctttgc	catggatgat	ttcgggtcga	ttagcgatga	aaagttatat	1200
gataatctac	tggagaagtt	cagaccgtgg	atcgatgaaa	caaaaagggt	aggcatcctt	1260
taa						1263

<210> 2165

<211> 1359

<212> DNA

<213> Enterobacter cloacae

<400> 2165

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gaataccttc	ctgaatgggt	tgtcagcga	cagggaaggc	cgctgtcatt	gtcccttctt	180
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aaacagcaga	cagaggcgat	gatagaggaa	atcatcgcca	gaaccccggg	tgctattgaa	1260
cgtgttagcg	ggcttcttcc	ggaccagttc	ccccagcagc	ttcgggaaag	tatttttgat	1320

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1359

<210> 2166

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 2166

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acatggcaac	tgcagttcac	ttacaccgct	tctcaaccgg	gtacgcacca	gaaaatcatt	180
gatatggcca	tgaatggcgt	tggatgcggg	gcaaccgccc	gcattatggg	cgttggcctc	240
aacacgattt	tccgccattt	aaaaaactca	ggccgcagtc	ggtaa		285

<210> 2167

<211> 1044

<212> DNA

<213> Enterobacter cloacae

<400> 2167

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<210> 2168

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 2168

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<210> 2169

<211> 234

<212> DNA

<213> Enterobacter cloacae

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<210> 2170
 <211> 2043
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 <213> Enterobacter cloacae

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<210> 2171
 <211> 2448
 <212> DNA
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 ataataacag aggccagggc caccctgact gacgaagtga ttgatctgca cgagcgtatc 360

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<210> 2172

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 2172

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<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 2173

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<210> 2174

<211> 1083

<212> DNA

<213> Enterobacter cloacae

<400> 2174

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<210> 2175

<211> 2628

<212> DNA

<213> Enterobacter cloacae

<400> 2175

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<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 2176

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<211> 750

<212> DNA

<213> Enterobacter cloacae

<400> 2177

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<210> 2178

<211> 1023

<212> DNA

<213> Enterobacter cloacae

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<211> 924

<212> DNA

<213> Enterobacter cloacae

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<210> 2180

<211> 1896

<212> DNA

<213> Enterobacter cloacae

<400> 2180

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<210> 2181

<211> 471

<212> DNA

<213> Enterobacter cloacae

<400> 2181

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gtcgcgcatc tggcgcggtt ctggcagcag gaagtgcagc ccggaccgtg gcgcaagcgt 420
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<210> 2182

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 2182

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ggttttatct ctgtttttcg tgatggcggc agtataacgc taaataattc ccgttgacgg 180
aaagcggcaa actottgctt ttgtgtcttc tcttgcgatg atagaaacag atttgaactt 240
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<210> 2183

<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 2183

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<210> 2184

<211> 2217

<212> DNA

<213> Enterobacter cloacae

<400> 2184

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<210> 2185

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 2185

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cataacatca	ttatgggttg	cggcggtctg	tacctgtgct	ggatgggcta	ccagatgctg	300
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<210> 2186

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 2186

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ggcgtgatgt	tatttaccag	ccgcgcgcgc	catcactatg	aacaggggca	gggtacgcaa	660
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tga						723

<210> 2187

<211> 645

<212> DNA

<213> Enterobacter cloacae

<400> 2187

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gccgcaggct	cgattgatct	gcatacgcct	tcccggacgc	aaacacgcgc	ccacctgttt	360
aaacgcgcgc	tggttcgttaa	cctgaccaac	ccgaaaagca	tcggtgttct	cgcgcgcctg	420

ttcccgcagt	ttatcgtgcc	gcatacagcca	caggtgatgc	agtacgtggt	gctggggcgca	480
accaccatta	ttgtcgatat	catttgtgatg	attgggttacg	cgacgctggc	gcagcgaatt	540
gcggcgtgga	tcaaaggggc	taagcagatg	aaggccctga	acaaagtgtt	tggttcgctg	600
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<210> 2188

<211> 1254

<212> DNA

<213> Enterobacter cloacae

<400> 2188

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acgtcacagc	cagagacgac	agacacaacc	ggtgagaaga	aaaacggcag	caataaaacc	180
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atcactgccc	tacagaaagc	gcaggagagc	caaaaagctg	agctggaagg	tgtgatcaaa	360
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<210> 2189

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2189

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aagctcgtgg	gcgagatttt	tgtgtaccac	atgcggttca	accgtgcact	gggtcttgag	180
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<210> 2190

<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 2190

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catcacatgc	togaagccag	cctgggctac	tttattaacc	cgctgggtcaa	tattttgtctg	360
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<210> 2191

<211> 756

<212> DNA

<213> Enterobacter cloacae

<400> 2191

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<210> 2192

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 2192

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ggctatcaat	ttgatctgaa	aggtgacgag	tgggtctgcg	accgcagcgg	cgaaacgttc	300
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<210> 2193

<211> 966

<212> DNA

<213> Enterobacter cloacae

<400> 2193

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<210> 2194

<211> 1224

<212> DNA

<213> Enterobacter cloacae

<400> 2194

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<210> 2195

<211> 1224

<212> DNA

<213> Enterobacter cloacae

<400> 2195

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<210> 2196

<211> 3081

<212> DNA

<213> Enterobacter cloacae

<400> 2196

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 <211> 819
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2198
 <211> 348
 <212> DNA
 <213> Enterobacter cloacae

<220>
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 <222> (152)

<220>
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 <222> (157)

<220>
 <221> unsure
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<220>
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 <222> (171)

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<210> 2199
 <211> 2013
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2200

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 2200

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<210> 2201

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<400> 2201

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<210> 2202

<211> 2424

<212> DNA

<213> Enterobacter cloacae

<400> 2202

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 <211> 1434
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2204
 <211> 537
 <212> DNA
 <213> Enterobacter cloacae

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 gttgataacg tggccgttgg cgcgaacgta cgcctgttgc agggcgctgt tttcattgag 180
 ccattttccg tcgaactggc ggttgttctt caaccgcgcg ccgctgattt tcagcagttc 240
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<210> 2205
 <211> 981
 <212> DNA
 <213> Enterobacter cloacae

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 gataaacctc atcagccacc gaaagtgtgg gaatggaaac agaataaccg cggcgcgttc 180
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 gaagagctgc tggcgctggg cgtgacgggc gcggaataac acgcatgggt gatccgcatt 360
 ggcgagggcg atcagttctc cagcggtttt gtcgacgtga acccgaactc gaagatcccc 420
 gccctgcgtg accactccac caaccgcgcg acgcgcgtct ttgaatccgg caatatcctg 480

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ggcgagctga	acgagcagtt	gcatgagcgt	cattcagcaa	gcgacttcga	taccagacg	960
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<210> 2206

<211> 281

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(180)

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<221>unsure

<222>(194)

<220>

<221>unsure

<222>(199)

<400> 2206

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tcaccggcgg	caagaaagac	accaccgtct	tcttcgcgcg	ggataaaacc	gtcgattatn	180
gaaaaaccca	nttnggggna	atgaaggtaa	tggacacgct	gcatcaggcg	ggctacctga	240
agatttgtct	ggtcggcgaa	gagaaagcgg	ccgcgaagta	a		281

<210> 2207

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 2207

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gccagcggt	ttccactggg	tgcgtctttg	ggccacgggc	tggaaaatgc	ccggcttgcc	120
gctgcccggg	ttttcacctc	cgggggtttc	accaccagga	ttctcaccgc	caggattttc	180
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ggaggtcaaa	atgcggtagc	tttggcccg	tttatagctg	gtttgcggat	ccagcgcggg	480
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<210> 2208

<211> 645

<212> DNA

<213> Enterobacter cloacae

<400> 2208

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cccacggtca	aagaacacat	cagcaatata	ttgaaaaaga	taggcgttaa	cagccggggt	600
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<210> 2209

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 2209

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gcgaaaaacg	tcccggataa	taagctgatg	tggtatgtga	ttatccacct	gacgtttgtg	480
ctgtcggcgt	ttgtgatggg	gtatctggat	aagatcagta	agaaataa		528

<210> 2210

<211> 1677

<212> DNA

<213> Enterobacter cloacae

<400> 2210

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<210> 2211
 <211> 1872
 <212> DNA
 <213> Enterobacter cloacae

<400> 2211
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<210> 2212
 <211> 390
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2213
 <211> 1062
 <212> DNA
 <213> Enterobacter cloacae

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cccaccaccg	agctgtaccc	gatgtcaaaa	atcaacgaag	cgatccagca	cgtgcgcgac	1020
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<210> 2214

<211> 2880

<212> DNA

<213> Enterobacter cloacae

<400> 2214

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<210> 2215

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 2215

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<210> 2216

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 2216

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<210> 2217

<211> 1572

<212> DNA

<213> Enterobacter cloacae

<400> 2217

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<210> 2218

<211> 4503

<212> DNA

<213> Enterobacter cloacae

<400> 2218

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<210> 2219

<211> 1428

<212> DNA

<213> Enterobacter cloacae

<400> 2219

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<210> 2220

<211> 1665

<212> DNA

<213> Enterobacter cloacae

<400> 2220

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<210> 2221

<211> 1032

<212> DNA

<213> Enterobacter cloacae

<400> 2221

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<210> 2222

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 2222

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<210> 2223

<211> 675

<212> DNA

<213> Enterobacter cloacae

<400> 2223

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<210> 2224

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 2224

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accattgagc	tgctgaatcg	ccagggtggto	cagttcatcg	atcttttcgct	gatcaccaaaa	180
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<210> 2225

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 2225

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<210> 2226

<211> 2328

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1615)

<400> 2226

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<210> 2227

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 2227

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<210> 2228

<211> 2583

<212> DNA

<213> Enterobacter cloacae

<400> 2228

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<210> 2229

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 2229

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<210> 2230

<211> 1224

<212> DNA

<213> Enterobacter cloacae

<400> 2230

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gtgcgcgccc	tgtgcgttaa	agagacgcgg	cagatcgctg	gcgatcccag	cagctggctg	180
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cgctacttcg	tgagcacgct	gcaaagcctg	ttcctggcgg	ggaatattcc	ggtagtgtg	1140
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aaaaccaaac ggcggttaga ttaa

1224

<210> 2231

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 2231

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gcggtgtctt	cgcaggctgc	cgacaaactg	gttgtggcga	cggacacggc	gttcgtaccg	180
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gcaactgaaa	ccaaaaacgt	tgacctggcg	ctggcaggca	tcaccattac	cgaagagcgt	360
aaaaaggcca	tgcattttct	tgacggctac	tacaaaagcg	gcctgctggt	gatggtgaaa	420
gcggataaca	acgatgtgaa	aagcgtgaaa	gatctcgacg	gtaaagtggg	cgccgtgaag	480
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ttcccgaaaca	tgcacaacgc	ttacatggaa	ctgggcacca	atcgcgcgga	tgcggtgctg	600
cacgatacgc	ctaacatcct	ttacttcac	aaaactgccg	gtaacggcaa	gttcaaagcg	660
gtaggtgatt	ctctggaagc	tcagcagtag	ggtattgcat	tcccgaagg	cagcgacgac	720
ctcgtaaca	aagttaacgg	cgcactgaaa	accctgaaag	agaacggcac	ctataacgaa	780
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<210> 2232

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 2232

cgccccgttg	cgcttacgct	taccgggcct	acgtttttcg	tttttcacca	cggtatacag	60
gaatacatca	tgcagtttga	ctggagcgcc	atctggcctg	ccattccact	cttgcttgaa	120
ggcgctaaaa	tgacctgtg	gatttcggct	ctcggtctgg	ttggcggggt	gattatcggt	180
cttgctcgccg	gtttcgcccc	cacctacggt	ggctggattg	caaatcacat	cgcactgggt	240
ttcatcgaa	tgatccgcgg	cacacccatt	gtggtgcagg	tcatgttcat	ctacttcgcc	300
ctgcgatgg	ccttcaccca	cctgcgcatt	gaccogttoa	gcgcgcgcgt	tgtcaccatc	360
atgatcaact	ccggcgcccta	cattgcggaa	attacccgcg	gtgcggtgct	gtcgattcat	420
aaagggttca	gtgaagctgg	cctggcgcta	ggtctttccc	gtcgcgaaac	catccgtcac	480
gtgatccctg	cgtggcgct	gcgcgcgatg	ctgcgcgcgc	tgggtaacca	gtggatcacc	540
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caggagatca	tcgcgggtaa	cttcgcgcgc	ctggaaatct	ggagtgcggt	cgcggttgct	660
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<210> 2233

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 2233

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ggtgaagggc	agattaattt	caccggagaa	attatcgatt	ctgcttgcca	ggtcgtgaat	180
ggattaagta	atccattaga	tgttcagttg	ggaaaagtat	ctaaaacggg	atttaccggg	240
gcaggctcta	ccagcacatt	aacgaagttt	gatattaagt	taaccaattg	tccggaaacc	300
gtaacctcgg	cagcgattaa	cttcgggtgg	accccgcatg	cggataataa	tgccgcgctg	360
gcgttaacgc	ccgataccga	tgcggctacc	ggtgtggcta	ttcagctggg	tgacacgtcc	420
gggcagcctg	tcagcctgta	tacctcttcg	aagcaatatc	ctttagcctc	cggcacggcg	480
gttaacgata	tggagttcgg	tgcgcgttat	attcaaacc	aggcggcagt	caccgcgggc	540
cctgctaact	ctgtatcaac	cttcaccggt	atttataact	ga		582

<210> 2234

<211> 684
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2234
 gaaatcttta tgcgccacgg ttatttactg agcattcttt tactggtagc agcctcggca 60
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 tctctcgggc tttcaaaccg ggataccacg gattatctgg tgcagtcctg ggtcgaattct 180
 ggcggtaaaa accaagccaa agccccgttc ctgatcaccg cgcgcgtttt tcgactggat 240
 gcgaaagagg ataacgtcct gcgcgtagtc cgtacggggg gaaatttacc ggaagacagg 300
 gaatctctgt actggctgaa tattaagcgc atccccgtct cgaagcatgt cgaaggggta 360
 aatacgtctg aaattgccat taataccgcg attaaattgc tctatcgccc gtcagcggta 420
 aaaggcagac cagaagatgt ggccgataaa cttgaatggc atcgcaagg gaatgattta 480
 gtggtgaata atccacacc tttctttatg aattttcaga ccgtcacccg gaatggacag 540
 aaagtcaaaa aagccacctg ggctgtgcgg aaaactgaaa cgcattttgc tttacctggc 600
 aacgtcggag gttctaccgt cgcgtattcc attattaccg attacggcag catcagtcag 660
 acatggtcta aaccggtca ttaa 684

<210> 2235
 <211> 1065
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2235
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 gccgcgttat ttatgccgca tgcgaaggcg acctgcacca cgcgggatct gcccaaatg 180
 attaacatgg cctccatttc tgtcccgcag acgctggcgg ttggtgcaac cattccgggt 240
 acagagcaga gcgttcattg tgcggggcac tgcgatcaga gtatcgacag cggactggaa 300
 attgtctcgt gttactacgg tacccgagcg gaaattccgg ggctgaaggg agtatacgaa 360
 tccggcgtac cgggtgtcgg tgcgcattg atgaacgac agggtcagcg aatcagcga 420
 gcaggcggag tacagtgcga ttacgcggga acgcctgttg gctatgtttc tggcgatggc 480
 acacagtcgt ttaactttga cgtcacgctt gaactggtea aaacaagcga cgcctgacc 540
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 tctgtttcgc caaaaaatct caccgttaac ttgggtgatt ttcccgtcag tgattttatg 720
 agcgtgggtt ttttatccag ccccgctcaa acgtttaata tcaccgttaa ctgtgacaca 780
 accgttcagc ctgagctaaa aatcaccagt gctaacagct acgagacggc attcaggggg 840
 gtgatcaaac tgacgaagca gacaggcatg gcaacggcg tcgggggtgag aatgctgttt 900
 gatgaccgca ttgcgacctt tgatacctac gtcaacactc aaagccaggc cgttgccaat 960
 gaaacgctgg agatccccct tcagggttcg taagagcaga tcagcgatgt ggtgacgccc 1020
 ggccccgcca acaccgtagc aaccatcact ctgcctata agtga 1065

<210> 2236
 <211> 1035
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2236
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 cagcaggatc gtggcctgac gctgtatggc aacgtggata tccgcaccgt gaacatgagc 180
 ttccgcgttg ggggacggct ggccctcgctg aacgttgacg aaggcgatgc catcaaagcc 240
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 gcaggcgtct ccgtcgacac ggcgcaatac gacctgatgc tggcgggcta tcgtgacgaa 360
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 aatttttata accgtcagca aggcttatgg aaaagccgta ctatttcgc caacgacctg 480
 gaaaatgcgc gctcatcccg cgaccaggca caggcgacgc tgaaatctgc ccaggataag 540
 ctaagccagt accgcaccgg taaccgtgcg caggacattg cccaggcgaa ggccagcctt 600
 gagcaggcgc aggcgcagtt agcccaggcg gagctggatc tgcacgacac cacgttaatc 660
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ggcagcaccg	tggttaacgct	ctccttaact	cgtccgggtgt	gggtgcgcgc	ttacattgat	780
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accgatgcgg	acgacgcgct	gcgtcagggc	atgcctgtta	ccgtgacctt	aaacgcaggg	1020
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<210> 2237

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 2237

acagatcagg	agaacatgat	ggcttcgggc	tgggcgaatg	acgacgccgt	taacgaacag	60
atcaacagta	ctattgaaga	tgccgtcgcg	cgtgctcgcg	gtgaaattcc	acgcggcgaa	120
agtttgacgg	aatgcgaaga	gtgcggagat	ccgattcctg	aggcacggcg	taaagccatt	180
cctggcgtag	ggctatgtat	tgccgtctag	caggagaaag	attcgaaaaa	tgcgacacat	240
tcaggatata	atcgagagg	atcgaaagac	agccagttag	gttga		285

<210> 2238

<211> 264

<212> DNA

<213> Enterobacter cloacae

<400> 2238

cctatgaaaa	ccatcaaata	tgctgttgcc	gctgttgccc	tgtccgctct	ctcttttcggc	60
gcttttcgcc	tagagccagt	ctcctctact	caggcacagg	atctgaacaa	aatcggggtg	120
gtgagtgtcg	aaggcgcgac	cacgctggac	ggtctggaag	ccaaactggc	ggaaaaagca	180
gccgctgcgg	gcgcaagtgg	atacaccatc	acgtccacta	acggtataata	caaactgagc	240
ggtactgcgg	ttatctacaa	gtaa				264

<210> 2239

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 2239

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cgggatatcg	ccgctcaggc	cgggcagaat	attgcggcca	tcacctacta	ttttggctca	180
aaagaggatt	catacctcgc	ctgcgcccag	tggatcgcg	attttatcgg	caccagcttt	240
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tataccggac	gggacgccag	cgataccgac	accattttgc	atacccacgc	cctgctgggc	540
gaagtgtcgc	ccttcogtct	ggggcgtag	accatcctgt	tacgtacggg	ctggacacaa	600
ttcgatgagg	ataaagccgc	gcaaattagc	caggtcatta	cctgtcacgt	tgatctgac	660
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<210> 2240

<211> 1755

<212> DNA

<213> Enterobacter cloacae

<400> 2240

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ccgggaatgg	ctaaaccggc	ggtgcgaccg	ctgaattgta	cgattcagaa	aggctatgtg	120
accgggctgg	tggggccgga	cggcgcggtg	aaaaccacgc	tgatgcggat	gctggcggga	180
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<210> 2241

<211> 1407

<212> DNA

<213> Enterobacter cloacae

<400> 2241

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ccggccgttt	tgcagggccg	tgacctgatg	gcaagcgcg	agaccggtag	cggtaaagacc	180
gcgggcttta	cctgcgcgt	gctggagctg	ttggtaaaaa	accagccgca	cgccaaaggc	240
cgtcgtccgg	tgcgtgcgct	gacctcacc	ccaaccccg	agctggcggc	ccagattggc	300
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ccggggcgct	tgtggatct	ggaacaccag	aacgcggtga	agctcgataa	catcgaaatc	480
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gcggcgatcc	acggcaacaa	gagccagggc	gcgcgtaccc	gtgcgctggc	ggacttttaa	900
tctggcgaca	ttcgcgtgct	ggtggcaacc	gacatcgccg	cacgcggtct	ggatatcgaa	960
gagctgcgcg	acgtggtgaa	ctacgagctg	ccaaacgtgc	cggaagatta	cgttcaccgt	1020
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gaacacaagc	ttctacgcga	cattgaacgc	ctgctgaaga	aagagatccc	gcgcattgaa	1140
accccgggct	atgaagtgg	cccgtagatc	aaagccgagc	caattcagaa	cggtcgtcag	1200
ggtggcgga	gcggtcaggg	cggcggtggt	cgcggtcagc	agccgcgctg	ttcagaaggt	1260
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ggaaacccgt	ggcgtagcgg	cgaaggga	ccggcaggcg	aggggcagcg	ccgacgccgc	1380
ccgcgtaaac	ctgctaacc	gcagtaa				1407

<210> 2242

<211> 309

<212> DNA

<213> Enterobacter cloacae

<400> 2242

accagcccga	tacgggtcgca	atactccgcc	tcgtccataa	agtgggtggt	gaccatcacg	60
gtcacgcctt	tttccaccat	gctattgata	tgcaaccaga	attcacggcg	ggtgagggga	120
tccacgcctg	acgtagggtt	atcaagaaac	aggatatccg	gctcgtgcat	caacgagcag	180
gccagcgcca	gccgctgttt	gaagccaagc	ggcagcgcg	cggtcgcctg	cgaggcgata	240
tcggtcaggc	cgaaggcgtc	gcacatgcgg	ccgatcttct	ggttctgcgc	ccgtccccgc	300
aggccatag						309

<210> 2243

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 2243

cccaggtgct	ggcgcgcctt	gccggagctg	actttgagat	ccatgttcag	caccagcgct	60
ttgccggacg	tcggtaccag	cagaccgcac	atcattttta	aggtggtgga	ttttcctgcg	120
ccgttcggcc	cgagcaggcc	aaatatctcg	ccgcgccttca	cggcaaaatt	gacgttatcg	180
gtggcggcga	aatcgccgaa	ttttttgggt	agcgatttct	cttcaatgac	cgtttcgccc	240
ggcgtacctt	ccaccgtgtg	cagaatggcg	ccaagcggtg	attctgaggt	ccccgccccg	300
cccagcagat	caataaacgc	atcttcaaag	cgcggcgagg	tctctgtcat	gtcgatctca	360
ggcatccctt	gcgcacgcgc	gatatcgctg	gcggtggcct	cttttttgag	gatcacgcgc	420
accgaacggc	cctga					435

<210> 2244

<211> 2256

<212> DNA

<213> Enterobacter cloacae

<400> 2244

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<210> 2245

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 2245

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<210> 2246

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 2246

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<210> 2247

<211> 444

<212> DNA

<213> Enterobacter cloacae

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<210> 2248

<211> 735

<212> DNA

<213> Enterobacter cloacae

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<210> 2249

<211> 771

<212> DNA

<213> Enterobacter cloacae

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<210> 2250

<211> 1110

<212> DNA

<213> Enterobacter cloacae

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<210> 2251

<211> 1209

<212> DNA

<213> *Enterobacter cloacae*

<400> 2251

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<210> 2252

<211> 498

<212> DNA

<213> *Enterobacter cloacae*

<400> 2252

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<210> 2253

<211> 645
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2253

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<210> 2254
 <211> 693
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2254

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<210> 2255
 <211> 753
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2255

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<210> 2256
 <211> 474
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2256

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<210> 2257

<211> 978

<212> DNA

<213> Enterobacter cloacae

<400> 2257

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<210> 2258

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 2258

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cgtctggagga	ttgcgaaatc	gcgatacct	cgcgctccac	ggaaaataac	cccatcgccg	180
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<210> 2259

<211> 2598

<212> DNA

<213> Enterobacter cloacae

<400> 2259

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<210> 2260

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 2260

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<210> 2261

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 2261

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gtcctggcgc	tttgtgctgg	cgacggcggg	cggtatgctc	tctacgggtg	tgatgatgcc	480
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<210> 2262

<211> 1257

<212> DNA

<213> Enterobacter cloacae

<400> 2262

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<210> 2263

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 2263

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<210> 2264

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 2264

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<210> 2265

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 2265

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<210> 2266

<211> 492

<212> DNA

<213> Enterobacter cloacae

<400> 2266

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<210> 2267

<211> 1161

<212> DNA

<213> *Enterobacter cloacae*

<400> 2267

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<210> 2268

<211> 1200

<212> DNA

<213> *Enterobacter cloacae*

<400> 2268

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<210> 2269

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 2269

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gccagccgt	atctcggcaa	atggtatgaa	gtcgcccgac	tggaaaaccg	ctttgagcgc	180
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tataacgtga	tcaagctgga	cgataagtac	cagtacgcgc	tggtcagcgg	ccggaaccgt	420
gactacctgt	ggattttatc	gcgcaccccg	accattccgg	atgcggtaaa	acaggactac	480
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<210> 2270

<211> 492

<212> DNA

<213> Enterobacter cloacae

<400> 2270

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tatgaaccgc	aattttttgt	ctatccgggc	aagagtattt	atatgcggat	caatgaacaa	420
cataatggta	actatatctt	taccttagga	acattaccga	catatgtgtg	tcgtggttca	480
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<210> 2271

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 2271

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<210> 2272

<211> 2379

<212> DNA

<213> Enterobacter cloacae

<400> 2272

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<210> 2273

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<400> 2273

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<210> 2274

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (942)

<400> 2274

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<210> 2275

<211> 183

<212> DNA

<213> Enterobacter cloacae

<400> 2275

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tcgggctcgt	cgcgatcgcc	cggtttgggt	accagcggaa	tggccgcaaa	ttcatcctgg	180
taa						183

<210> 2276

<211> 303

<212> DNA

<213> Enterobacter cloacae

<400> 2276

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gcagagggcg	cctgccagag	cagtaaccaga	cccacggtct	caatgacaag	tgacgacacg	180
gccaccttca	cgcgcgcaaa	gcgatccagc	atccagccaa	acagcacgcg	catcaataca	240
aacgcgcccgc	caaaggccgt	cagcgtaaag	cccgccatcg	cccagccgcg	gctcatgaaa	300
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<210> 2277

<211> 2172

<212> DNA

<213> Enterobacter cloacae

<400> 2277

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<210> 2278

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2278

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<210> 2279

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 2279

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<210> 2280
 <211> 822
 <212> DNA
 <213> Enterobacter cloacae

<400> 2280
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 ctgatccgcc cgatgattgt tgcgtctcgc gcggtgatga gcgccaaact tctttatgac 780
 agccatggac aggagatcct cacctggttg gggatgaact aa 822

<210> 2281
 <211> 366
 <212> DNA
 <213> Enterobacter cloacae

<400> 2281
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<210> 2282
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 <212> DNA
 <213> Enterobacter cloacae

<400> 2282
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1218

<210> 2283

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 2283

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<210> 2284

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 2284

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<210> 2285

<211> 2151

<212> DNA

<213> Enterobacter cloacae

<400> 2285

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<210> 2286

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 2286

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aaaatagtag ctgttatcgg cctgctcctg gagcagacgt ttgacgggaa cctcgtgat 60
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cagctggcgg aagagagcct gatcctcctc gctgagcgat gttttctttt tcattcgtca 180
ttctcatctc gtatttccga tagtgtaccc gactaa 216

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<210> 2287

<211> 975

<212> DNA

<213> Enterobacter cloacae

<400> 2287

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<210> 2288

<211> 912

<212> DNA

<213> Enterobacter cloacae

<400> 2288

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ccggtccaca gaattgccct cggcattgaa tacgatggca gtaaatacta tggctggcag 180
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<210> 2289

<211> 1281

<212> DNA

<213> Enterobacter cloacae

<400> 2289

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<210> 2290

<211> 288

<212> DNA

<213> Enterobacter cloacae

<400> 2290

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<210> 2291

<211> 1344

<212> DNA

<213> *Enterobacter cloacae*

<400> 2291

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<210> 2292

<211> 1023

<212> DNA

<213> *Enterobacter cloacae*

<400> 2292

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<210> 2293

<211> 1146

<212> DNA

<213> *Enterobacter cloacae*

<400> 2293

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ccgggccaca	cgattaaccg	cgctggcgat	gaagttgaga	tgatcaccaa	agggcgctac	1020
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atggatcact	tcctgcgcca	gcgcgcgcag	aatgcggatg	tgacgaccac	cattccacgc	1140
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<210> 2294

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 2294

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ggttatctgt	atcggcctct	atttcttact	catgccaaag	ctcggggaag	aagatcgaca	180
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cggctctgctg	ctgtttatca	ttggcgggcaa	ggttatctgg	gcaaccgggt	ttgtgatgat	420
ggcagggcag	tttttggggc	cgcgcgcagg	ctcgctctctg	gtattaagca	aagggcaaaa	480
gctgatccgc	ccgatgattg	ttgtcgtctc	ggcggtgatg	agcgccaaac	ttctttatga	540

<210> 2295

<211> 588

<212> DNA

<213> Enterobacter cloacae

<400> 2295

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gacgcgcgca	cccaggggca	gtttgaagat	gtggaggtga	aacccagggc	gctggaatgg	360
ctgtttctgc	tgggcggggg	tttcccgctt	aacgtgagct	gtgacaacct	cgaaggcgac	420
ttcgagccag	accgtatcgt	cttcacgcgc	cgcgttcatg	cgcaggtgat	ggaatatctt	480
gagaaaggca	tcccggcacg	tccggcacgc	ctgatcgagg	ctttacagaa	ttattaccac	540
acgcgcggaga	tcacggcgga	acgttctccg	tgcccggaag	atctttta		588

<210> 2296

<211> 1239

<212> DNA

<213> Enterobacter cloacae

<400> 2296

aggtatagta	gaagggagcc	gcgcggctcc	ctttttttat	gcctgaacac	ggagttatgc	60
atgaaggctg	ttacccttga	gaagagcgct	ccttcgggga	acctttccct	tttccgcata	120

gccttttgccg	tgttttctgac	ctatatgacc	gttggcctgc	cgctgccggt	gatcccccttg	180
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gtggccgtgt	cgtcacttgt	cattgagacc	gtgggtctgg	tactgctctg	gcaggcgccc	960
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cttgcaacgt	cgtttggcta	tccttccgta	ttctcgcgcg	gtgcggtgtc	agcgggtggt	1200
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<210> 2297

<211> 1167

<212> DNA

<213> Enterobacter cloacae

<400> 2297

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ccggtcagcg	aactggacga	tgcagacgcc	ctgatggtgc	gctcgggtgac	ttaaagtaaat	180
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tccctgtatg	tcatgtgcga	tgacgcgtca	gcggcggggc	tgctgcataa	actgggattt	1140
aacgccgttc	accaccgggc	acgttaa				1167

<210> 2298

<211> 1020

<212> DNA

<213> Enterobacter cloacae

<400> 2298

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cgtaccgaca	gcgcaggaga	acagctgcgt	ttcggcgggg	aatccttgat	ggtgcaggac	180
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ctgttctccc	tggagccgga	tgtgtcgtcg	gtgggtgccg	acgtcaaccc	gtttgtgctg	360
gctgactacc	gcaaccgcaa	catcattgca	gtaccgaaca	gcctcaccag	ccagctgctg	420
accgcgctga	agccgctgat	cgacgacggt	ggcctgtcgc	gtatttccgt	gaccagcctg	480

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atgctgccgc	tactgccgga	tcgtgaaggt	tcggtgcggg	aagagcgctc	tatcgtcgat	660
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aacgattacg	gtatgcctga	gcaggtgcag	ttctggtctg	ttgccgacaa	cgtgcgtttc	960
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<210> 2299

<211> 672

<212> DNA

<213> Enterobacter cloacae

<400> 2299

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ctgatgatca	tcgccgcgat	tgttggtgat	gcggccaact	acaccatcgg	gcgggtgttt	300
ggcgagcggg	tgttcagtaa	tccggactcg	aagattttcc	gccgcagtta	tttagataag	360
acccatgcgt	tctatgagcg	ccatggcggg	aagaccatta	tccttgcccg	ttttgtgcct	420
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gtgctttccg	tactgcctgg	cgtcatcgaa	attatccgtc	acaaacgcgc	ggcggcgaag	660
caagcgaagt	aa					672

<210> 2300

<211> 339

<212> DNA

<213> Enterobacter cloacae

<400> 2300

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caggatgaat	ttgcggccat	tccgttggtg	cccaaacccg	gcgatcgcca	cgagcccgat	180
atgctgccag	cggcaacgca	ggcgctgcct	gccagccgcg	cagaaggcgc	agcgggaagag	240
gtgcgcgcag	gtgatgcagc	cgcgcgcgtc	ctcgatccct	cgcgcctggc	gacgaacaat	300
cacattcttc	accaaggggag	ctgccgctcc	gcatacacac			339

<210> 2301

<211> 771

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (755)

<400> 2301

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cgtccactga	agcgcataaa	gtctcctcgt	gacgaagatg	acgttgaaga	cgacatcgac	120
ggctcttgac	acgacggcgt	gggtgaagtt	cgtgttctac	gggtcaatac	tgcccccggc	180
gcagcgcatg	gagacgcata	agccccccgc	gctccgcagc	accagtatca	accaccgtat	240
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cgcaccagc	ctgtgcaaca	gcagcccggt	gcgccacagc	ctgtacagcc	gcaacctgtc	360
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caaccgcagc	cgcagcctga	accgcctgcg	ccacagcccg	ccccgcgcgc	tgagccagag	480
ccggttgacg	agccagaacc	ggttggtgaa	aagccgcagc	gtaaaagaagc	ggtgatcatt	540

atgaacgtgg	ctgctcatca	tggcaccocat	ctgaacgggtg	atgtgctgct	taacagcatc	600
caacaggcag	gcttcaagtt	cggcgacatg	aataattttcc	atcgccacct	gagtcctgac	660
ggcagcggtc	cggcgctgtt	cagcctggcc	aatatggtca	atccaggcac	gttgggtcttc	720
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<210> 2302

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 2302

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cgtgctacca	cgcggctatg	tattcagtg	ggactttttc	tcttacaaca	cggggcagaa	120
agcgccctcg	tcgaagaact	ttccacacgc	cttgggtctg	cgtggggat	ggacagcgtt	180
gagagctcca	tctcgtcaaa	tgccattgta	ctgaccacca	ttaaagacgg	acagtgcctc	240
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cacattgtga	tccttgctga	acacaggctg	ctcgatctgc	gggaaataga	gaaacgcttc	360
aaccagatca	aacctctccg	gtatccacgc	tggtggttg	tgctgatgg	gggactctcc	420
tgcgctgct	tctgcaagct	caacgcgggc	ggctgggacg	gcgctgtcgt	gaccttcttt	480
gccagcagca	tcgcgatgta	tgtccgccag	ttgttgacgc	acaggcaact	gcatccgcaa	540
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ccttacttcg	ccagcacggc	tactgttgcg	atggccgccca	gcgtattgct	gctgggtgccg	660
ggttttccct	taatcaatgc	cgtecgctgat	atgttcaaaag	gccacatcaa	caccggtctg	720
gcgcgctggg	cgatagccag	cctgctgacg	ctggcgacct	gtatcggggg	ggtaatggcc	780
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<210> 2303

<211> 1479

<212> DNA

<213> Enterobacter cloacae

<400> 2303

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ggcgaagccg	aaatccatca	ggcggttgce	gcccgcacaa	aggcgttccc	gaaatgggcc	180
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aacgtgccgg	acattgccgc	gatggagacc	gcgcacaccg	gcctgccgat	ccaccagacc	300
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cagatgaacg	gcaaaaacct	ccgggtcgac	gacaagatgc	tcaactacac	cctgggtgcag	420
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gggcgcgaag	gcggcgagta	cagcttcgag	gtattcgcg	agatgaagaa	cgtgtgcac	1440
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<210> 2304

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 2304

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gaaaggccac	aagatcggcc	ttacctccaa	agcgatgcag	gccagctcgc	agatcagcga	120
gccggactac	ggtgcgctgc	tggacgatat	gttcttccac	gacggcagcg	acatccccgt	180
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gcgcggcccg	aactgcacga	tcttcgacgt	ctacaacgcc	acggattacg	tcacccccgc	300
cctggagctg	atcgacgcc	gctgccataa				330

<210> 2305

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 2305

gggccgtacg	gacaaagaaa	ccccgtacgt	gccggtgccg	gaaggcggcg	tgaagacctc	60
ctcacaccat	taattaagca	tgttactgta	ggcccggtac	gctgcgcgcc	tccgggcttc	120
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gcggcgaaaa	tgttgattgg	cattccggac	tatgacaact	acgttgagca	tatgaagacc	240
aaccatccgg	ataagccgta	catgacttac	actgaattct	tccgcgagcg	tcaggaagcg	300
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<210> 2306

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 2306

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actaacgcgc	ttctgctgga	taaccagctc	tgttttgccc	tctattcggc	aaatctggcg	120
cttaacaagc	tctaccggca	actgctggcg	ccgtttaacc	tgacctacce	gcaataacctg	180
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cgggcgctgc	aacagcaggc	cgtgacgata	ccccacgcgc	tgggctgtgc	agcgcagtgt	420
gataccgaca	ccatgctggc	gctcaagcac	cagctcgaac	ttttgcgcca	acagcttcat	480
cgcgcgtaa						489

<210> 2307

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 2307

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cccaaagaga	tgggtggcat	gggggggtgaa	gtaaccaacc	ctgaacagct	gttcgctgcg	180
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gtgacgctga	acatcatcgc	gtaa				444

<210> 2308

<211> 756

<212> DNA

<213> Enterobacter cloacae

<400> 2308

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aaggctcag	cgcaggggca	gatgaacgcc	ctcaaccagg	cgcgccagta	tgtggatgaa	300
tttgacggca	acattgccag	cttcattctt	agcggaaaac	ccggcacggg	gaaaaatcac	360
cttgccggcc	ctatctgcaa	cgagctgctg	ctgcgcggga	agtcagtgtc	gattatcacc	420
gtggccgata	ttatgtccgc	catgaaggac	accttcagca	accgcgaaac	cagcgaagaa	480
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<210> 2309

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 2309

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gagagcggca	cttccagagg	cgggctgtca	gcctcgctcc	tcaccggcct	gctgagtaac	180
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<210> 2310

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 2310

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tcgtgacgt	taacgacgtt	togtgaatgc	ccgtggaatg	cgccttctca	caggcgatta	420
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<210> 2311

<211> 1314

<212> DNA

<213> Enterobacter cloacae

<400> 2311

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<210> 2312

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 2312

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<210> 2313

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 2313

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<210> 2314

<211> 2319

<212> DNA

<213> Enterobacter cloacae

<400> 2314

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<210> 2315

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 2315

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cgcctgacgc	gcattaaactc	gcgtgcgccc	atcttatacgg	tgacgcacgg	cgatatcgat	660
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<210> 2316

<211> 588

<212> DNA

<213> Enterobacter cloacae

<400> 2316

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<210> 2317

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2317

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<210> 2318

<211> 2334

<212> DNA

<213> Enterobacter cloacae

<400> 2318

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<210> 2319

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 2319

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<210> 2320

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 2320

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<210> 2321

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<400> 2321

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<210> 2322

<211> 1365

<212> DNA

<213> Enterobacter cloacae

<400> 2322

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<210> 2323

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 2323

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<210> 2324

<211> 1686

<212> DNA

<213> Enterobacter cloacae

<400> 2324

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<210> 2325

<211> 1704

<212> DNA

<213> Enterobacter cloacae

<400> 2325

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<210> 2326

<211> 1788

<212> DNA

<213> Enterobacter cloacae

<400> 2326

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<210> 2327

<211> 456

<212> DNA

<213> Enterobacter cloacae

<400> 2327

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<210> 2328

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 2328

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<210> 2329

<211> 1503

<212> DNA

<213> Enterobacter cloacae

<400> 2329

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taa

1503

<210> 2330

<211> 822

<212> DNA

<213> Enterobacter cloacae

<400> 2330

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cgctactggc	tgcaatgtga	gcgagcgta	acttatcagc	ccatctaccg	taccgacggt		180
cggttaatgg	cgattgaggt	gttaacggtc	gtcactcacc	catcgaatcc	ttcacagcgt		240
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gagcagctga	gaatgctggc	gacgaagcag	gcgttcttca	agcagcacgg	tattctggcg		360
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gactcctcgt	ttgctcgat	gtgtgagttt	ggcccgctgt	ggctggatga	tttcggtacc		540
ggtatggcca	atttctccgc	cctgagcgaa	gtgcgttatg	actacatcaa	agtggcccgc		600
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<210> 2331

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 2331

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gaggcgcagg	a	agttgtgcg	cgaaattgag	ggaaaaggcg	gaaaagcggc	agcattgcag	180
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<210> 2332

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 2332

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gatgggtatt	t	aattcgtga	taatggtgtg	gctttactgg	aagagattat	ggatcgcttt	300
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gcggccggag	a	gtccaataa	agagattgga	cgtaatctca	atatcagtgc	ggcaacggta	600
aaagcccata	t	tgagacgct	tttccggcgt	cttgatgtca	aaaaccggac	gcaagccgcg	660
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<210> 2333
 <211> 2229
 <212> DNA
 <213> Enterobacter cloacae

<400> 2333
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 gcgtttatga ccaatccatt actgacgctt ttttcgttgc caccgttttc taaaatcctc 240
 cctgagcatg tggttccagc gggttacgaa tcgctggaca actgccgcgc gccggtagaa 300
 agcgtggctg cgcagggcgc gccgtacacc tgggaaaatc tgtgtcagcc gctggccgaa 360
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<210> 2334
 <211> 462
 <212> DNA
 <213> Enterobacter cloacae

<400> 2334
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 ggatgtatga ttagcacctg cgcattgttt tgggcgttat gcgtggtttg catagtgaat 180
 atggcgcgct acttctcctc gttacgtgag ctgttagtgg tacttcgtgg ttgcgatccg 240
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 cagatgcgtc tgggtggggt tatctactac caacgctacc gcgatcacca cgatgaagag 360
 tttatccgtc gctgcgagcg cctgcgtcgt cagttcattt tgaccagcgc cctctgtggt 420
 ctgggttggtg tgagtatgat tgcgctgatg atttggcact ga 462

<210> 2335
 <211> 1287
 <212> DNA
 <213> Enterobacter cloacae

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 gcgctggcgc gctataccca gtgggatttt atcgaactgg tgggtaaaca cggtatcgcg 360
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<210> 2336
 <211> 861
 <212> DNA
 <213> Enterobacter cloacae

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 gaacgggctc gtcagctggc gacgaagcgt gtggtggtga agcgcctga ctatgcgcgc 780
 ccgctggcgg acgttgcgac cactaacgcg gtgaccagca aagggcaccg gtttgatatt 840
 tattcgggaa caccggaata a 861

<210> 2337
 <211> 852
 <212> DNA
 <213> Enterobacter cloacae

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 gttaaatccc gtggaaaccg ttcgatagtc tttggcctta agacgtttcg aaaccatcat 180
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<210> 2338

<211> 945

<212> DNA

<213> Enterobacter cloacae

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<210> 2339

<211> 2085

<212> DNA

<213> Enterobacter cloacae

<400> 2339

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<210> 2340

<211> 1701

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1661)

<220>

<221> unsure

<222> (1689)

<400> 2340

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<210> 2341

<211> 1506

<212> DNA

<213> *Enterobacter cloacae*

<400> 2341

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<210> 2342

<211> 1443

<212> DNA

<213> *Enterobacter cloacae*

<400> 2342

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<210> 2343

<211> 1332

<212> DNA

<213> Enterobacter cloacae

<400> 2343

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gttgccctcg	tgtgacgat	ggggatctcc	accgtcgcca	tggcctgct	gccgacctat	360
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<210> 2344

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 2344

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tggagcaaac	tgatgtcttc	cgcgcgccag	ctgattaaca	ccgttcacgt	ggatatgctg	420
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<210> 2345

<211> 1707

<212> DNA

<213> Enterobacter cloacae

<400> 2345

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<210> 2346

<211> 351

<212> DNA

<213> Enterobacter cloacae

<400> 2346

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<210> 2347

<211> 675

<212> DNA

<213> Enterobacter cloacae

<400> 2347

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<210> 2348

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 2348

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<210> 2349

<211> 882

<212> DNA

<213> Enterobacter cloacae

<400> 2349

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aagctcgaag	cacagatgaa	caacgtgctg	ccgtggctgc	acaaaacgct	ggtgccagcc	840
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<210> 2350

<211> 573

<212> DNA

<213> Enterobacter cloacae

<400> 2350

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<210> 2351

<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 2351

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caggcattcg	aaaacgcgct	gggcacgcag	ctgctgcacc	gcactaccgc	ccgcgtcagc	180
ctgacgcagg	acggcatgg	ttattacgag	cgcgccaaag	atctgctgat	gaatctggac	240
gaactggacg	gcatgttcc	gcacgaccct	tcaaccatca	gtggtcggct	acgtgtggat	300
atgcccggtg	ccattgcgcg	aaatgtcgtc	attccgaaac	tgcttcgatt	tttacaacag	360
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<210> 2352

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 2352

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gaagtcagcc	gcggttttgg	tggcgatata	ttgaacacct	ccgtttacat	tgcccgtcag	180
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gcggcgggag	attctttcag	cgcgggggtat	ctggcggtac	gtctgacggg	aggtacgccg	900
gaagcggcgc	cgcagcgcgc	tcattttaacg	gccagcacgg	tgattcagta	tcgcggagcg	960
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<210> 2353

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 2353

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cagcagatcc	ggatcgctta	tcaacgcccg	cgccagcagc	aaccgcgtat	gctgaccgcc	120
gctcagcgtg	gcggattgca	gcgcggtttc	ctgcgtcgta	aagcccattc	cggccagcag	180
cgtctcggcc	ttccagcgaa	gactgtcgcg	ctcaccggtc	ggcagctgcg	ccagcaccgc	240
atccagcatg	gtcaggggat	aaaggggtctc	cggcagatgt	tgttccacgc	gcgccagcag	300
gcaatgtcca	gccagtga					318

<210> 2354

<211> 702

<212> DNA

<213> Enterobacter cloacae

<400> 2354

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coggaaccgt	ggttgatttt	tgcgcgtacg	atgtttggca	atgccggggg	gtttgcctgg	180
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ctgccggcag	cgatcttata	cttctcagcg	atgacctctc	tgttgatgta	tggttattta	660
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<210> 2355

<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 2355

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<210> 2356

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 2356

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gccgattcca	tcgataccac	ggcggatgtc	tccttgata	aaaccgacag	cggttttgce	300
atcagcaaat	tgccgttaca	aagcaagggt	acggtaaccg	gtatcgatcc	gcagcagttc	360
gacggcatta	ttcagaaaag	gaaggcgggt	tgtccgggtat	cgcagctggt	gaaagccgaa	420
atcacgctgg	attacaaaact	gaactga				447

<210> 2357

<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 2357

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gcaggaaaaa	tcgctctggg	gaccgggtgg	agcaccggta	ttggctctgc	aacggcacag	120
gagctggcgg	cgcaggagc	gaaggctctat	atcaccggac	gtcgtcaggc	cgaactggat	180
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atggcgcaaa tctag 795

<210> 2358
<211> 378
<212> DNA
<213> Enterobacter cloacae

<400> 2358
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ccagggccag cagcaaagag cagaaggcca gttccagcgt gccggggaaa aaggctttca 180
aatcttccgc aacggggcga ccgggtgcga tggatgtgcc cagatcgcca tgcgccagcg 240
cctctacata gcggccaaac tgaatataga gcggttgate cagccccagc tgctggcgga 300
tgccctgcac gatttcatcg ctggcgcggt caccggccag caggcggggc ggatcgccgg 360
ggatcaggtg tgaaataa 378

<210> 2359
<211> 1506
<212> DNA
<213> Enterobacter cloacae

<400> 2359
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<210> 2360
<211> 1215
<212> DNA
<213> Enterobacter cloacae

<400> 2360
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gtcgacaga	gcattgagca	gataggagcg	tggtgctgta	ttcgtccacg	aggagaccag	1200
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<210> 2361

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 2361

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ctggatctgg	cacggaagat	gtatcgaaaa	gcgcctgaca	cgttccagat	cgaagttcag	480
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<210> 2362

<211> 1536

<212> DNA

<213> Enterobacter cloacae

<400> 2362

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<210> 2363

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 2363

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<210> 2364

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 2364

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<210> 2365

<211> 1785

<212> DNA

<213> Enterobacter cloacae

<400> 2365

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<210> 2366

<211> 1716

<212> DNA

<213> Enterobacter cloacae

<400> 2366

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<210> 2367

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 2367

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<210> 2368

<211> 867

<212> DNA

<213> Enterobacter cloacae

<400> 2368

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<210> 2369

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 2369

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<210> 2370

<211> 1548

<212> DNA

<213> Enterobacter cloacae

<400> 2370

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<210> 2371

<211> 1044

<212> DNA

<213> Enterobacter cloacae

<400> 2371

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<210> 2372

<211> 930

<212> DNA

<213> Enterobacter cloacae

<400> 2372

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<210> 2373

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 2373

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<210> 2374

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 2374

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1023

<210> 2375

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 2375

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<210> 2376

<211> 2112

<212> DNA

<213> Enterobacter cloacae

<400> 2376

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<210> 2377

<211> 2709

<212> DNA

<213> Enterobacter cloacae

<400> 2377

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<210> 2378

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 2378

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<210> 2379

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 2379

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<210> 2380

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 2380

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<210> 2381

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 2381
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<210> 2382

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 2382
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<210> 2383

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 2383
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<210> 2384

<211> 1362

<212> DNA

<213> Enterobacter cloacae

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<210> 2385

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 2385

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<210> 2386

<211> 2655

<212> DNA

<213> Enterobacter cloacae

<400> 2386

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<210> 2387

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 2387

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cacatacgag	aaacctttga	ccagaatgac	aactatagcc	atgaagtcag	taaatacagt	240
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<210> 2388

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 2388

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<210> 2389

<211> 219
 <212> DNA
 <213> Enterobacter cloacae

<400> 2389
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 tcggttatca cttactccga gatgcgcttt ggccgcacag gtccgaaggc ctccccaccc 180
 cgcgagcagt tgggtgacgc gttctgtgtg ccgttctga 219

<210> 2390
 <211> 288
 <212> DNA
 <213> Enterobacter cloacae

<400> 2390
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 cgtatcaaag gtcagattgc agcgctggaa caggcgattg aaaacgaagc ggaatgttct 120
 tcattgtttg agcaactggc ttccgtacga ggagccgtta aaggcctgat gactgttggt 180
 ctggaaagct atctcaggga agaatttccc gatacgaaca aaagaagggg gtcgcagacg 240
 aaatctatca acgacgctat ttccattgtt cgctcatatc tccgttaa 288

<210> 2391
 <211> 621
 <212> DNA
 <213> Enterobacter cloacae

<400> 2391
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<210> 2392
 <211> 633
 <212> DNA
 <213> Enterobacter cloacae

<400> 2392
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<210> 2393
 <211> 603
 <212> DNA

<213> Enterobacter cloacae

<400> 2393

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<210> 2394

<211> 1446

<212> DNA

<213> Enterobacter cloacae

<400> 2394

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<210> 2395

<211> 231

<212> DNA

<213> Enterobacter cloacae

<400> 2395

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<210> 2396

<211> 2031

<212> DNA

<213> Enterobacter cloacae

<400> 2396

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<210> 2397

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 2397

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 <212> DNA
 <213> Enterobacter cloacae

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 <212> DNA

<213> *Enterobacter cloacae*

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<211> 960

<212> DNA

<213> Enterobacter cloacae

<400> 2401

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<210> 2402

<211> 1983

<212> DNA

<213> Enterobacter cloacae

<400> 2402

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<210> 2403

<211> 1170

<212> DNA

<213> Enterobacter cloacae

<400> 2403

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<210> 2404

<211> 1674

<212> DNA

<213> Enterobacter cloacae

<400> 2404

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<210> 2405

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 2405

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ctgccgttac	cgctggaaat	cgaatttacc	catctgcctg	aaaaactgcg	cagacgcttt	240
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<210> 2406

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 2406

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<210> 2407

<211> 1062

<212> DNA

<213> Enterobacter cloacae

<400> 2407

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cgccgccaga	tcctgaaaat	gcttggcatc	agcgccactg	ccctgacgct	caccctcgcg	180
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<210> 2408

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 2408

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aaagatatct	agcattttac	gggtcggatg	gctctgaaat	ttttgctggc	gaccttgctc	180
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<210> 2409

<211> 1425

<212> DNA

<213> Enterobacter cloacae

<400> 2409

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tccttccccg	ccagtgcggc	actgccttcg	cagggtgcctg	gacaagaagc	cattcccagc	180
cttgcgccga	tgttgaaaa	agtcctgcct	gcggtagtca	gcgttcaggt	ggaaggagac	240
gcacgccaaa	gccagcgtat	tcccgaagag	ctgaagaaat	attttggcga	agacgcgcgc	300
gatcagcagg	ctcagccgtt	tgaaggctgc	ggctcagggg	tgattatcga	cgcgggctaag	360
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<210> 2410

<211> 219

<212> DNA

<213> *Enterobacter cloacae*

<400> 2410

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caacatcaac	cagtcgaagg	tctctcgcat	gttaaccaag	tttggagcgg	tgcgtacgcg	180
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<210> 2411

<211> 984

<212> DNA

<213> *Enterobacter cloacae*

<400> 2411

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<210> 2412

<211> 474

<212> DNA

<213> *Enterobacter cloacae*

<400> 2412

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cacatggcga	aaagctccag	cagcctgctg	ccggaaatga	ccgcggagac	caacccttc	360
cgcaatcgtc	tggctgattc	tgaagccggg	aacgatcagg	caccggttca	gatgccacgc	420
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<210> 2413

<211> 438

<212> DNA

<213> *Enterobacter cloacae*

<400> 2413

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ttcgaacagg	agctgtaa					438

<210> 2414
 <211> 270
 <212> DNA
 <213> Enterobacter cloacae

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 aaagcggaag aacaggggtgc gtcattctat cgcattcatcg aagcgcgcag tggcgaccac 240
 tggcacgcta ccgcagaact gtacaaataa 270

<210> 2415
 <211> 537
 <212> DNA
 <213> Enterobacter cloacae

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 ggcgtgatag cagcaaccac cccgacaggt tcacgagtg cagaataacg ggagccaggt 480
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<210> 2416
 <211> 930
 <212> DNA
 <213> Enterobacter cloacae

<400> 2416
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<210> 2417
 <211> 1731
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2418

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 2418

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<210> 2419

<211> 1107

<212> DNA

<213> Enterobacter cloacae

<400> 2419

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<211> 1566

<212> DNA

<213> Enterobacter cloacae

<400> 2420

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<211> 1539

<212> DNA

<213> Enterobacter cloacae

<400> 2421

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<211> 330

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<210> 2423

<211> 942

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<213> Enterobacter cloacae

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<211> 504

<212> DNA

<213> Enterobacter cloacae

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<212> DNA

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<212> DNA

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<210> 2427

<211> 1785

<212> DNA

<213> Enterobacter cloacae

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<213> Enterobacter cloacae

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<210> 2430

<211> 2034

<212> DNA

<213> Enterobacter cloacae

<400> 2430

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<210> 2431

<211> 2046

<212> DNA

<213> *Enterobacter cloacae*

<400> 2431

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<210> 2432

<211> 1338

<212> DNA

<213> *Enterobacter cloacae*

<400> 2432

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<210> 2433

<211> 678

<212> DNA

<213> Enterobacter cloacae

<400> 2433

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<210> 2434

<211> 3111

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(64)

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<400> 2434
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<210> 2435

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 2435

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attgccgatt	tgcagatcca	tccggtgaaa	cgcattgagg	aagttctgac	tctcgactg	480
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<210> 2436
 <211> 360
 <212> DNA
 <213> Enterobacter cloacae

<400> 2436
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<210> 2437
 <211> 501
 <212> DNA
 <213> Enterobacter cloacae

<400> 2437
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 atgaaatgtg gaatcaaagc actgttaatt acactggcta ttgccacttc cgggatgagt 180
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<210> 2438
 <211> 381
 <212> DNA
 <213> Enterobacter cloacae

<400> 2438
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 gattaccgtt atctcagaga ggggtgtctgg gagttgaagg ttgatagtgg tcccggttat 240
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<210> 2439
 <211> 843
 <212> DNA
 <213> Enterobacter cloacae

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 gagcgtgaag ttaccctgac gtttgctact ggtcgtcatg tgctggagat gcgccatctg 180
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<210> 2440

<211> 375

<212> DNA

<213> Enterobacter cloacae

<400> 2440

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<210> 2441

<211> 1119

<212> DNA

<213> Enterobacter cloacae

<400> 2441

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<210> 2442

<211> 462

<212> DNA

<213> Enterobacter cloacae

<400> 2442

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<210> 2443

<211> 1383

<212> DNA

<213> *Enterobacter cloacae*

<400> 2443

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<210> 2444

<211> 1350

<212> DNA

<213> *Enterobacter cloacae*

<400> 2444

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<210> 2445

<211> 1653

<212> DNA

<213> *Enterobacter cloacae*

<400> 2445

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<210> 2446

<211> 1350

<212> DNA

<213> *Enterobacter cloacae*

<220>

<221> unsure

<222> (1261)

<400> 2446

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<210> 2447

<211> 1389

<212> DNA

<213> Enterobacter cloacae

<400> 2447

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<210> 2448

<211> 1566

<212> DNA

<213> Enterobacter cloacae

<400> 2448

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<210> 2449

<211> 2280

<212> DNA

<213> Enterobacter cloacae

<400> 2449

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<210> 2450

<211> 1371

<212> DNA

<213> Enterobacter cloacae

<400> 2450

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ggtaaccoga	cgttggaagc	tgaagttcat	ctggaagggt	gtttcgctgg	tatggcagcg	180
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<210> 2451

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 2451

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caggcagaac	tgggtaaaaa	agcgcgtttc	cggcagtgga	tactggcgaa	agcggcaagc	900
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<210> 2452

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 2452

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attttcgccg	cgggtgagtg	ctttattttt	gtagctctgg	gcgcgttttg	cgcgcatgtc	120
ttaaagcaat	ctctgggcgt	tgtggagatg	gggtggatcc	agaccggcct	tgaatatcag	180
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<210> 2453
 <211> 606
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2453
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 attatcgctt cgcaggatga ttacgttatc tggcaaccga aaccgttcat gggcgagcag 240
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<210> 2454
 <211> 792
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2454
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 actattcgcg cggggctgga caaggtctgg atgcaggcgc tgtcacagtt tggctggctg 720
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 caagcgaat aa 792

<210> 2455
 <211> 465
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2455
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 tatgaagatc cggagctggc ggactgggaa aagtataaag ataaatacat cctggtggtg 180
 acctccacca ccgggcaggg cgatctaccg gacagcatcg tcccgtttt ccagggcatt 240
 aaagaccagc ttggctatca gccagatgtt cactatggca tcattgccct cggcgatagc 300
 tcttacgcca atttctgcgg cggcggtaaa cagttegcag cgctgttgca ggaacagagc 360
 gctcagcgcg tcggagagat gttgctgatt gatgcgggtg aacaccctga gccagaaagc 420
 gagtcaaatc cctgggttga aactggggcc acgtccttga actaa 465

<210> 2456
 <211> 1155
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2456

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<210> 2457

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 2457

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cagactttcg	ccaccatttc	gccttacacg	ctggaagaga	cctacgaagt	gctggacgcc	180
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<210> 2458

<211> 1374

<212> DNA

<213> Enterobacter cloacae

<400> 2458

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tcacttgccg	tactgaactc	cggaagcctg	accgacaaca	gtaaagagct	gctgtcccgc	180
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<210> 2459

<211> 1371

<212> DNA

<213> Enterobacter cloacae

<400> 2459

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tcccgaaagc	gttgccgcaa	aacggatacc	atgtggatgc	ttggcctgta	cggcacagca	180
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<210> 2460

<211> 774

<212> DNA

<213> Enterobacter cloacae

<400> 2460

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<210> 2461

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 2461

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<210> 2462

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 2462

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<210> 2463

<211> 1299

<212> DNA

<213> Enterobacter cloacae

<400> 2463

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<210> 2464

<211> 1398

<212> DNA

<213> Enterobacter cloacae

<400> 2464

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<210> 2465

<211> 2769

<212> DNA

<213> Enterobacter cloacae

<400> 2465

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<211> 1383

<212> DNA

<213> Enterobacter cloacae

<400> 2466

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<210> 2467

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 2467

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<210> 2468

<211> 822

<212> DNA

<213> Enterobacter cloacae

<220>

<221>unsure

<222>(725)

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<222>(794)

<400> 2468

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<210> 2469

<211> 222

<212> DNA

<213> Enterobacter cloacae

<400> 2469

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aaactgcgcg	atcacatcg	cctgctgacg	gaaaagctga	aggccacgca	gcggtcaaac	180
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<210> 2470

<211> 654

<212> DNA

<213> Enterobacter cloacae

<400> 2470

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gccgtgacca	ccgcagcagc	cgtcatggcc	gtgatcgtgg	tcattggtcgt	gaccgtgcgc	180
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catgccaaac	tgcaactcgt	caacgccccat	gaatacgtct	ttaggaacgc	gctgaaccag	420
gttgctcgta	tactgaccgt	aagcgtcggt	cgcgcctaca	gcaacgtcga	atttgtcgcc	480
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gtagtcacgc	ggcgcaactca	ccggagactc	atcaaccaac	acaccgtctt	ctgtacgtac	600
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<210> 2471

<211> 222

<212> DNA

<213> Enterobacter cloacae

<400> 2471

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aacgatgtta	agcgccagct	taaaagcggc	gacgtgggtg	tggtatgggc	cgaactgcat	180
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<210> 2472

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 2472

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cagcttaact	tacggggcgc	cgaggtagaa	ggcgacagct	ttcaccgcta	cacgcgccc	180
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<210> 2473

<211> 639

<212> DNA

<213> *Enterobacter cloacae*

<400> 2473

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tgctcccgtg	aaacagtggt	ccgtatcctg	aagatgctgg	aagatcagaa	cctgatctcc	600
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<210> 2474

<211> 2145

<212> DNA

<213> *Enterobacter cloacae*

<400> 2474

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<210> 2475

<211> 1938

<212> DNA

<213> Enterobacter cloacae

<400> 2475

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gagataagcg	cggatggcgg	taactttacc	ttcccgggca	actggcagct	cgccctgggtg	240
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<210> 2476

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 2476

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<210> 2477

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 2477

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<210> 2478

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 2478

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<210> 2479

<211> 573

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (32)

<220>

<221> unsure

<222> (33)

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<210> 2480
 <211> 690
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2481
 <211> 594
 <212> DNA
 <213> Enterobacter cloacae

<400> 2481

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<210> 2482

<211> 1266

<212> DNA

<213> Enterobacter cloacae

<400> 2482

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<210> 2483

<211> 411

<212> DNA

<213> Enterobacter cloacae

<400> 2483

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<210> 2484

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 2484

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<210> 2485

<211> 309

<212> DNA

<213> *Enterobacter cloacae*

<400> 2485

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<210> 2486

<211> 828

<212> DNA

<213> *Enterobacter cloacae*

<400> 2486

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<210> 2487

<211> 963

<212> DNA

<213> *Enterobacter cloacae*

<400> 2487

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<210> 2488

<211> 1950

<212> DNA

<213> Enterobacter cloacae

<400> 2488

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<211> 1671

<212> DNA

<213> Enterobacter cloacae

<400> 2489

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<210> 2490

<211> 837

<212> DNA

<213> Enterobacter cloacae

<400> 2490

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<210> 2491

<211> 1059

<212> DNA

<213> Enterobacter cloacae

<400> 2491

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<210> 2492

<211> 792

<212> DNA

<213> Enterobacter cloacae

<400> 2492

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<210> 2493

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 2493

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ttccagcatc	cgttttatac	atacagctgt	ccggcattgc	tgaaagagtg	gctggaccgc	300
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cggagtgtca	ttaccaccgg	tgagccggaa	agcgtttacc	gtcacgacgg	gctgaaccgt	420
taccccatga	gcgacattct	gcggccggtt	gagctgacgg	cggcgatgtg	ccgtatgcac	480
tgatgagcc	cgattattat	ctactgggca	cggcggcagg	atccgaaagc	gctggcgagc	540
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<210> 2494

<211> 564

<212> DNA

<213> Enterobacter cloacae

<400> 2494

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atcttccagc	atcttcagga	tacggcccac	tgtttcacgg	gagcagccga	cgatctgacc	120
gatttccctg	cgggtaattt	taatttgcac	accgtcagg	tgagtcattg	cgtctggttg	180
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acctaccttc	tcagaggtca	cttgccagac	gcgtgccatc	tgggaagaga	gacgcacag	300
gatgtcagg	ttgacctgaa	tcagctgacg	gaatttctta	taagaaattt	cagccacttc	360

acatgctgtt	tttgcacgaa	cccaggcgct	acgttccctgg	ccttcttcaa	acaggcccag	420
ttcacggata	aaatcgccct	ggttcagata	agaaaggatc	atctctttcc	cttcttcac	480
tttgatcagc	acggccaccg	agcctttaac	gatgtaatac	aacgtttccg	ctttttcacc	540
ctggtgaatc	agcgtgctct	ttga				564

<210> 2495

<211> 198

<212> DNA

<213> Enterobacter cloacae

<400> 2495

tgggtactta	tgaatgtggc	aatgagacaa	gaaccattcg	agagtcgggt	ctgtttgcgg	60
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catccggact	ctgggggttg	aatcgaattc	ttaccatac	ctgggaagtc	ggctgtcgta	180
acgtttcgca	gccagtaa					198

<210> 2496

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 2496

agccgtgctg	ctgttgagct	ccatactgtg	tatcctgtcg	ctgccgctgt	ttatctcgct	60
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gcgcgcgacg	ccctggaagg	gattactgaa	tcctgggtgg	acgcggcctg	gcataccggg	180
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gctcagctca	gtcgtgcgtt	gtgccgggcg	gatacacagg	tggatacgcc	cgagggcgga	600
ttcgcgctgg	cggaatggtt	acgcgacggc	aaaacgctgc	taaaaacgca	atatggggcg	660
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<210> 2497

<211> 672

<212> DNA

<213> Enterobacter cloacae

<400> 2497

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caggtaacga	cagaagacgg	tgtgttggtt	gatgagtctc	cggtagagtgc	gccgctggac	180
tacctgcatg	gtcacggttc	cctgatttcc	ggcctggaaa	cggcgctgga	aggccatgaa	240
gttggcgaca	aattcgacgt	tgtctgtaggc	gcgaacgaac	cttacgggtca	gtatgacgac	300
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gacgaccacg	ttgtggttga	cggcaaccac	atgctggcgg	gtcagaacct	gaagttcaac	480
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ggtgcgcacg	gtcacgacca	tgaccacgat	cacggccatg	acggctgctg	cgggtgtcac	600
ggccacgacc	atggctcatg	ccacggccac	ggtaaagggt	gttgcggtaa	cggcggctgc	660
ggttgccact	ga					672

<210> 2498

<211> 423

<212> DNA

<213> Enterobacter cloacae

<400> 2498

cgggtggaag	gaggttgccg	gtacgccaca	actgatgcag	gacgccgtct	aatgagtaac	60
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tccacctacg	gtaaccaggg	cggtcatgtc	ctgggtccgc	aaagtaatag	cgatatcaat	420
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<210> 2499

<211> 1713

<212> DNA

<213> Enterobacter cloacae

<400> 2499

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gtggcaggcg	ctgccgccat	tgcgatcggt	gtcgcgatgg	tcttatgggc	aaaaagccccg	180
gattaccgca	cgctctacag	caacctttcc	gaccaggatg	gcggtgccat	cgtaaccacag	240
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gtgatgagcc	agcgcatctg	cgaaatgtca	gataacgata	cgcgctcgt	cgcgctggtc	1680
atccgcggtt	ggatgggtaa	cgaacatgag	ttaa			1713

<210> 2500

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 2500

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accactggca	aaggcaaaaga	tgctccgctg	acgctggccg	atctaaaagc	ggcgggaagc	180
aagctgtcga	cagcggcaca	ggaaaaaaac	ggtgatacca	cgctccaggc	caaaatcgcc	240
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accggggaga	tgcggcccg	tgcggccctc	ccctctgcgc	tagcccagac	ggataacggc	540
cagcatcagc	cgcttagcca	tgcgttaacg	ggtcaggaaa	aatgcccgtt	tcaggacagc	600
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atttcgctta	agctggatga	caaccaggca	cagttgcaga	tggtttcgcc	ccacagccac	960
gttcgogcgg	cgctggaagc	ggccctgccg	atcctgcgca	cgcagcttgc	ggaaaacggc	1020
attcagcttt	ctcaaagcag	cgtcagcagc	gagggtttg	ccgggcagca	gcagtcctca	1080
tcggggcagc	aacagcacgc	ttcgcgttcc	ggccagcatg	gcgggtttaa	cgatgagagt	1140
gaagagttat	tgccctgccc	tgccgcctcg	caatccgccc	cacgcggcag	ccgtgccgta	1200
gacatctttg	cctaa					1215

<210> 2501

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 2501

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ctccagggtga	gcggcgcgct	gttcgggtatt	attgccttta	tccttatcgc	cgccctggtg	180
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acggtggagg	ctaacgcca	ggccctgcg	gatttccagt	ccgttatgaa	gagtttgctc	420
aagcgtcccc	ggagatcctg	a				441

<210> 2502

<211> 387

<212> DNA

<213> Enterobacter cloacae

<400> 2502

tggttccgcc	cgcgaccatt	gccctgcctt	ttaagatcat	gctgttcgtg	ctggtcgacg	60
gctggcagct	gctggtcagc	tcgctggcgc	agagtttcta	cagttgagga	gcgcgcaatg	120
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gcgcccctgc	tgtctggttg	gctagtcacc	ggctctgatta	tcagtattct	ccaggccgcc	240
acgcagatta	acgaaatgac	cctgtcggtc	atcccggaaga	tcattgcgct	cttcgtggcg	300
attatcggtg	ccgggccatg	gatgctcaat	ttgctgctgg	actatatgcg	caacctgttc	360
accaatctgc	cttacatcat	cggtcga				387

<210> 2503

<211> 792

<212> DNA

<213> Enterobacter cloacae

<400> 2503

cggacgatgc	tgcatttcac	cagcgatcag	tttgttcagt	ggctcgggat	ctatttcttg	60
ccgatgctgc	gcatcatggc	gctgatctcc	accgccccca	tactcagtga	aaagtcgggtg	120
cctaaacgcg	tcaaaattgg	gctgggcatg	gttatcacga	ttatcgttgc	cccttccctg	180
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atgattggcg	tagcggctgg	attcacgatg	cagctcgctt	tcgccgcggt	acgaacggcg	300
ggtgaactta	tcggtttgca	aatgggcctg	tcttttcgca	cgttcgttga	cccgggcagc	360
cacctgaata	tgcccgtgct	ggcagctatt	atcgacctgc	tggcgatgct	gttgtttctc	420
tgtttcaacg	gcaacctgtg	gctcatctcg	atgctggttg	acaccttcca	cacgctgccg	480
attggcgaca	accgggtaaa	cagcaacgcg	tttctggcgc	tggtgagggc	tgccgggctg	540
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<210> 2504
 <211> 633
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2504
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 gaactcgcag ccgcttgtga cgcccacaag cccggcgtgg tgtttattaa tgaggactgt 180
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 accctgttta ttgtttttat ggcgatcgcc aatattcatt tcgatgagta tttgttgggtg 300
 cgtaaaaact tattaatcag ctcgaaatcg attaaaccag agtcacttga tgacattctg 360
 ggcgattatt tgaataaaga agttaagaat gtagggcgga ttaacttacc caccctatca 420
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<210> 2505
 <211> 927
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2505
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 ctggacagcg taggcttcgc cgtggtggtg aaaggcttca accgggaggg catcagcctt 840
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 gagggacttg attacttttt gaggtga 927

<210> 2506
 <211> 1422
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2506
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 acttcttata cagcaaaact tagtgccctac ggcacgctga aaagtgcatt ggaatccttc 180
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aacaatttaa	ctaagcaata	taacgcggcc	agcgagcgta	tcgacaccat	ggtagcgcg	1320
tataaagaac	agtttacgca	attagacgtc	atgatgaact	cgctgaactc	taccagcagt	1380
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<210> 2507

<211> 438

<212> DNA

<213> Enterobacter cloacae

<400> 2507

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tttgatggag	ccctcagcgc	gctggtagcgc	gcgcgtctgt	tccttgca	cggtaatatc	180
ccggcaaaaag	ggctggcgct	ctcaaaaagcc	atcaacatta	tcgaaaacgg	gctgaagggtt	240
ggcctgggtgg	aaaataatgg	ggatgagctt	acgcaaaaacc	tgattgccct	ttatgcctat	300
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gaaaacctgc	tgcgcaatat	cgctgacggg	tggaaggagg	ttgccgggtac	gccacaactg	420
atgcaggacg	ccgtctaa					438

<210> 2508

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<400> 2508

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<210> 2509

<211> 1443

<212> DNA

<213> Enterobacter cloacae

<400> 2509

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gggagtcgtc	tgatgaccgc	tcgccttacg	cgctggctta	acacgcttga	taattttgaa	120
acgaagatgg	cgcagctgcc	atccgttcgt	cgttatggac	gcctgacgcg	cgccaccggt	180
ctggtttctg	aagccacggg	gctgcaactt	ccgctcggcg	ccacctgcgt	gattgagcgg	240

caggacggggg	gggagacgcg	tgaagtggaa	agcgaagtgg	tccgggttcaa	cggtcagcgc	300
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tttgaacgcg	ccgactggga	agattccctc	caggcactgg	agctgatttt	cccgcagggtg	1440
taa						1443

<210> 2510

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 2510

cacaggtgga	gggcgaaggt	catggcgcag	aacagcgcgt	tatcaacgct	gaaagatctg	60
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caggctgaag	aacagttgaa	gatgttaatc	gactatcagc	atgaatatcg	caccaacctt	180
aacaccgaca	tgacgcaggg	cattggtagc	cagcgcctga	ttaactatca	gcagttttatc	240
cagacgctgg	aaaaggcgat	tgagcagcat	cgccagcagc	ttaaccagtg	gacgcaaaaa	300
gtcgataccg	cgctgaattt	ctggcgcgag	aaaaaacagc	ggttgcaggc	ctggcaaaacc	360
ctacaggacc	ggcagattgc	agcctcgacc	ctggcggaaa	accgtctgga	tcagaaaaaa	420
atggatgagt	ttgccacgcg	cgcataaatg	aggaaaacctg	aatga		465

<210> 2511

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 2511

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attaccctcg	cggcctgcgc	caccgcaggc	tacagttact	ggcgtatgca	gcaggaaccc	180
tcagcgcggg	ccgccaaaag	tgaagcgccg	cctccaccgg	cgcgggtctt	ctaccgcgtg	240
gatacgttca	ccgtgaacct	gggcgatgcg	gatcgcgtgc	tttacgtggg	tattacgctg	300
cgtctgaaag	atgaagcgac	ccgtgcacgt	ctaaacgact	acctgccaga	agtgcgtagc	360
cgtctgctgc	tgtgtttttc	tcgtcaggat	gcctccgcgc	tcgccaccga	tgtgggcaag	420
caaaagctgg	tcgatgccat	caaacagacg	ctggcgaccc	cgttggtaaa	cggccaacct	480
aagcaggaag	tcactgacgt	tctgtatata	gccttcattc	tcgcgtaa		528

<210> 2512

<211> 426

<212> DNA

<213> Enterobacter cloacae

<400> 2512

ggaacagccc	aaatgagtga	catgaacaat	ccgtccgatg	aaaacagcgg	agcaactggac	60
gatctgtggg	ctgacgcgtt	aaacgagcag	aaaacgacgc	cgacgaaaag	cgcggcagac	120

gcggtctttc	agcagtttagg	cggcggcgac	gtcagcggca	cgttgcagga	catcgacctg	180
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gagctgctgc	gcctgacgca	gggttcctgt	gtggcgcttg	acggttttagc	gggtgagccg	300
ctggatatct	tgatcaacgg	ctacctgatt	gcacaaggcg	aagtgggtggt	ggtggccgat	360
aaatacggcg	tacgtatcac	cgacatcatt	accccttcgg	aacgtatgcg	tcgtctgagc	420
cgtaa						426

<210> 2513

<211> 1560

<212> DNA

<213> Enterobacter cloacae

<400> 2513

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ggcgggtgaac	tgtggcgaga	agtcacggca	ttagcccca	atctgaacga	aatcggcacc	180
aatatggtct	ggttaccgcc	ggcctacaaa	ggggcatcgg	gcggctattc	cgctgggtat	240
gactcttatg	accttttcga	cctcgggtgag	tttgaccaga	aaggcagcgt	cgccacccaaa	300
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gtgcagcgcg	tggatgcgca	ggatcgcacc	caaatacagcg	atgagatcat	cgaatgcgaa	480
gcctggagcgc	gctacacctt	tcccgctcgg	gcgggccagt	attcgcagtt	catctgggat	540
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ctgtcgaatg	gtgatgacgg	cgagaagacg	atctgcctcg	gggaaaatta	cggaataaag	1440
acctggcggtg	atttttttagg	caaccgcgag	gaaaccgtga	ccacggcggc	ggatggcgaa	1500
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<210> 2514

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 2514

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gccggggcgg	gcgaaccoga	gctgagtga	gaggaacagc	gcgccagtt	gctggcccag	180
atgcaaatac	aggcgacga	acagggtctc	aatgcaggga	tgaacgaagg	ccgtcagacc	240
gggcacgcac	agggttatca	ggaagggtcg	gcgaaagggt	tagagcaggg	catcgagcag	300
gcgcgccagc	agcaggcgcc	gctacatgcc	cgcatgcagc	agctggtgag	cgagtttcag	360
catacgcctg	atgcgctcga	cagcgtgatt	gcctcgcgcc	tgatgcagat	ggcgctggag	420
gcggcccgtc	aggtgatcgg	ccagacgcgg	atagtggata	acgccgcgct	gattaagcag	480
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cctgatgatt	tgcagcgcgt	ggaagagagc	ctcggcgcca	cgctgagcct	gcacggctgg	600
cggctgcgcg	gcgacccgct	acttcacat	ggaggctgta	aggtctcggc	ggatgagggc	660
gatctggatg	ccagcgtcgc	gaccgcgtgg	caggaaactgt	gccgcctggc	ggcaccggga	720
gtcgtctga						729

<210> 2515

<211> 1068

<212> DNA

<213> Enterobacter cloacae

<400> 2515

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gataagagtg	acgaaccgaa	accgggtctg	accggcgacg	ataatattcg	tccctacgat	180
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cgtttcgcac	gtcagttccg	tatggggctg	tttaacctgc	tgcgtcgtag	cccgatatc	300
accgtcgggtg	ccatccgcac	tcagccgtat	catgagtttg	cccgcacact	gcccgtgccca	360
accaaactta	acctgatcca	tctgaaaccg	ctgcgcggta	ccggcctggg	gggtgttttcg	420
ccaagcctgg	tgttcacgcg	agtggacaac	ctgttcgggtg	gcgatggtcg	tttcccgacc	480
aaagtggaa	gccgcgagtt	taccataacc	gaacagcgcg	tgattaaccg	catgctgaag	540
ctggcgctgg	aatcctacag	cgacgcgtgg	aaagcgatta	acccgctgga	agtggagtag	600
gtgcgttccg	agatgcaggt	gaaatttacc	aacatcacca	cctccccgaa	tgacatcgtc	660
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cgtcacgaag	atcagaactg	gcgtgagaac	ctgggtgcgtc	aggtgcagca	ctcgcagctg	840
gagctggtag	ccaactttgc	cgacatctcc	atgcggttat	cgcagatcct	gaaattacaa	900
cccggcgacg	ttttgccgat	agataaacc	gaccgcatta	ttgcccattg	ggatggcgta	960
cccgctgctga	caagccagta	cggcacgatt	aacggccagt	atgcgttaacg	cgttgagcac	1020
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<210> 2516

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 2516

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atcctgatgc	gccgtttgtt	attccttaacg	ctggcaggcc	tgggcctgtt	cgcgccctct	120
gtgtatgcgc	aactgccggg	gctggtttcc	acgcgcctgg	cgaacggggg	acaaagctgg	180
tccctgtccg	tgcagacgct	ggtgttcac	acctgcctga	cctttatccc	ggcgatcctg	240
ctgatgatga	ccagcttcac	cgcacatcac	attgtgtttg	gtctgctgcg	aaatgcgctc	300
ggcacaccgt	ccgcacccgc	caatcagggtg	ctgctgggtt	tagccctgtt	cctgaccttt	360
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gataaaaatt	ccatgcaggt	tgccttgaa	aagggggctc	agccattacg	tgaatttatg	480
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gtgatcgcca	gcgtcctgat	ggcgcctcgg	atgatgatgg	ttccgcccgc	gaccattgcc	720
ctgcccttta	agatcatgct	gttcgtgctg	gtcgacggct	ggcagctgct	ggtcagctcg	780
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<210> 2517

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 2517

ctgttgagac	ggttaaatga	ggagcccgc	atgaagactg	acaaagagta	cagcgacacc	60
attaagcgtg	aggttgaa	ggatgtcgat	gcccgtgctg	ccgccatcaa	tgaaattagt	120
gagtcggaag	ttcatcgccg	ggaggataat	tcagaccgtg	tcgtgggtcaa	tggtcgggat	180
taccatacct	accgtgaact	ggctgaagca	ttcgagctgg	atatccatga	ctttagcgtc	240
tcggaaacga	accgctaa					258

<210> 2518

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 2518

tgggtgtcgt	gtactctttg	tcagtcttca	tggcgggctc	ctcattttaac	cgctctcaaca	60
gctaagtata	gaccgcacac	aaaaacgccca	ttcgcgccag	gcggcgatgc	caggcaatgt	120
aattttgttct	acactggctc	aaaaccacag	gaggaatgta	tgaagggtcaa	cgatcgggta	180
accgtcaaaa	cggacgggtg	gccgcgccgc	ccggggcgtg	ttctggcaat	agaagagttt	240
aatgaaggca	caatgtatct	ggtgtcgtg	gaagattacc	cgctcggcat	ctggttcttc	300
aacgaactgg	ggcacccgga	tgggatcttt	gtggaaacgg	cggaatag		348

<210> 2519

<211> 309

<212> DNA

<213> Enterobacter cloacae

<400> 2519

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cgctggccgc	gtcccacggg	gagcagggcg	ttaatcggcc	gcacgcgggt	atccagtag	120
tgtctgattg	gcgtgcgttg	cagcgggttg	aaggggtggg	tgatcagcgc	gccggtttgc	180
gtgggtatcag	gggagggcag	gccatcgagc	ggtttgccgc	ttccgtccag	gacgcggccc	240
agcagcgccg	gaccgagcgg	gagctgtttg	ccgctttgca	ggcgcgcacc	gctaattgtt	300
ttcgcgtag						309

<210> 2520

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 2520

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caggcaacag	cgatgaccgc	ccgtaatcag	agcgtggctg	accagccgcc	gggcgtcagt	120
ttcgccggtc	aactgcatgc	ggcgctggac	cggatcagcg	acaagcaaaa	cgcagcccgt	180
accagggctg	agagatttac	ccttggcgaa	ccggcgctgg	cgctcaacga	tgtgatggcc	240
gatctgcaaa	aagcgtcggg	gtcattgcag	atggggttgc	aggtgcgtaa	caagctgggtg	300
tcggcatacc	aggaagtgat	ggggatgcag	gttttaa			336

<210> 2521

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 2521

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tgctttcagg	tcgaaaaacta	tcaggaagtg	gttaagcatc	cggcaccttc	gcaactggca	180
ggttactggc	agtcgaaagg	tccgcagagc	gcgatggtga	gcccgggaagc	gatcgccacg	240
ctggtgggtga	cgccagaagg	ggatacgcgt	gattgccgctc	agtggcagcg	cgttatcgcg	300
gtgccgggta	agatcatgct	gcgttcagat	gattattata	acgtgacgcg	taagctggat	360
gtctatccgc	tggagcgtga	tggggcggcg	ctggagtatg	acggtatgga	actgtacaag	420
gttgaccgtc	caacgggtgga	atgcgcagat	tacctgagta	agaatccgct	ggagagtaag	480
cttccgtaa						489

<210> 2522

<211> 810

<212> DNA

<213> Enterobacter cloacae

<400> 2522

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atggataaac	actcgtgtg	gcagcgttat	gttccgctgg	tgcgtcacga	agcattgcgc	180
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gggttattga	atgcagttga	ccggtacgac	gctctgcaag	gaacggcatt	tacgacttac	300
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cgcagcgttc	gccgcaacgc	gcgcgaagtg	gcgcgatgca	tggggcagct	ggaacaggag	420
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ggcgccgtgc	tggaggtggg	cgagtcacgg	gtgagccagc	tgcacagcca	ggccattaaa	780
cgcttgccga	caaaactggg	taagttatag				810

<210> 2523

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 2523

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aaagacttta	aacacagcca	gacgcattgc	gccactgta	aaaaattact	cgaccgcctc	120
acgctgggtc	gtcgcggtga	aatcgtgaat	aagattgcga	tttccgcct	cgacacgctg	180
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ctgtttgaac	aaaccgagat	gagtcacggc	accgtgcgtg	aatacgtggg	tcgcctgcgc	360
cgcttggtgc	agcatttgac	catgcaaaat	atctccgcgc	atctgctgac	gaccggatac	420
ctggatgaaa	atctggagcc	ctggctgccc	gccaccagta	ccaacaatta	ccgcctgcgc	480
ctgcgaaagt	atgcacaata	taaagtccag	atgcgcggcg	tcataaagca	gaaagtccgc	540
gccggaacaa	cttctgatat	atatttaa				567

<210> 2524

<211> 1059

<212> DNA

<213> Enterobacter cloacae

<400> 2524

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<210> 2525

<211> 690

<212> DNA

<213> Enterobacter cloacae

<400> 2525

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<210> 2526

<211> 509

<212> DNA

<213> Enterobacter cloacae

<400> 2526

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gcgtgagtgc	gtcgtttggc	gtctctggtg	cgagggagaa	gggcaattat	cacttcgaaa	420
atctgcaatc	caccgccgat	gcgcgtctgt	atgaggcgaa	acagcgcggg	cgtaaccggg	480
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<210> 2527

<211> 1728

<212> DNA

<213> Enterobacter cloacae

<400> 2527

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1728

<210> 2528

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 2528

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<210> 2529

<211> 759

<212> DNA

<213> Enterobacter cloacae

<400> 2529

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<210> 2530

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 2530

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<210> 2531

<211> 933

<212> DNA

<213> *Enterobacter cloacae*

<400> 2531

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accactttta	ccgttatcgc	tgatatggcg	aaaaacgtgg	cgggggatgc	cgcagaggtc	180
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<210> 2532

<211> 1167

<212> DNA

<213> *Enterobacter cloacae*

<400> 2532

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<210> 2533

<211> 1380

<212> DNA

<213> *Enterobacter cloacae*

<400> 2533

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<210> 2534

<211> 3885

<212> DNA

<213> Enterobacter cloacae

<400> 2534

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<210> 2535

<211> 954

<212> DNA

<213> Enterobacter cloacae

<400> 2535

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<210> 2536

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 2536

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cagcagtgcg	agttgccccc	gggctggcgc	gtggctctgc	aaccgcaatc	taaggaggcg	180
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cgcgcatga

249

<210> 2537

<211> 1521

<212> DNA

<213> Enterobacter cloacae

<400> 2537

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<210> 2538

<211> 2043

<212> DNA

<213> Enterobacter cloacae

<400> 2538

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<210> 2539

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 2539

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<210> 2540

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 2540

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<210> 2541

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 2541

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<210> 2542

<211> 1263

<212> DNA

<213> Enterobacter cloacae

<400> 2542

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<210> 2543

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 2543

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<210> 2544

<211> 1320

<212> DNA

<213> Enterobacter cloacae

<400> 2544

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<210> 2545

<211> 663

<212> DNA

<213> Enterobacter cloacae

<400> 2545

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<210> 2546

<211> 1059

<212> DNA

<213> Enterobacter cloacae

<400> 2546

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<210> 2547

<211> 1593

<212> DNA

<213> Enterobacter cloacae

<400> 2547

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<210> 2548

<211> 720

<212> DNA

<213> Enterobacter cloacae

<400> 2548

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<210> 2549
 <211> 978
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2550
 <211> 327
 <212> DNA
 <213> Enterobacter cloacae

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 cttcaccctg ctgcgcgacg cgggcgcgaa tgccttgcgc cagcgtgccg ccgagggaat 180
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<210> 2551
 <211> 2265
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2552

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 2552

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<210> 2553

<211> 1722

<212> DNA

<213> Enterobacter cloacae

<400> 2553

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<210> 2554

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 2554

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<210> 2555

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 2555

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<210> 2556

<211> 1899

<212> DNA

<213> Enterobacter cloacae

<400> 2556

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<210> 2557

<211> 945

<212> DNA

<213> Enterobacter cloacae

<400> 2557

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gccgatgaag	atgaggtaca	tctcagcaat	ctgcaacggc	aaatcctctt	cacgacagaa	420
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<210> 2558

<211> 357

<212> DNA

<213> Enterobacter cloacae

<400> 2558

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ctgccgggta	acctgatcac	cgttcattct	caggaccacc	tgatgaacgc	gatggtaatt	300
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cagaacctga	tgccgacggt	gtcgtctatc	tctctggcgg	acacagtagg	gcgccatctg	480
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gaaccgctgg	aacaatttat	cggtagcgta	gatgaagcgc	tgtataaccgc	taaacaacag	1620
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<210> 2562

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 2562

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gatccgctcg	gaaaaaaggt	cgcggctcatc	gacatgatgg	attacggcat	gatgaaaggt	300
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<210> 2563

<211> 1734

<212> DNA

<213> Enterobacter cloacae

<400> 2563

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atcgtagaat	ccaggggatt	taccatgcaa	caacgtcgtc	cagtcgcgcg	cgctctgctc	180
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02/18/99

1001

ctgaaaatca	ctgcgggcaaa	acagaatgtg	cgcgtgctgg	tttgcggtca	gtgggcgga	1260
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atcacctgtg	tgatccagcc	tggcggttca	atccgtgatg	acgaagtgat	tgccgctgcc	1680
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<210> 2564

<211> 1308

<212> DNA

<213> Enterobacter cloacae

<400> 2564

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gaagcgcaga	aacgcgccta	tgcgctgatg	gcggatatcc	actggaacgg	cagcttcagc	1260
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<210> 2565

<211> 717

<212> DNA

<213> Enterobacter cloacae

<400> 2565

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ctggaaaaccg	gcgtcggcag	tatgcgcgtg	gtcagcgcta	tcaccaggc	cgcagactgg	660
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<210> 2566

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 2566

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<210> 2567

<211> 4167

<212> DNA

<213> Enterobacter cloacae

<400> 2567

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<210> 2568

<211> 612

<212> DNA

<213> Enterobacter cloacae

<400> 2568

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<210> 2569

<211> 276

<212> DNA

<213> Enterobacter cloacae

<400> 2569

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<210> 2570

<211> 4266

<212> DNA

<213> *Enterobacter cloacae*

<400> 2570

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<210> 2571

<211> 1092

<212> DNA

<213> Enterobacter cloacae

<400> 2571

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<210> 2572

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 2572

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<210> 2573

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 2573

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<210> 2574

<211> 366

<212> DNA

<213> Enterobacter cloacae

<400> 2574

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<210> 2575

<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 2575

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<210> 2576

<211> 708

<212> DNA

<213> Enterobacter cloacae

<400> 2576

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<210> 2577

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 2577

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<210> 2578

<211> 915

<212> DNA

<213> Enterobacter cloacae

<400> 2578

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<210> 2579

<211> 2403

<212> DNA

<213> Enterobacter cloacae

<400> 2579

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<210> 2580

<211> 1329

<212> DNA

<213> Enterobacter cloacae

<400> 2580

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c c g t a c c c g c	a c g t t g a c g a	t g t g a t c c c g	c t g a t g g c g g	a a g g c a a a a t	c c t g c c g t a t	780
c t g g a t a t c c	c g c t a c a g c a	t g c c a g c c c g	c g c a t t c t g a	a g c t g a t g a a	a c g t c c t g g c	840
t c c g t t g a c c	g c c a g c t g g c	g c g c a t c a a g	c a g t g g c g t g	a g a t c t g c c c	g g a t c t t a c c	900
c t g c g t c c c a	c c t t t a t t g t	c g g c t t c c c g	g g t g a a a c c g	a a g a a g a t t t	c c a g a t g c t g	960
c t c g a c t t c c	t g a a a g a g g c	g c g t c t g g a t	c g c g t c g g c t	g c t t c a a g t a	c a g c c c g g t t	1020
g a a g g c g c a a	c g g c c a a c g a	g c t g g c g g a c	c a g g t a c c g g	a a g a g g t a a a	a g a g g a g c g c	1080
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g g c c g c g a a a	t t c t g g t g a t	t a t c g a c g a a	g t g g a c g a a g	a a g g c g c g a t	t g g c c g c a g c	1200
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<210> 2581

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2581

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g a c c a c g a t a	g a c a g a c c g g	t t c c c g g c a g	a a t a t g g c t g	a a c a g g a t g g	t g g c a t c g c t	120
g g c t c c c a t g	c t g c g c g c c g	a c t c g a t a a a	g g t c t g c t g c	t t c a g c a c c a	g c g t g t t g c c	180
a c g t a c c a g a	c g c g c g a a a g	c g g g a a t c g a	g a a t a c c g c c	a c g g c g a t g a	t g a c g t t c g c	240
c a t g c c g c t g	c c c a t c a c c g	c c a c c a c g g c	a a t c g c c a g c	a g a a t a c c g g	g a a a g g c a a a	300
c a g c a c a t c a	c a g a t a c g c a	t g a t g a t g c g	g t c c c a c c a g	c c t t c g t a g t	a c c c g g c c g c	360
c a g c c c a a a c	a c g g t g c c a a	t t g c t g c g c c	c a t c a g c a c c	g c a a a g a c c c	c g g c c g c c a g	420
c g a g a t c t g c	g c c c c t a c c a	g c a c g c g g c t	g a a a a t a t c g	c g c c c g a g c g	a g t c c a c g c c	480
a a a c c a g t g c	a t c a t c g a c g	g t c c a t c g t t	c a g c c g g t c g	t a a t c g a a g t	a g t t t t c c g c	540
a t c a a a c g g g	g c t a a					555

<210> 2582

<211> 1173

<212> DNA

<213> Enterobacter cloacae

<400> 2582

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a t t a a g g c g c	a c a a a a c g g c	t c t g g t g c a t	a t c g t g a a g c	c g c c g g t c t g	t a c c g a g c g c	120
g c c a g c a t t	a c a c c g a a a t	g t a c c a g c a g	c a c a t g g a c a	a g c c g a t c c c	g g t g c g c c g c	180
g c c c t g g c g c	t g g c g c a t c a	c c t g g c c a a g	c g t a c c a t c t	g g a t c a a g c a	c g a c g a g c t g	240
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t c c t g g a t t g	a g a a a g a g a t	t g a c g a c c t g	g c g g a c c g t c	c g g g c g c g g g	c t t t g c g g t g	360
a g c g a a g a g a	a c a a g c g c g t	g c t g c a t g a g	a t c t g c c c a t	g g t g g c g c g g	c c a g a c g g t g	420
c a g g a t c g c t	g c t a c g g c a t	g t t c a c c g a c	g a g c a g a a a g	g c c t g c t g g a	a a c c g g c a t c	480
a t c a a a g c c g	a a g g c a a c a t	g a c c t c c g g c	g a c g c g c a c c	t g g c g g t g a a	c t t c c c g c t g	540
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a a c c t g a c g g	t g c t g g a a g a	c c t g c a c g g c	g a t c a g t t c c	t g a a a g c c a t	t g a t a t t g t g	660
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a t c g c c c a c g	a g c c g c c a a a	a a c c t t c t g g	c a g g c g c t g c	a g c t g t g c t a	c t a c a t t c a g	840
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t c g c a c t c c a	a a g c c t c t g g	c g g g c a g c c c	g c t g t a t c a g	a a c g t c a c c a	t c g g c g g c c a	1080
g a a g c t g g t c	a a c g g c g a g c	c a a t g g a c g c	g g t c a a c c c g	c t c t c c t a c g	c g a t t c t g g a	1140
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<210> 2583

<211> 879

<212> DNA

<213> Enterobacter cloacae

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 gacgcgttcg tggcgctgat gtcaaagcac tatcacgctt taaagcgcat cagcgattac 480
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<210> 2584

<211> 1347

<212> DNA

<213> Enterobacter cloacae

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<210> 2585

<211> 1236

<212> DNA

<213> Enterobacter cloacae

<400> 2585
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<210> 2586

<211> 690

<212> DNA

<213> Enterobacter cloacae

<400> 2586

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<210> 2587

<211> 1287

<212> DNA

<213> Enterobacter cloacae

<400> 2587

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<210> 2588
 <211> 1455
 <212> DNA
 <213> Enterobacter cloacae

<400> 2588
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 cgctaccacg cgggcatgag caacgacttc ctgcagcctt gcgtgcaggg gatccgctgc 240
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<210> 2589
 <211> 1293
 <212> DNA
 <213> Enterobacter cloacae

<400> 2589
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<210> 2590
 <211> 1887
 <212> DNA
 <213> Enterobacter cloacae

<400> 2590
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 cagggcaatg cattctcgcg gttataa 1887

<210> 2591
 <211> 414
 <212> DNA
 <213> Enterobacter cloacae

<400> 2591
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 aatttcatgc gtgaaaaagc acccatcctg aaagcgcact acgctgaaag cgaatttagt 240
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 cagactgcc cgaattttat tgccgttaac gcggataagc ttgaaaactg cctgactacg 360
 ctgcgcgttt gcatcatgtg totgaacaag ccggaaacgc ttgcccgga ctga 414

<210> 2592
 <211> 690
 <212> DNA
 <213> Enterobacter cloacae

<400> 2592
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cagcagttta	ttacctctcc	ggcgggtgat	gcggcaattg	tgaagtttga	gcaggactgg	660
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<210> 2593

<211> 945

<212> DNA

<213> Enterobacter cloacae

<400> 2593

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<210> 2594

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 2594

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<210> 2595

<211> 1152

<212> DNA

<213> *Enterobacter cloacae*

<400> 2595

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<210> 2596

<211> 345

<212> DNA

<213> *Enterobacter cloacae*

<400> 2596

tgcgctatta	ctcatcgctt	cttgcgacac	ggtgattgtg	acgtgatttt	tagaatggac	60
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gaaggtaacg	ccgacgaaaa	actcgacccg	gcgagcctga	cgaaaattat	gaccagctat	300
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<210> 2597

<211> 1632

<212> DNA

<213> *Enterobacter cloacae*

<400> 2597

tgcgcgcttt	atcacacttt	tgcaggaat	ctctccgtgt	tagttaccag	caacgtcact	60
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<210> 2598

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 2598

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gtgctggcgg	ggaaagcgaa	taccagcgaa	aaagcgcgtg	caaaggtgct	ggcgtgcgcg	180
cgcgagctgg	gggtaatgga	cggcatggcg	gcagggcgtc	tgctgcttaa	cagcctgggtg	240
gtttttgccc	cgcagcgcgc	tttcgacgag	cggtecgaca	tcttttacta	ccgcgtgata	300
cagagcgtga	gcaaaagcact	tgcttcccac	gaggtecggt	tgcgtacttg	cgcgtggag	360
gagaacgaca	gcgacgcccc	gctgtttctg	gcgcggatga	acgagccgga	cacgcaggcg	420
gccattcttc	ttgggtattga	cgatccgcct	atccacgata	tggcgggtgga	cgtgggcaaa	480
ccctgcatgc	tgattaaactg	cgcgcgaccg	cacatgcgtc	tgcttgcctg	tgccgcggat	540
caccgcgcca	tcggcgagcg	ggcggcgagg	tcctgttctg	agatggggca	ccgcgagggtg	600
atgaacgtgc	tgtgcctacg	tcgctacacc	atggagctgc	gcctgtcggg	gattcgcgac	660
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<210> 2599

<211> 1623

<212> DNA

<213> Enterobacter cloacae

<400> 2599

ggtgggtccc	ggtcattttg	tcgcaccacc	gcgtcagggc	aatgcattct	cgcggttata	60
acttacaaca	ggcaggagaa	cacaatggtt	ccttttgttg	ctcgtcaatg	gctgcttgcc	120
gcgagcgtga	cggctgcgct	ggcgcgcgcc	cccgcgttcg	cggcgaaaga	tgtggtgggtg	180
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aacgtgctgg	cggaaggcta	taccgtgtcg	gaogatgggc	tggctctatac	cgttaagctc	360
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ctgaccggtt	tttacatcat	gccggatacg	ggcttttagct	ttgatgaagc	ggatttaaaa	1620
taa						1623

<210> 2600

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 2600

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cgcaccccg	ggattgagtt	ctggcgctga	ttccgtcgtc	agcccgtcgc	tatggtcgcc	180
gggttggttg	tgttactgct	gacccctggg	gcgattatcg	ccccctgggt	agcccgttt	240
gatgcggaag	actacttcga	ttacgacggc	ctgaacgatg	gaccgtcgat	gatgcactgg	300
tttgccgtgg	actcgctcgg	gcccgcata	ttcagccggc	tgcctgtagg	ggcgcagatc	360
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ctggcggtta	atttactggg	ggatgggctg	cgcgacgcgc	tggatccggc	gataaaaggg	960
tag						963

<210> 2601

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 2601

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gtcggcgcg	tgatcatcac	gtcgtgctg	ataatccctg	ccgccacggc	gcgcggtttt	660
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ggcgggttaa	ccttcctcgg	gttttatgac	acgccagcgg	ggccgctcgg	ggtattgtgc	780
gcggcggtgt	tgtttatttt	cagtatgatg	aaaaagaccg	cgcagtag		828

<210> 2602

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 2602
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 atgttcgttg agctggtcta tgacaagcgt aatgttgatg gtttggttg cgccagagag 120
 attattcttg cagagctgac gaagcgagt caccagatct tccctgatgc cgaagtgagg 180
 gtgaagccga tgcaggcgaa cggcttgaat agcgatgcca gcaaaagcga tcgggaaaag 240
 ctgaaccgca tgctggagga aatgtttgaa gacgcaaata tgtggtggt gaatgattag 300

<210> 2603

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 2603
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 gtccctttctg acgtgtcgct gaatctgaag cccggcaaaa tactcacgct gtcgggccct 120
 aacggtgcag gcaaactgac gctggtgcgc gtogtattag gcctggtagc cctgacgca 180
 ggtgttatcg tccgcgaaga caaattgcgt atcggtatg tgcgcgcaaaa attacatctt 240
 gatgccaccc tgccctgac ggtgagccgc ttccctgcgc tccgtcccgg tacgcgtaaa 300
 gcgatatcc tcccggcgt gaaacgcgtt caggcgggac atcttggtga ggccgccctt 360
 caaaagctgt cgggcggtga aaccacgcgc gagggtgttg acgtcaacgg tcagggttgcg 420
 cctcagctgc tggctcctgga cgagccgacg caggtgtgtg acgtcaacgg tcagggttgcg 480
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 tgttggtccg gcacgcccga agtggtgtca atgcataccg aatttatctc catgtttggc 660
 catcgtggcg ccgaacagct gggcatctat cgcataate acaatcaccg ccatagttta 720
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<210> 2604

<211> 594

<212> DNA

<213> Enterobacter cloacae

<400> 2604
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 gatgtggtca gccgcgctgc gcgcctggca gaaaaatgcc gcgccagcgg ctgcctggtt 180
 gttatggtgc gcgtgggtgc gtccgctgat ttgcgcgaag cggttaaaaca gccggttgat 240
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 aatatcggtg tggaatccac cgcgcgtaac gcctgggagc tgggctttta cctggtgatc 480
 gcggaagatg cgtgcagcgc agcctctgog gatcagcacc agtgcagcat gaccataatc 540
 ttcccgcgta tcgggtcgcgt gcgcagcagc gatgagatcc tcagcgcggt atga 594

<210> 2605

<211> 822

<212> DNA

<213> Enterobacter cloacae

<400> 2605
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 ggacgaattt tgtgtagctc tggatatctc ggaaccgcag gcgcgggagc aatgacatat 180
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 agcgaggcga tcatacgcga ggatctggaa aaggttctgc ccgttgctgt aagtctctgc 660

gggactggca	ctacgccagc	aggagaggaa	attaacgacc	ttaaaaccgt	ggactacagt	720
gctatgagcg	ccctgtatgt	tgaggccatc	aaggagctga	ccgaacgggt	aaaaatcatc	780
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<210> 2606

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 2606

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gatctggacg	ctgctttcct	gtccgccgac	cagggctggt	ccggtgcata	cgggttgctg	120
cttctcaata	acgccagcgc	aaccggagag	caataccgct	accgccaggc	aaagaatcat	180
atttttcata	gtggttatat	cccaggggcg	tcata			216

<210> 2607

<211> 396

<212> DNA

<213> Enterobacter cloacae

<400> 2607

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gcagtcgaaa	ccttcagctg	gtgcccaaag	gttgccctct	aggttgatac	aagtttcgt	120
acccgaaagg	cgcagtttgg	cgatggctat	gcgcagggtg	ccggagacgg	tatcaaccct	180
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tcaggcttat	ggcgcgcgga	atccttccag	atatctaccc	acggcaacaa	gaaatatacc	360
ctcagcagta	cattcatata	ggcataccat	ccatga			396

<210> 2608

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 2608

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cgggaaattg	gcggcgccat	tatatccgcc	ggggtttatg	cagaagatca	gcaataa	597

<210> 2609

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 2609

agaaggaaga	gaaaaactga	tatggcatat	aagcgtcccg	tttcggttct	ggtggtcatt	60
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cagtcggtta	ccggcagcct	ggaagagggg	gagaccgcac	cgcaggccgc	cgcgcgtgaa	180
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gaacacctga	cctaccgctg	ggtggatgcg	gcggatgccg	ccgcaactgac	caagtcgtgg	420
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<210> 2610
 <211> 768
 <212> DNA
 <213> Enterobacter cloacae

<400> 2610
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 gcggtggata aagccctgtc caacaacatg acgcgtgaca ccctgaaccg tgcaatcgca 240
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 cctggcggtga cggcggtgat ggttgagtgt ctgtccgaca accgtaaccg taccgttgcg 360
 gaagtgcgcc acgcgttcac caaaaccggc ggcaacctgg gcaactgacg ttctgtagcg 420
 tacctgttca gcaaaaaag cgtcatctcc ttcgagaaaag gcgacgaaga tgcgatcatg 480
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 accgcaccga aactgctgcg tctgatcgac atgctcgaag actgcgacga cgtacaggaa 720
 gtgtaccaca acggtgaaat ctctgatgag gttgcagcga ctctctga 768

<210> 2611
 <211> 870
 <212> DNA
 <213> Enterobacter cloacae

<400> 2611
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<210> 2612
 <211> 3492
 <212> DNA
 <213> Enterobacter cloacae

<400> 2612
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<210> 2613

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 2613

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<210> 2614

<211> 3873

<212> DNA

<213> Enterobacter cloacae

<400> 2614

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<210> 2615

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 2615

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<210> 2616

<211> 543

<212> DNA

<213> Enterobacter cloacae

<400> 2616

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<210> 2617

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 2617

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<210> 2618

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 2618

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<210> 2619

<211> 1821

<212> DNA

<213> Enterobacter cloacae

<400> 2619

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<210> 2620

<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 2620

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cagatggaga	ttttcatcca	ggcggcaaaag	ctgcgcggcg	atgcgctcga	tcacctgctg	180
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<210> 2621

<211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 2621

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cttgccgtgc	tgcgccagtt	ggtcgagcgg	cggcgcgcgg	cgttggccca	tctggacgcg	540
caactggcct	ccatgccagc	cgagcggggc	cacgaggagg	cattgccgtg	a	591

<210> 2622

<211> 1323

<212> DNA

<213> Enterobacter cloacae

<400> 2622

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cgtgcgcgcc	gtcgtgcgga	gatcatcagt	ccgttggcgc	agtcggagac	ggtcgggcac	180
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<210> 2623

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 2623

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gacgcggatc	gcccgcagca	cctcaagaca	tcagctcggc	cggacaagcc	cgttcgcgcc	420
gatacggata	ttgcgcagcc	gcaggcagac	aacttgccac	ccgccaaacc	gttcgaccag	480
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<210> 2624

<211> 1563

<212> DNA

<213> Enterobacter cloacae

<400> 2624

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<210> 2625

<211> 1020

<212> DNA

<213> Enterobacter cloacae

<400> 2625

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gatctgctcg	gccattccga	cgtctctacg	acgatgattt	acacgcattg	gctgaaagtt	960
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<210> 2626

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 2626

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aacctgaccg	cgatgcgggc	cgtggtgttc	accgaccgcg	aagtggcgac	cgtaggctac	180
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gaaggcagcg	gacgactgat	cggcgtgcag	gcagtggccc	cggaagcggg	cgaactgatc	360
cagacggcgg	cactggcgat	tgcgaaccgg	atgacgggtg	aggaactggc	cgaccagttg	420
ttccctacc	tgacgatggt	cgaagggttg	aagctcgcgg	cgcagacctt	caacaaggat	480
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<210> 2627

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 2627

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<210> 2628

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 2628

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cgtaacagca	aagctgcata	cgggtttctg	ggtaaaatcc	tcaacaacgt	gaagaagtgg	420
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<210> 2629

<211> 276

<212> DNA

<213> Enterobacter cloacae

<400> 2629

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cacgctggac	atggctcgct	acctgctcac	acgcagcgag	ggcaccatag	gggaactggc	180
gcacttgctg	atggcgggcg	ccatcgctgc	cgtggagagc	ggcgagggaag	cgatcaacca	240
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<210> 2630

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 2630

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ccatggtcag	ccactacctg	tttgatgcgc	agttctgtaa	tccagcatcg	ggttgggaga	120
aaggccagat	tgagaagaac	gtgcaggatt	cccgccaacg	cctgtggcaa	ggggcaccag	180
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<210> 2631

<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 2631

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ggcatggcac	acgccattga	ggagttgggc	aatcagaatt	caccagcatt	taatcaagcc	120
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gccattggta	cacaagcagt	gatgcacttg	aaccgacggg	tgcgtttctt	ctccaccgtg	420
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acagcgttgt	tggaccgact	aaccaccacc	tgccacatcc	tggaaaccgg	caatgaaagt	720
taccgcttca	aacacagttc	aactcagaat	aagcaggagg	aaaaacagac	ccgcaaaactg	780
aaaatcgaga	cataa					795

<210> 2632

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 2632

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<210> 2633

<211> 3024

<212> DNA

<213> Enterobacter cloacae

<400> 2633

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<210> 2634

<211> 1032

<212> DNA

<213> Enterobacter cloacae

<400> 2634

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<210> 2635

<211> 561

<212> DNA

<213> Enterobacter cloacae

<400> 2635

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ccgattctcg	ccgccgtgct	ggccgggacg	accgccggtg	ccttccttgg	cgagcattgg	480
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<210> 2636
 <211> 873
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2636
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<210> 2637
 <211> 618
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2637
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 tacctgcggg aagactga 618

<210> 2638
 <211> 435
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2638
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 cccggcgcgc ggatacttcc gctcaagggc gtcgggaagc gcaacgcgcg tgcggccctc 360
 ggcttggtcc ttcagccacc atgcccgctg acgcgacagc tgctcgcgca ggctgggtgc 420
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<210> 2639
 <211> 447
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2639

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aagctgggcg	aacaaacgat	gctcgccttc	cagaaaaccg	aggatgcgaa	ccacttcatc	180
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gctgctgccc	aagggttgcg	ggtgacgcac	accgtggaaa	cggatgaagg	cacgaaccca	420
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<210> 2640

<211> 930

<212> DNA

<213> Enterobacter cloacae

<400> 2640

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ggagatctgc	gaagcgcaat	caccttctcg	gaaacctcg	cgaatttctg	cagtcgcgac	900
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<210> 2641

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 2641

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cacatagagt	cctacaggct	cgcattgcac	tcactcgggg	cggaaaaggt	tgaggctctt	720
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<210> 2642

<211> 387

<212> DNA

<213> Enterobacter cloacae

<400> 2642

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gttatcgcaa	tagttggcga	agtaatcgca	acatccgcac	taaaatctag	cgagggtctt	120
actaagcttg	ccccttcgcg	cgttgctcata	atcggttatg	gcattgcatt	ttattttctt	180

tctctggttc	tgaaatccat	cctgtgcggt	gttgcttatg	cagtctggtc	gggactcggc	240
gtcgtcataa	ttacagccat	tgcttggttg	cttcattggc	aaaagcttga	tgctggggc	300
ttttaggta	tggggctcat	aattgctgcc	tttttgctcg	cccgatcccc	atcgtggaag	360
tcgctgcgga	ggccgacgcc	atggtga				387

<210> 2643

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 2643

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ccgaacgttc	gggtcgccctg	ctcggtgat	atcgacgagg	ttgtgcggct	gatgcacgac	180
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<210> 2644

<211> 411

<212> DNA

<213> Enterobacter cloacae

<400> 2644

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tgtaggtcac	gagcggcatt	ctggccttcc	cgcggcgcca	tgaccttgcc	cgggtcaagg	360
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<210> 2645

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 2645

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accagatccg	tcacgaggcc	gctgccttgc	cgggcacgcc	ggatcagaac	gtatacctgg	180
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<210> 2646

<211> 210

<212> DNA

<213> Enterobacter cloacae

<400> 2646

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tcgcacgac	ggcgcgccag	ctcccaagcc	tcatacaggca	gagtggccac	gccttgttct	120
ggaatccgtg	gggtgtccgc	cgccatgtct	acctcgcttt	ggtgcacacg	agtattgagc	180
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<210> 2647

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 2647

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ggcggcgaga	atcggcagat	ggcaggggca	ggtcaacacg	gccagcgcac	cccacaggta	180
gccggaaaacg	ggttgggcgcg	tctcggggcg	cagtttgtca	ggggcggttca	cggaatgcc	240
tcctcgtgcg	cccgtcgcgc	tggcatggag	gccagttgcg	cgtccagatg	ggccaacgcc	300
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tccgctgcgt	cgagcgcacg	gcacagccgc	gccagggcat	ccaggccgat	accgcctcg	420
aaggccgcgc	gcacgaagca	cagccgttgc	aaggccgcgt	cgtcgaacac	gccgtag	477

<210> 2648

<211> 411

<212> DNA

<213> Enterobacter cloacae

<400> 2648

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<210> 2649

<211> 1548

<212> DNA

<213> Enterobacter cloacae

<400> 2649

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cgaatcgatg	cctatatcca	ctggtacaac	gagcgcgcga	tcaaagtgtc	gcttggcggg	1500
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<210> 2650

<211> 714
 <212> DNA
 <213> Enterobacter cloacae

<400> 2650
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 gtacttaatc tgtcgggtgt caacgtcaga cgggcaccgg ccttcgcgtt tgagcagagc 180
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 aatcgtggag tgatcgacat tcaactccgg ttcagccagc atctcctgca gctcacggta 540
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 ccggcctttg aatgggttca tgtgcagctc catcagcaaa aggggatgat aagtttatca 660
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<210> 2651
 <211> 1233
 <212> DNA
 <213> Enterobacter cloacae

<400> 2651
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 gcttccggtt cttttggtag ccggggggacc tatgccaatc tgggcttgcc cggtagcggg 180
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 accgaccggg ggctcagaca ggcgcttgag caggaagccg ctgaactcat gtcagcggta 300
 accgcaatcc gtaatatcca cgagctgacg ccggatccaa aaacaggcat cagctgggca 360
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 gaaacgattg ttgcatttga agtaaaagcc gagctatcag cagtcctgct ggacgttgat 840
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 attgatccgg ttgaagcgtt aggcgatcac ccggttatcc gaaagatgag cagtaccttc 1200
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<210> 2652
 <211> 651
 <212> DNA
 <213> Enterobacter cloacae

<400> 2652
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 tttctcggcg ggatcctttg taaaaaagaa gaagaatacg accttgatgt gatcgctttc 180
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 gaaaagctcc agcagcactt tggtaaagtt cagaatgcct tcatccgggc agtagatgcc 480
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tccatggtct ttgccgagct gatacgcgag gctacaggct ggaaactcag ggcaattggt 600
gagccttcag aatcagattc gtttgtctcg cacctgagga attacatgtg a 651

<210> 2653

<211> 1152

<212> DNA

<213> Enterobacter cloacae

<400> 2653

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gaaagacgta acccgaaaacg cgcctttctg tttgtcagca aagtactcgg caggcacatt 180
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acctatgaat aa 1152

<210> 2654

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 2654

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aaacacgcgt tcaccaaaga agatggtgaa aaagtcgttg atgatgcagg taaacgactg 180
aaataa 186

<210> 2655

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 2655

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gcgcgaggag ctggccgagg tggatgtgga ctggctgac gccgagcgtc ccggcaaggt 120
aaaaaccttg aagcagcatc cgcgcaagaa caaacggcc atcaacatcg aatacatgaa 180
aaccagcatc cgtgccaaagg tggagcacc gtttcgcatc atcaagcggc agttcggctt 240
cgtgaaagcc agatacaagg ggctgctgaa aaacgataa 279

<210> 2656

<211> 1191

<212> DNA

<213> Enterobacter cloacae

<400> 2656

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cacctgcggc cgatctcggc catgaggtct ccgtccacaa gggggaacgt attctggttc 120

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ggcgacagcc	tgagcgatca	tcgttttatg	aaactgtgca	gctggtttgg	catcccgctg	1140
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<210> 2657

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 2657

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cagggagcaa	tgtgtgaacc	cgccacacat	cgcgctggg	cggctggcat	tctggacaga	960
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<210> 2658

<211> 501

<212> DNA

<213> Enterobacter cloacae

<400> 2658

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accagtctgg	aatgctcaga	gccgacatta	acccgggccc	tcaaagagct	acgcgagtca	180
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<210> 2659

<211> 747
 <212> DNA
 <213> Enterobacter cloacae

<400> 2659
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 aaaaatggcg ttcagacgct gcttaccacg ctgaaacagg atccgtatgc actcgaaacg 240
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<210> 2660
 <211> 687
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2661
 <211> 1125
 <212> DNA
 <213> Enterobacter cloacae

<400> 2661
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 tcagagtcca tgattggtga aaacctgaaa aaaatgactg atggtctgca aatgatcgtc 180
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<210> 2662

<211> 1590

<212> DNA

<213> Enterobacter cloacae

<400> 2662

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<210> 2663

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 2663

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 <211> 1236
 <212> DNA
 <213> Enterobacter cloacae

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 <211> 420
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2666
 <211> 786
 <212> DNA
 <213> Enterobacter cloacae

<400> 2666
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<210> 2667

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 2667

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<210> 2668

<211> 384

<212> DNA

<213> Enterobacter cloacae

<400> 2668

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<210> 2669

<211> 711

<212> DNA

<213> Enterobacter cloacae

<400> 2669

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<210> 2670

<211> 483

<212> DNA

<213> Enterobacter cloacae

<400> 2670

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<210> 2671

<211> 1623

<212> DNA

<213> Enterobacter cloacae

<400> 2671

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<210> 2672

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 2672

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<211> 423

<212> DNA

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<400> 2673

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<211> 2742

<212> DNA

<213> *Enterobacter cloacae*

<400> 2674

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<210> 2675

<211> 747

<212> DNA

<213> Enterobacter cloacae

<400> 2675

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ttcagcgtgc	cgttcgtggt	cgttcgcgcg	atctctgacg	tagcggacca	gcagtccac	660
atcagcttcg	acgagttcct	ggcggttgcg	gccaaagcagt	ccaccgtgat	ggtggaaacc	720
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<210> 2676

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 2676

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<210> 2677

<211> 831

<212> DNA

<213> Enterobacter cloacae

<400> 2677

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gagccgtttg	tgaaccgggg	cgtcagcact	ggcgaactgg	atcgcatctg	taacgactat	180
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gccggtgact	accgcatccg	caccatgaaa	gacggctgga	cggtgaaaac	caaagacaga	720
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<210> 2678

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 2678

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cagcttaaaa	ttccggtcat	cgcactcaac	agcgactggg	ttgaacgcgc	cagcccgct	780
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<210> 2679

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 2679

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<210> 2680

<211> 1545

<212> DNA

<213> Enterobacter cloacae

<400> 2680

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<210> 2681

<211> 1491

<212> DNA

<213> Enterobacter cloacae

<400> 2681

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<210> 2682

<211> 648

<212> DNA

<213> Enterobacter cloacae

<400> 2682

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<210> 2683
 <211> 582
 <212> DNA
 <213> Enterobacter cloacae

<400> 2683
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<210> 2684
 <211> 1428
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2685
 <211> 585
 <212> DNA
 <213> Enterobacter cloacae

<400> 2685
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gaaaaaacgc	gtcgcggcct	gactcgcttc	aaaggcgtag	ctatgggtga	cggcaaagtt	540
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<210> 2686

<211> 792

<212> DNA

<213> Enterobacter cloacae

<400> 2686

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<210> 2687

<211> 3501

<212> DNA

<213> Enterobacter cloacae

<400> 2687

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<210> 2688

<211> 972

<212> DNA

<213> Enterobacter cloacae

<400> 2688

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<210> 2689

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 2689

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<210> 2690

<211> 777

<212> DNA

<213> Enterobacter cloacae

<400> 2690

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<210> 2691

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 2691

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<210> 2692

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 2692

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330

<210> 2693

<211> 768

<212> DNA

<213> Enterobacter cloacae

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<210> 2694

<211> 861

<212> DNA

<213> Enterobacter cloacae

<400> 2694

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<210> 2695

<211> 1449

<212> DNA

<213> Enterobacter cloacae

<400> 2695

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<210> 2696

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 2696

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<210> 2697

<211> 561

<212> DNA

<213> Enterobacter cloacae

<400> 2697

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<210> 2698

<211> 1029

<212> DNA

<213> Enterobacter cloacae

<400> 2698
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 gtttattcct ccggtattcc gctgcaaccg aacaaggctc ggcgtaaac agctgcaactg 960
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<210> 2699

<211> 630

<212> DNA

<213> Enterobacter cloacae

<400> 2699
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 ctggacctca cttatccgcg gtatgggttc gccagcaca agggatatcc aacggccttc 540
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<210> 2700

<211> 2136

<212> DNA

<213> Enterobacter cloacae

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 gccgacctgc tgaaatttat cgaacacaat ccgcgcacat gtggcgatgat attcgactgg 180
 gacgaatacg acatggagtt gtgcagcgat atcaataagc tcaacgaata tcttcgctg 240
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tggtcgggtg	ggcgccacta	tcccggtctt	gaaacggata	ttcatggcgc	gaaacgcgac	2100
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<210> 2701

<211> 402

<212> DNA

<213> Enterobacter cloacae

<400> 2701

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cgcacactgg	ccttcagcgt	cgatgacctg	gacagcgcg	taaaacatct	ggaagctcac	300
ggcgtggcct	gcgaagcgat	tcgtgtcgat	ccctttaccg	ataaacgttt	cacttttttc	360
aacgatccgg	acggcctgcc	gctggagcct	tatcagcagt	aa		402

<210> 2702

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 2702

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aacgtaatgg	atgcccggtg	gcgcattatc	ggcagcggcg	atcgtgagcg	tattggggaa	180
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<210> 2703
 <211> 1272
 <212> DNA
 <213> Enterobacter cloacae

<400> 2703
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 actctcgacg ttgtacgtca taatcctgac agctacaccg tagccgcgct tgtggccgga 180
 aaaaacgtgc agcgaatggt cgaacagtgc ctggagttta cccccggtt tgccgtgatg 240
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 gaggtgctca gcgggcaaca ggccggcggtc gatatggccg cgcttgatga agttgatcag 360
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 gaggtgctgg ccgtggatga acaggcacgc attgttgcgc gtaaacaggt gacacgtctc 1260
 gcaagctggt ga 1272

<210> 2704
 <211> 1176
 <212> DNA
 <213> Enterobacter cloacae

<400> 2704
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 cgtgtaccca atgcccgtt tgtgggcgtg gctgggcgcg taatgcaggc cgaaggctgc 180
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<210> 2705
 <211> 1077
 <212> DNA
 <213> Enterobacter cloacae

<400> 2705
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 cgtgagcctg acgtccagct gcgggcgatg catatccatc acggcttaag ccccatgcc 180
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 tacgcccgtt tttctggcgc attacagcct ggagaagcgt tggtcaccgc gcagcatctg 360
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 tccgccatgc ctgagcgcgc tgattttgct gaaacagagc tcatccgccc gctactgggt 480
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 ctgagtgage gctgggcgca tttttccgaa gcggcgccca gaagcgccat gctgtgtgct 660
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 gacgttgtgc tcgactggcc gtgcgcggaa aaagcattaa cgtaccgat gaatgcgggt 1020
 gtcgttgctg taagtcattc gttcttcacc cacaggggat ggcagcaccg cgttag 1077

<210> 2706
 <211> 273
 <212> DNA
 <213> Enterobacter cloacae

<400> 2706
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 cgtgaaaagt tccgtgtacg tcagcacgaa ctgccttcaa tggatttcgt ggtggtggcg 180
 aaaaaagggg ttgcgcacct cgataaccgt gctctctcgg aagcgttgga aaaattatgg 240
 cgccgccact gtgccttggc tcgcgggtcc tga 273

<210> 2707
 <211> 1137
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (378)

<220>
 <221> unsure
 <222> (504)

<400> 2707
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tcaggtctgg	tgctgtacta	tatcgtcagc	aacctggtga	ccatcatcca	gcagcagctg	1080
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<210> 2708

<211> 1377

<212> DNA

<213> Enterobacter cloacae

<400> 2708

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gaactgctgg	cggaagagct	gcgtctggcg	caacagaacc	tgagcgagat	caccggggag	1320
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<210> 2709

<211> 1287

<212> DNA

<213> Enterobacter cloacae

<400> 2709

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cgggcaggcg	tgccagctc	ggtgctgggc	attgcgcagg	tctgcgggtc	ttcgtctatgg	1140
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gaagcccatc agcagtcctcg atcttaa 1287

<210> 2710

<211> 777

<212> DNA

<213> Enterobacter cloacae

<400> 2710

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atccgcaaac	tgaacggcgc	ggcgtcagac	gacgccagcc	tggtgcagct	gctccccggc	540
tccggacgcc	tgcgcgcgac	aaaagcctcg	ctggtagagg	cgctcagcga	cgctgaggac	600
gtactgatct	ggtcogttgc	ggtgagcccc	gccatcgaa	ggctgaaaat	ctgggaattt	660
gacagtattc	gcggttggcg	tagtcttcgc	gatgtccctg	agcgcgccaa	cgagccccgc	720
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<210> 2711

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 2711

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cacctgcgtc	agatcctggt	gttcctggat	gcgatggtga	tgaacaagcc	ggaatttatg	480
ggcggcggtg	ttcagaacaa	ggtcgacccg	cagacgggtg	aagtgggtga	tcagagtacg	540
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taa						603

<210> 2712

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 2712

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accacgcaga	ccacgaccac	cgcagcgggt	agcgcgcgcg	accagggcgt	accggccagt	180
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ccgttccagt	tactgaaaac	cacgcctgaa	tttatctacc	aggcgcagag	cggcctgacc	360
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gacacctttg	tgctggctga	tggccaaaac	gaactcgtta	tcccgatgac	ctataccgac	480
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<210> 2713

<211> 306

<212> DNA

<213> *Enterobacter cloacae*

<400> 2713

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gcgcctggca	ggagatcgag	caggccgacc	gcgtgctgtt	tatggtggac	ggcaccacaa	180
ccgacgccgt	tgaccggct	gaaatctggc	cagactttat	cgcccgtctc	ccggctaacc	240
tgccgatcac	cgtggtgcgc	aacaaggccg	acgttacccg	cgaaacgctg	ggcatcagcg	300
atgtga						306

<210> 2714

<211> 1029

<212> DNA

<213> *Enterobacter cloacae*

<400> 2714

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gagcgcagcg	tcaccaaagc	cgcgaagcgg	atgaacgtga	cgccgtccgc	ggtgagtaaa	180
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ggcaaccaga	tcctcgataa	attccaccat	agctctcctg	gcgggcttaa	gtttgtgctc	360
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caggcagaaa	agctcaccgt	acccttcacg	ctgatctggc	ataaacggaa	cagccataat	960
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<210> 2715

<211> 288

<212> DNA

<213> *Enterobacter cloacae*

<400> 2715

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tgcgctttca	cgccaacatg	ctcaagctac	ggaattgagg	cattgcgcag	gtttggagtg	180
ataaaaaggca	gttggttgac	ggtgaaacgc	gtattaaaa	gccacccttt	acaccaggt	240
ggagacgacc	ccgtccctcc	aggacccttt	gataccagag	aacactaa		288

<210> 2716

<211> 741

<212> DNA

<213> *Enterobacter cloacae*

<400> 2716

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gtcgacagtg	aggtcatttg	ttcccgcgcg	tatgtcgcca	tgttccagga	atttggtatt	180
acgctcgatc	tcgaagaggt	gtttaaacgc	tttaaggggc	tgaagctgta	cgagatcatc	240
gacatcatta	acgaagagca	cggggtggat	ctggcgaaag	cgatctgga	accggtgtac	300
cgcgcgcagg	tcgcacgcct	cttcgacgcc	gagctggaag	ttatcgctgg	cgctaacacg	360
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cagcactcgc	tcggcaagct	gaatatgttg	caccacttcc	cggaaaaact	gttcagcggc	480
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aacgtcaacg	tggagaactg	catcctgggtg	gatgactcgt	ctgcggggcg	gcagtcgggg	600
attgatgcgg	ggatggaggt	gttttacttc	tgcgcgatc	cgcacaacaa	gccgatcgat	660
catccaaaag	tgacgacctt	taccgatctg	gcgcaactgc	cagcgttgtg	gaaggcgcg	720
gggtgggata	ttactcgtcg	a				741

<210> 2717

<211> 594

<212> DNA

<213> Enterobacter cloacae

<400> 2717

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ctgttttcag	gtgcgacatt	agcggctgac	ggtagctgtt	atttccgtgg	cgaggtgatt	120
gattctactt	gtacagtcac	gactgatacc	agtaatcaga	ctgttaatat	tggctcgtgta	180
tcggtaaaaa	ccttcgcggg	tattgattcc	accgcgtctg	ttaaagattt	ccacatccgt	240
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aaagatacca	tcggtaaagg	ttatctttca	atcggtacgc	cggtgaacga	agacggtacg	360
gacgggtgagt	tcactggcag	cggcgacgcc	attgcggcga	cgggcgtggc	gataaaaactg	420
ttcaacctga	gcgatgatac	cgcgatccct	ttgtataaca	attctaaata	cgttgccatt	480
gcagatggta	aagcggatat	gggattcaag	gcgaaattcg	tccagactct	ggcaacagtg	540
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<210> 2718

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 2718

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tccctgattt	tctctctctg	gccgagcatt	caaaaatttg	gtttcgcctt	cctgtggacc	180
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taa						963

<210> 2719

<211> 831

<212> DNA

<213> Enterobacter cloacae

<400> 2719

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cttaataaac	acatttccgg	ccagtttaac	gcagagctgg	aaagcattcg	caccaggtg	180
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caggacagcg	agctggcgaa	gcgcgttatt	gaaggcgacc	acaacgtcaa	tatgatggaa	300
gtcgccatcg	acgaagcctg	cgtgcgcctc	attgcgaagc	gtcagccgac	ggcgagcgac	360
ctgcgtctgg	tgatggcgat	catcaaaaact	atcgccgagc	tggagcggtat	tggtgacgtg	420

gcggataaaa	tctgccgcac	cgcgctggag	aaattctccc	agcagcacca	gccgctgctg	480
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tgccagaaca	tttgogaata	catcttctac	ttcgtgaagg	ggcaggattt	ccgacacgtg	780
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<210> 2720

<211> 399

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (10)

<400> 2720

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ccatgggcca	ttttccacat	cctgatcatt	acgctgcaag	cctttatctt	catgggtctg	360
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<210> 2721

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2721

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tttgccgctg	aggtgacgaa	aaacgaacaa	atggccgagt	tgctttctgg	tgcgttagcg	180
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cgtcgggtg	atatgggtcat	tgatggcagc	gtacgcggcc	gtcttgagcg	ccttgcagac	540
gtcttgcagt	cttaa					555

<210> 2722

<211> 1554

<212> DNA

<213> Enterobacter cloacae

<400> 2722

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<210> 2723

<211> 915

<212> DNA

<213> Enterobacter cloacae

<400> 2723

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atggtggcga	tgaagccgcg	gaccgataat	ggcggcagcc	tgattaaaga	gctgcagttg	840
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<210> 2724

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 2724

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ccgggtcagc	caccgctgct	caccgccatt	aagcctggta	tgatccgcat	cgttaaaccag	180
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gaatcgaagc	gtaaggctga	agagcacatt	aacagctctc	atggtgacgt	ggattacgct	360
caggcgtctg	cggagctggc	caaagcgatc	gcgaaactgc	gcgttatcga	gttgacccaa	420
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<210> 2725

<211> 1425

<212> DNA

<213> Enterobacter cloacae

<400> 2725

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<210> 2726

<211> 1845

<212> DNA

<213> Enterobacter cloacae

<400> 2726

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<210> 2727
 <211> 786
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2728
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 <212> DNA
 <213> Enterobacter cloacae

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<210> 2729
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 <212> DNA
 <213> Enterobacter cloacae

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<210> 2730

<211> 258

<212> DNA

<213> Enterobacter cloacae

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<210> 2731

<211> 507

<212> DNA

<213> Enterobacter cloacae

<400> 2731

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<210> 2732

<211> 1506

<212> DNA

<213> Enterobacter cloacae

<400> 2732

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<210> 2733

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 2733

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<210> 2734

<211> 2538

<212> DNA

<213> Enterobacter cloacae

<400> 2734

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<210> 2735

<211> 1086

<212> DNA

<213> Enterobacter cloacae

<400> 2735

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<210> 2736

<211> 1074

<212> DNA

<213> Enterobacter cloacae

<400> 2736

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<210> 2737

<211> 909

<212> DNA

<213> Enterobacter cloacae

<400> 2737

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<210> 2738

<211> 303

<212> DNA

<213> Enterobacter cloacae

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<210> 2739

<211> 2181

<212> DNA

<213> Enterobacter cloacae

<400> 2739

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<210> 2740

<211> 18048

<212> DNA

<213> Enterobacter cloacae

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<210> 2741

<211> 1197

<212> DNA

<213> Enterobacter cloacae

<400> 2741

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<210> 2742

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 2742

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<210> 2743

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 2743

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<210> 2744

<211> 1335

<212> DNA

<213> Enterobacter cloacae

<400> 2744

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<210> 2745

<211> 1728

<212> DNA

<213> Enterobacter cloacae

<400> 2745

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<210> 2746

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 2746

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<210> 2747

<211> 1155

<212> DNA

<213> Enterobacter cloacae

<400> 2747

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<210> 2748

<211> 1821

<212> DNA

<213> Enterobacter cloacae

<400> 2748

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<210> 2749

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 2749

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<210> 2750

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 2750

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<210> 2751

<211> 1095

<212> DNA

<213> Enterobacter cloacae

<400> 2751

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atgaccgatt	taattgcacg	tccccgtcgc	ctgcgcaagt	cacccgcact	gcgcgccatg	180
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<210> 2752

<211> 1959

<212> DNA

<213> Enterobacter cloacae

<400> 2752

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<210> 2753

<211> 183

<212> DNA

<213> Enterobacter cloacae

<400> 2753

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agcagagtca	tgaacgtgc	gtcactgatc	ctgcggcgta	cagccttcac	cagcagtcga	180
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<210> 2754

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 2754

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gtcaaaacac	cttcgaccgg	cagtgccttac	gtatcactgc	cagttcctcc	tgcacggcct	420
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<210> 2755

<211> 423

<212> DNA

<213> Enterobacter cloacae

<400> 2755

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cgggcatgcc	gcaggtcact	gccgctcagg	ttctccaccg	tcacaccogg	tggtgattgtt	300
gggtttctca	tcgtgagtta	ccggttcaat	attccagaca	gactcgcggg	tcattttaagc	360
atccatgccc	gccctgaact	ccgggcacac	tatacgtcac	atcgccgcac	cacacctgat	420
tag						423

<210> 2756

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 2756

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ttctcgttaa	tcgaaaaact	cagagcgcag	tatcctgtgg	tcacactctg	ccagggtgtc	120
gggggttcac	gcagcagcta	caaatactgg	gtgaaaagcc	ccgaaaagcc	agacggcaag	180
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ggcagactca	tgaaagaact	gggactgggt	agttgtcagc	aaccaccca	ccgtataaaa	360
cgtggtggcc	atgaacacat	tgctatccca	aaccaccttg	agcgacagtt	cgcagtgaca	420
gagtctaate	aggtgtggtg	cggcgatgtg	acgtatagtg	tgcccggagt	tcaggggcggg	480
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<210> 2757

<211> 1530

<212> DNA

<213> Enterobacter cloacae

<400> 2757

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cccgaaggta	atccctatct	gaggacggag	accagaaaca	cgtatacatc	gcgctttaca	1500
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<210> 2758

<211> 210

<212> DNA

<213> Enterobacter cloacae

<400> 2758

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cactttcttg	ctgaatgctt	aaccctgtct	gttgaacggc	ggcataaccc	taaaggctat	180
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<210> 2759

<211> 957

<212> DNA

<213> Enterobacter cloacae

<400> 2759

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acgattatcc	cgttggggcc	gtacattggc	gcgcaagtgt	cgggcctgga	cgtaaccctg	180
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<210> 2760

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 2760

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gatggtcagt	cttacgacag	tatgcgttat	gaagtccggc	tggatgcagg	ttataccttc	180
aatacggggc	gcgagcaggc	attaacgcct	tacttcaaac	tggcttacgt	gtatgacgat	240

gctgacaaca	atgctgatat	caacaacgac	agcattgata	acggcgtaga	aggctctgcg	300
gttcgcgtgg	gactgggtac	tcagttcagc	ttcacgaaaa	acttcagtg	ttacactgat	360
gogacttata	tgggcggcgg	cgacgttgac	cagaactggg	gagcaaacct	gggtgtgaaa	420
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<210> 2761

<211> 1239

<212> DNA

<213> Enterobacter cloacae

<400> 2761

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atcaccaacg	tctttggtca	ggttcgcggt	tcgttccagt	atctgattag	ctcctggact	1140
acgcttgtgg	agctgatgtc	catctacaaa	cgtttacgca	gtttcgagcg	tgagctggac	1200
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<210> 2762

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<400> 2762

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ccggttttcc	tggtacatac	cgcccttaaa	atcacctcgc	caaacggtaa	aagctatagc	420
gaacggctgg	atacggtgaa	aaccgagaag	cagcttagcg	ccatttttga	tgatttcata	480
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<210> 2763

<211> 396

<212> DNA

<213> *Enterobacter cloacae*

<400> 2763

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ctaaagaaaa	agctacaacg	cattgaaatg	gaaaacgaca	tattaaaaaa	ggctaccgcg	360
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<210> 2764

<211> 1425

<212> DNA

<213> *Enterobacter cloacae*

<400> 2764

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<210> 2765

<211> 1038

<212> DNA

<213> *Enterobacter cloacae*

<400> 2765

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<210> 2766

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 2766

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<210> 2767

<211> 2391

<212> DNA

<213> Enterobacter cloacae

<400> 2767

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<210> 2768

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 2768

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<210> 2769

<211> 507

<212> DNA

<213> Enterobacter cloacae

<400> 2769

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cgcgatgact	ataacgggtg	gttaccacca	aacgaatcgg	aaaaccgata	ctggaaaaac	480
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<210> 2770

<211> 276

<212> DNA

<213> Enterobacter cloacae

<400> 2770

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gcgcgaagtc	atcgtctggg	ttttctctca	gccagcgccg	catggctatc	catttttgcgg	180
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<210> 2771
 <211> 951
 <212> DNA
 <213> Enterobacter cloacae

<400> 2771
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<210> 2772
 <211> 783
 <212> DNA
 <213> Enterobacter cloacae

<400> 2772
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 tccggctgcg ggaaaacgac gctgctgaac ctgacgcgcg ggtttgtacc gtatcagcac 180
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<210> 2773
 <211> 252
 <212> DNA
 <213> Enterobacter cloacae

<400> 2773
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 ctgggatttg aagcgaaagg ctggcaaacc tatgcggttg ggctggtgac ctgggtaatc 180
 agtttctggc tggcgggatt cattatccgc cgtcgccccg atgagacgac gacggcagag 240
 aaaaccgact aa 252

<210> 2774
 <211> 672
 <212> DNA
 <213> Enterobacter cloacae

<400> 2774

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<210> 2775

<211> 1167

<212> DNA

<213> Enterobacter cloacae

<400> 2775

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<210> 2776

<211> 732

<212> DNA

<213> Enterobacter cloacae

<400> 2776

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<210> 2777
 <211> 1389
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2777
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 gtggcgggctt cgccgagcgt ggcccgaat gaacggctga gcggctatgc gggcaatgca 180
 ggcggtgcga aggtacaaaa actttcggat atcagccttg aggcgtgccc gcgcttctca 240
 accggattca aagaatttga ccgcgtgctc ggcggtggcg tagtgccggg cagcgctata 300
 ctcatcggcg gtaacccggg ccgcggtaaa tcgaccctgc tctgcaaac gctctgcaag 360
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 atcgagcaga tctgcatgat cgccgaagaa gagcagccga agctgatggt gatcgactcc 540
 attcagggtga tgcattatggc tgacattcag tcgtcacccg gaagcgtggc gcagggtgcgt 600
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 ggtcatgtga ccaaagacgg ctgcgtggcg ggaccgaaag tgcttgaaca ctgtatcgac 720
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 aaccgcttcg gcgcgggtgaa tgaacttgcc gtctttgccg tgaccgagca ggggcttcgc 840
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 gaggtagggc tggccggcga gatccgcccg gtgccgagcg gtcaggagcg tatctccgaa 1260
 gcggcaaaaac atggcttcct ccgcgcgatt gttccggccg ccaacgtgcc gaaaaaatt 1320
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 gacttataa 1389

<210> 2778
 <211> 906
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2778
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 agccagctgg agcagcaggt ggggatccgt ctgttgaatc gcacgacgcg cagaataagc 180
 ctgacgtttg cggcgagca ctatctgggt cactgtcgcg agatgctggc ggccagcgag 240
 cgcgcggagt atgccattca gcggctgcga gaaaaccca gcggcgcgct gcggatcacc 300
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 tatccggacg tgtcactgga tgtgtcgatc tcagacgacg tgggtggatct ggtcgagtct 420
 ggctttgacg tggcgtgctg caccggcaaa ccgcaggatt cttccctgat tggccgcatg 480
 attgggcact gtcgcgccta catgtctggc tcgcccgact acctggcacg ccgggagccg 540
 ttaattcatc ccagacagct ggtggagcat cgctgcatta cgcaccgggc atggtcggag 600
 tggcttctgc gaagcgagaa tgaggattac cgctacctgc cggataacgc tcatatgacg 660
 gataatctgg tgtacgccag ggaatgcgcc attgccgggg cggggatcac gctgttacc 720
 gcattcctgc tgggaagata gatcgaaaag ggcgcgctgg tgaaggtgtt gtcggcggtg 780
 agcgttgagg gaaacgatct ctggctggcc tacccgagtc gtaagctcaa ttcgcctgcg 840
 ctgatgagct atatcgactt tgcgatgcag tttgatgagg tgaagcggta ttacgtgggc 900
 ggggtga 906

<210> 2779
 <211> 414
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2779
 gcgatgcga gtggcagaga cgttactgat cggcgcgggg tgtgttatgc tgtactcgt 60

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gaacagcgtc	atcaggagtg	gcttcgtttt	gtggagttgc	tccgccagtc	ttacgacaaa	180
gatctgcatt	taccgttgct	acagctgatg	ctgacgccc	atgaacgcga	agcgctgggc	240
acgcgggtac	gcattattga	ggaactgctg	cgcgcgcaaa	tgagccagcg	cgagctgaaa	300
aacgagctgg	gcgcgggcat	cgcgaccatt	acccgtgggt	caaacagcct	gaagtcggcg	360
ccggttgaac	tgcgtcagtg	gctggaagcg	gtattgctga	aaaacgcccg	atga	414

<210> 2780

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 2780

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gccaatcgcc	ccctctttac	gaccaatata	atcaatgccg	gtgtagtgcg	acattaccgg	120
accagcgcc	tcaccgcgcg	ggactttctc	cagtatgacc	tccggcagcg	gcagcggtgg	180
agaacgcgct	tcgcccgcgt	gctcgcggct	ttcgatgaca	acccagctga	aggctcgctcc	240
ttcgtcgata	ccagcatcaa	tcgcgaccca	gaagtcagcg	tctggcgcg	cggtttttgc	300
attcgccacg	cgatttcgtg	cgccagcgcg	tgtttcctcg	ctgccaaacg	gctgttccgg	360
cacaccgctc	tcgacgcgca	cggcgctcaat	atggcaggat	ccttcgccaa	agatctcttc	420
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<210> 2781

<211> 571

<212> DNA

<213> Enterobacter cloacae

<400> 2781

cggaaaaaaa	gcatgtttaca	ggtatacctt	gttcgccacg	gtgaaacgca	gtggaacgcc	60
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tggcaggtgg	cggagcgcg	cagaacgctg	ggcatcactc	acgtcatctc	cagtgattta	180
ggccgcacac	agcagacggc	acgcatcatc	gccgatgcct	gtggctgcga	cgtgaccctc	240
gaaccgcgct	tgcgcgagct	ggatatgggc	gtgctggaaa	aacgtcctat	cgatacgctg	300
acggaaaccg	aagaaggctg	gcgcgcgacg	ctggtgaacg	gcactgaaga	tggtcgcate	360
cctgaggggt	aatccatgca	ggagctgagc	gtgcgcgatg	atgccgcgct	ggccgagtg	420
ctgaaactcc	cggcaggtag	ccgaccgctg	ctggtgagcc	acggtatcgc	gctgggttgt	480
ctggtgagca	ccattctggg	actgccagct	tacgccgaac	gccgtttg	tctgcgcaac	540
tgttccattt	cccgtatcga	ctatcatgag	a			571

<210> 2782

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 2782

tgggcaaaac	acaggaataa	atcgatgaat	atgacaagac	tgaagatttc	taaaactctg	60
ctggctgtaa	cgttgggtag	tgtcctggta	agcggttctg	ctctggcgga	atccagcacc	120
atggataaag	cgaaaagttc	cgccaatacc	gcaggggaaa	aaatcgatag	ctctatgaat	180
aaagtcggta	atttcatgga	tgacagctca	atcacagcaa	aagtgaagc	cgactgggtg	240
gatcacgact	ccattaagag	caccgatatt	tctgttaaaa	ccgacaacaa	ggttgtcacc	300
ctgagcgggt	tcgttgaaag	ccagaccag	gctgaagaag	ccgttaaagt	ggcgaaaggt	360
gttgagggcg	taagctccgt	cagcgacaaa	ctgcacgtac	gtgacagcaa	agaatcgctc	420
gtgaagggct	atgccggaga	tgacgcaact	accagcgaaa	tcaaagctaa	actgttagcc	480
gacgacatcg	tgccatcccc	tatggtgaaa	gttgaaacca	ccgatgggtg	ggtccagctg	540
tccggtacgg	ttgagaatca	ggcacaagc	gatcgtgccg	agtcaattgc	aaaagctatt	600
gatggtgtga	aaagcgtcaa	aaacgatctg	aaaacgaagt	aa		642

<210> 2783

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 2783
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attgtgcccc ctattgaagc ggcgagattc gacaaagttc tggcgcttgc ccgggggacac 180
gatgcgctgt atgccgcgtt gggctctgcat ccgatcgtta ttgagcacca tottgatgac 240
catctcgaca ggctggatgc cagctgcaa aacgcggata cgaagctggg tgccatcggg 300
gagatcggcc tcgatctcta tcgttaa 327

<210> 2784
<211> 468
<212> DNA
<213> *Enterobacter cloacae*

<400> 2784
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aagcgcacgc acgtgcgcgc caggggctgt gtccatgggt tcgctggaag ccttcagcag 180
gcgcagcgtt ttatcgagct gggctataaa attggcgtcg gtggcaccat tacctatcgg 240
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gcggcgcgcg tttttgatgt gctgtgtgag ttgcgtcagg agcctgaaga tgtgattgcc 420
agcgcgctgc tggaaaatac ccgagcggtc ttccggcatca cgctatag 468

<210> 2785
<211> 1239
<212> DNA
<213> *Enterobacter cloacae*

<400> 2785
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gaagcctgtg caaaaggcga agcggacaac ggtcgtaaag gccctctgaa cctgccaaac 180
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gccaacctgc cgggctacct cggtaactgc cactcttccg gtaccgtgat tctggaccag 480
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ttccagatcg cctgccatga agagacgttt ggctgggata aactgtacga gttgtgcgaa 600
atcgcgccgtg aagagctgac cgaaggcggc tacaacattg gccgcgttat cgcgcgtccg 660
tttatcggcg acaaagcggg taacttccag cgtaccggca accgtcacga tctggctgtg 720
gagccaccgg cgcgcacagt gctgcaaaaa ctgcgtcagc agaaagacgg tcacgtgggt 780
tcggtgggta aaatcgcgga catttacgcc aactgcggca ttaccaaaaa ggtcaaagcg 840
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ggctcgtctg gtcaccgtga aaccttcgcg gacatcggcc agacgattgc gaaatacttt 1200
ggtacgtctg acatggaata tggcaaggct atgttctaa 1239

<210> 2786
<211> 1071
<212> DNA
<213> *Enterobacter cloacae*

<400> 2786
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tgogacctgc caacgatgt ctctttatgg ccaggattgc cgtctctttt aagtggcgat 180

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ctggataagc	aacgcctcac	ccagtatcaa	accaaactgg	gcgcagcgat	ggtcacggtt	300
gcggcctggt	gtgtggaaga	ttatcaggtc	attcgccctgg	cgggttccct	gacgcagcgc	360
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accgtcgcca	tcggcgatgg	cggaacgat	ctgccgatga	tcaaagttgc	cgggctgggt	960
attgcctacc	atgccaaacc	gaaagtgaat	gaaaagacgg	aagtcaactat	ccgtcatgct	1020
gatctgatgg	gggtgtttctg	tattctctcc	ggcagcatta	atcaaaaata	a	1071

<210> 2787

<211> 1770

<212> DNA

<213> Enterobacter cloacae

<400> 2787

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gttaccttcg	aagaactcca	ccttaccttc	gtcctggtag	tccaggatgt	gggtcgcgat	180
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cgagatattt	ttaagaatat	gacgtttcgg	cgggacaact	ttgccgacac	gatgcaggtt	1680
ataaacgaat	tgagccacgt	tggacttcgc	ctctttttatc	gtgatgagaa	tgaatttcag	1740
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<210> 2788

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 2788

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catgcagacc	agcttgcgct	ggtctgtgaa	gggggcgggc	agcgcggtat	ttttaccgcc	180
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cctgccgttg	tggccaatga	cgcggtggcg	atgccgctgg	tggacgcgcc	gcaggccaac	1080
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<210> 2789

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 2789

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acagaccgcg	aaggtaaaat	ttatacggca	ctgccgttgg	agaatgttat	gaccgatttta	180
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gccgactggg	cggactcccg	ccactaccgc	ttcggcgctg	ccagcctgct	ggccagcctg	900
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<210> 2790

<211> 1422

<212> DNA

<213> Enterobacter cloacae

<400> 2790

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taccgcgcgc	cattcaaccg	attccgcgat	gaggttaccg	tgtttctcgc	acaagaaatt	120
attcgtaaaa	aacgtgatgg	tcatgcatta	agcgacgaag	aaatccgctt	ctttatcaat	180
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<210> 2791

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 2791

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<210> 2792

<211> 1236

<212> DNA

<213> Enterobacter cloacae

<400> 2792

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<210> 2793

<211> 1983

<212> DNA

<213> Enterobacter cloacae

<400> 2793

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<210> 2794

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 2794

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<210> 2795

<211> 1041

<212> DNA

<213> Enterobacter cloacae

<400> 2795

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<210> 2796

<211> 321

<212> DNA

<213> Enterobacter cloacae

<400> 2796

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<210> 2797

<211> 1629

<212> DNA

<213> Enterobacter cloacae

<400> 2797

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<210> 2798

<211> 1764

<212> DNA

<213> Enterobacter cloacae

<400> 2798

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<210> 2799

<211> 663

<212> DNA

<213> Enterobacter cloacae

<400> 2799

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<210> 2800

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 2800

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<210> 2801

<211> 696

<212> DNA

<213> Enterobacter cloacae

<400> 2801

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cgcgtttgcg	tggcgggtgca	gaaaactgac	accctggcaa	ttaccgacga	taccccgatc	660
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<210> 2802

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 2802

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<210> 2803

<211> 864

<212> DNA

<213> Enterobacter cloacae

<400> 2803

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<210> 2804

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 2804

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ccgattattg	tcggcagcga	cgatacgtc	gatatctttg	gtgtagtgac	gtatatcggtg	300
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<210> 2805

<211> 570

<212> DNA

<213> Enterobacter cloacae

<400> 2805

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cgtcggaaga	cgtcggcaat	gccgatccgc	gcgccatgca	ggtcgcgctt	tccgcctggg	180
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<210> 2806

<211> 2451

<212> DNA

<213> Enterobacter cloacae

<400> 2806

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<210> 2807

<211> 1152

<212> DNA

<213> Enterobacter cloacae

<400> 2807

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<210> 2808
 <211> 768
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2808
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 acgaatccag aatggacgaa ggtagccgg gctaaacgca tcacctga 768

<210> 2809
 <211> 1095
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2809
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<210> 2810
 <211> 468
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2810
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 cgtcgactgg aaagacaggg ttttatccag ggctatacgg ctctgctgaa cccgcattat 180
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<210> 2811
 <211> 3705
 <212> DNA
 <213> Enterobacter cloacae

<400> 2811

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<210> 2812

<211> 621

<212> DNA

<213> Enterobacter cloacae

<400> 2812

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aaaaaacacg	gccagcttgc	tgccgtcgcg	ccgctgcgt	ctgcgcactt	cacaaagccg	540
agtattgtga	ttaaacctaa	cgccaacagc	cgtccgacgg	gggacaccac	cggctacctg	600
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<210> 2813

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 2813

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cggcgttcat	gtaaacggta	tgcttaatt	aaggagaaaa	agatgacggc	aattgccccg	180
gtaatcacca	ttgatgggcc	aagtggcgca	gggaaaggta	ctctgtgcaa	agcgatggcg	240
gaagcattgc	aatggcatct	tttagattcg	ggagcaatct	atcgctgct	ggcgctggct	300
gcgctgcac	atcatgtgga	tggtgcgtct	gaagaagcgc	tggtaccgct	ggctgcgcac	360
ctggatgtgc	gctttgtctc	gaccgatggc	aaccttgaag	tgatcctgga	aggggaagat	420
gtcagcgggtg	aaatccgtac	ccaggaagtg	gccaatgcgg	cctctcaggt	ggcggttttc	480
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<210> 2814

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 2814

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gaaagacttg	ccagtcagca	accgcatatc	cctgccaagg	ctgtggaaga	tgccgttaaa	120
gagatgctgg	agcatatggc	taccactott	gcccaggcg	agcgattga	aatccgcggt	180
ttcggtagtt	tttccctgca	ctatcgtgca	ccacgtaccg	ggcgtaacct	gaagactggc	240
gataaagtgg	agctggaagg	aaagtatggt	ccgcacttta	agccgggtaa	agaactgcgc	300
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<210> 2815

<211> 993

<212> DNA

<213> Enterobacter cloacae

<400> 2815

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gcgggtgaa	acggcaaaac	cccgggtgtg	atctggctgg	tagagcagct	ccagaggcgc	240
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cgtacaggcg	cgccgggttc	ggtatcgccg	gtgcgcagtg	atgccgtgaa	ggcactgctt	420
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aacgggtgtg	aagccagagc	ggtcgaaatc	ccaatgcttc	ttcgccccgg	acaggccgta	660
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aaagaaaact	ggtggtatct	gccggttgac	gctgaactca	gcggcgcaaca	gccggaacat	960
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<210> 2816

<211> 780

<212> DNA

<213> Enterobacter cloacae

<400> 2816

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attgtgcatg	tccttgaaaag	ggcacgcgaa	tggggcgccg	gacgtgtcat	cgtcgccacc	180
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gccgatcatc	agtcaggcac	cgagcgccctg	gcggaagtgc	tcgaaaaatg	cggtttcagc	300
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ggctttattc	gtcgctacgt	cgcctgggca	ccaagcccg	tggagcatat	tgaaatgtct	660
gaacagcttc	gcgtgctgtg	gtacggcgag	aaaattcacg	ttgcggttgc	ccaggaaatc	720
cccggcaccg	gcgtggatac	ccctgaagat	ctcgagcgcg	tacgcgtcga	aatgcgttaa	780

<210> 2817

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 2817

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agcgtctggg	ctgatgcagc	cagcgacctt	aaaagccgac	tggataaagt	gagcagcttc	120
cacgccagct	tcacgcaaaa	agtgactgac	ggcagcggca	acgcggtgca	ggaaggctcag	180
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cagtccagcg	actggcagca	gtacaacatc	aaacaaaacg	gtgatgagtt	cgtcctgacg	420
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cagcaaaacg	gcgtgttaga	tgcttcgaaa	ttcaccttta	ccccgcgcga	gggcgtaacg	600
gtggacgacc	aacgtaataa	gtaa				624

<210> 2818

<211> 1182

<212> DNA

<213> Enterobacter cloacae

<400> 2818

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atctcggcgg	ttacctccgg	cgtgaaggag	atccgcgagg	cgatcgagcg	cgcacggcaa	300
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agtcagcagg	atgcgtttct	gccgcacatt	gaagacggca	cgattttctt	catcggcgca	420
accacggaaa	acccgtcggt	tgaactcaac	tcgcgcgtgc	tttcccgcgc	ccgcgtttac	480
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cgtgaacgtc	cggattacga	cgttcgggta	caccttcgca	atgcccccta	caaagctgat	1140
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<210> 2819

<211> 1314

<212> DNA

<213> Enterobacter cloacae

<400> 2819

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gaagagcgtc	gtaaagtgtt	gcaggataca	actgaaaatc	tgcaagcaga	gcgtaattct	180
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<210> 2820

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 2820

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gggcagtgcg	tgccggggcg	gtttatcggt	cttgcgctgg	cgctgttaaa	agggaacctc	180

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<210> 2821

<211> 1296

<212> DNA

<213> Enterobacter cloacae

<400> 2821

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aatctgcctg	gttcaaaaag	tgtctcgaac	cgcgctctgc	tgctggcagc	tttggcaaac	120
ggcaccaccg	tcctcaactaa	tctgctggac	agcgatgacg	tgcgccatat	gotcaatgca	180
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<210> 2822

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 2822

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<210> 2823

<211> 1683

<212> DNA

<213> *Enterobacter cloacae*

<400> 2823

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<210> 2824

<211> 2280

<212> DNA

<213> *Enterobacter cloacae*

<400> 2824

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<210> 2825

<211> 1749

<212> DNA

<213> Enterobacter cloacae

<400> 2825

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<210> 2826

<211> 1245

<212> DNA

<213> Enterobacter cloacae

<400> 2826

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<210> 2827

<211> 228

<212> DNA

<213> Enterobacter cloacae

<400> 2827

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gagctgattt	gcaaactgga	cagcctggcg	ttcccgtctgc	gtgacgggat	tccggctcgtg	180
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<210> 2828

<211> 900

<212> DNA

<213> Enterobacter cloacae

<400> 2828

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<210> 2829

<211> 777

<212> DNA

<213> Enterobacter cloacae

<400> 2829

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<210> 2830

<211> 302

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (18)

<400> 2830

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<210> 2831

<211> 1968

<212> DNA

<213> Enterobacter cloacae

<400> 2831

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<210> 2832

<211> 969

<212> DNA

<213> *Enterobacter cloacae*

<400> 2832

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<210> 2833

<211> 2298

<212> DNA

<213> *Enterobacter cloacae*

<400> 2833

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<210> 2834

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 2834

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<210> 2835

<211> 1689

<212> DNA

<213> Enterobacter cloacae

<400> 2835

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<210> 2836

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 2836

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<210> 2837

<211> 222

<212> DNA

<213> Enterobacter cloacae

<400> 2837

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tcgctagtaa	tcgtggatca	gaatgccacg	gtgaatacgt	tcccgggect	tgtacacacc	180
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<210> 2838

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 2838

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<210> 2839

<211> 1560

<212> DNA

<213> Enterobacter cloacae

<400> 2839

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<210> 2840

<211> 1503

<212> DNA

<213> Enterobacter cloacae

<400> 2840

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<210> 2841

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 2841

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<210> 2842
 <211> 288
 <212> DNA
 <213> Enterobacter cloacae

<400> 2842
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<210> 2843
 <211> 942
 <212> DNA
 <213> Enterobacter cloacae

<400> 2843
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<210> 2844
 <211> 1854
 <212> DNA
 <213> Enterobacter cloacae

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tggacgccga	aagatcgcca	gcgcgaagtc	tccttcgccc	tgcgcgccta	cgcgagcctt	1800
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<210> 2845

<211> 426

<212> DNA

<213> Enterobacter cloacae

<400> 2845

cccgaagat	gccccgcgac	gcgtggcgtt	ttggcgccga	tgggacgtg	ttttctaacc	60
atgtgccccg	ccagcttgat	gggtgtttt	tcctccgccc	gcgccttgc	ggccattgce	120
gatgcggtga	aaggcgatat	tgcgatcctg	gccgatagcg	gcacccgtaa	cggtctggac	180
gtggtgcgca	tgattgcgct	cggcgccgac	agcgtgctgc	tgggcctgct	ttacctgtac	240
gcgctggcca	ccagcggcca	ggcgggctgt	gcgaatctgc	tgaacctgat	cgagaaagag	300
atgaaagtag	cgatgaccct	gaccggggcg	aagtcgatta	gcgaaatcaa	caaagactcg	360
ctggtgcagg	agctcagtaa	gctgcctgcg	gcgctggccc	ctctttctca	gggaaacgcg	420
gcctga						426

<210> 2846

<211> 1428

<212> DNA

<213> Enterobacter cloacae

<400> 2846

gaaaatttga	cacaccccg	ccctccgcaa	ttgtatagac	aagcaaatac	aagaacacaa	60
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gtgatcgatg	aaagtccctt	ttcagggttt	cactggcttc	ttattgtgct	gggctttctg	180
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acggagtggg	gaatacataa	acaggatctg	gggcgggtgc	tgagtgcggc	gctgctgggg	300
ctgtcgctgg	gagccctgat	tgcaggctcc	gtatcggacc	ggatgggacg	caagcgcgtg	360
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caggcagaca	gtattttaat	gatcctcagc	gtgctgctc	tcgtggccgc	ggcggaacc	1380
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<210> 2847

<211> 483

<212> DNA

<213> *Enterobacter cloacae*

<400> 2847

gggggagcga	tgcttaacat	cgtcttattc	gaaccagaaa	ttccgcgcaa	caccggcaat	60
attatccgcc	tgtgcgcaa	caccggtttt	cgtctgcaca	tcattgaacc	gatgggcttt	120
acgtgggacg	acaaacgtct	gcgcgcgcgc	gggctggact	accatgagtt	tactgcccgc	180
gttcgtcatc	acgattacgc	cgcgtttctg	gacgcagaga	agccgcagcg	catgttcgcc	240
ctgaccacca	aaggcacgcc	agcacacagc	gccgtaagct	atcaggacgg	ggattatctg	300
atgtttggtc	cggaaacccg	cggcctgccg	gccaccattc	tggatgcctt	gccagccgag	360
cagaaaattc	gtattccgat	gatgcgcgac	agccgcagca	tgaacctgtc	gaatgcggtg	420
tcggtggtgg	tgtatgaggc	gtggcgccag	ctgggttattc	ccggcgcgat	actgcgtagc	480
taa						483

<210> 2848

<211> 855

<212> DNA

<213> *Enterobacter cloacae*

<400> 2848

atcataacga	caaataat	tgccgagaaa	gatgtggata	cggaattgct	aaaaactttc	60
ctcgaagtga	gcagaacgcg	acactttggg	cgagcagctg	aagccctcta	cctgacgcag	120
tcagcagtca	gttttcgtat	tcgacagctg	gaaaatcaac	tgggtgtgaa	cctttttacc	180
cgccatcgca	acaatatctg	tttaaccccg	gccggtgaaa	agctattgcc	ttatgcagaa	240
accctgatga	atacctggca	ggcagcgccg	aaggagggtg	cgcacacctc	ccggcataat	300
gaattctcga	tcggtgccag	cgcctcacta	tgggaatgca	tgctcagcca	gtggcttatg	360
cggctatatc	gctcacacaa	ccatctgcaa	tttgaggcga	ggattgcgca	acgccagtcg	420
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gcggataata	aaccgcact	ccatgttgct	accgattcga	caactctctc	caggccgctg	780
tatgccat	ggctgcaaaa	cagcgataag	cagtcgcaga	taaaagatct	gttaaaaaacc	840
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<210> 2849

<211> 909

<212> DNA

<213> *Enterobacter cloacae*

<400> 2849

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cagatccagc	gccttgagga	agacctcggc	cagccgctgt	tcgtgcgcga	taaccgcacc	180
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cgcaatcgcg	tgatgat	agaacgcagc	gatgagaaaa	cgccgttcga	gctcggcggtg	840
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aaccactaa						909

<210> 2850

<211> 228

<212> DNA
<213> Enterobacter cloacae

<220>
<221> unsure
<222> (34)

<400> 2850
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 gataccttga cccggaagat gccccgcgac gcgtggcggt ttggcgccga tgggatcggtg 120
 ttttctaacc atgtgccccg ccagcttgat ggggtgtttt tctccgccc gcgcctgccc 180
 ggccattgcc gatgcggtga aaggcgatat tgcgattcctg gccgatag 228

<210> 2851
<211> 1551
<212> DNA
<213> Enterobacter cloacae

<400> 2851
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 gccatcggcg tgaaggcacc gcttatttct gtagaggttc atttaagtaa tggactgccc 120
 ggactgacgc tggtcggcct accagaaacg accgttaaag aggcgaggga tcgcgtgcgc 180
 agcgcaatta ttaatagcgg ttatgctttt ccggcgaaag agatcaccat caaccttgcg 240
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 cataacctgt tactgatagg tccgccaggc acggggaaaa cgatgctggc gacgagattg 720
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<210> 2852
<211> 189
<212> DNA
<213> Enterobacter cloacae

<400> 2852
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 cgtcgcctag gtgagccgtt accccaccta ctagctaate ccatctgggc acatccgatg 120
 gcaagaggcc cgaaggcccc cctctttggt cttgcgacgt tatgcggtat tagctaccgt 180
 ttccagtga 189

<210> 2853
<211> 1488
<212> DNA
<213> Enterobacter cloacae

<400> 2853

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tttatgaccg	tggggccacgc	gtatcagatg	ctggaaaagtc	agggggcgcat	tgttgccaga	240
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caggtgatgc	gcgatgaagt	ggtcgacatc	aacacctata	tcttcgacgt	gctacaggcc	360
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atccatcaaa	tcagcattgc	gcccggaag	atgttttcca	cctccaatat	ctggacaccg	1380
tttttcggtt	tcaatacctc	atggggatgg	ggcgagcggg	aagagcaggc	ggtcgtccag	1440
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<210> 2854

<211> 267

<212> DNA

<213> Enterobacter cloacae

<400> 2854

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ttctacgcaa	tcattggcctc	catctgcgca	ttaatcacct	ggttcctgtc	taaagatcgt	180
aaacgtattc	gcctgttgag	cgcattcctg	gtgggatcta	cctggccgat	gagctttcct	240
gttgccctgt	tgatctctct	tttctga				267

<210> 2855

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 2855

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ggactgcac	tcaacaaccc	gcgggacatc	gccccagacg	ttttttatcc	cattaccagc	180
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<210> 2856
 <211> 1461
 <212> DNA
 <213> Enterobacter cloacae

<400> 2856
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 gtgctgctgg agattgctga agcgtcggaa gcacagggtg acgctgccgt ccaggctgcc 180
 gatcgcgctg ttacagagtg gggacaaacg acgcccgaata cgcgcgcga atgtctgttg 240
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 ttatccggtt acggaaaaga tatgtcggtc tacggacttg aggattacac ggtagtcoga 1440
 catgtcatgt ttaaacta a 1461

<210> 2857
 <211> 243
 <212> DNA
 <213> Enterobacter cloacae

<400> 2857
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 agcgtgatta cccacatgaa cgaactgctg atcgaattaa gcgacgatgc agagctcagc 120
 cgtgaagatc gttataccca gcagcagcgc ctgctgaccg cgattgcgca tcatggcaag 180
 caacataaag aagaggcgga ggcacgcat gccaccta cgcagggtgg gactatcctg 240
 taa 243

<210> 2858
 <211> 585
 <212> DNA
 <213> Enterobacter cloacae

<400> 2858
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 cgcgccatga tccataagat tgaacggggg gacagtagcc caacggcgac gctgcttgcg 180
 cggttatccg gtgccttcgg tattagcatg tctacgtca ttgcgcgcgc ggaaatgcag 240
 gagggcaaac tattacgtct ggcaaccag cccgtctggc gcgatccgca aaccactat 300
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 ccgcaggca gcgatgtgcc gatgcccgct tcctcttaac cgtggcgcg acagctgatt 420
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 ggagattgtc tggaaactcg gcccgcgaac gactgccggt ttatcaacga aacggatgaa 540
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<210> 2859
 <211> 1101
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2859
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 ggcgcgccgg ttgccgaaaa tttccgcctg gaagagcagc cgatccccac gcccgcagag 180
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<210> 2860
 <211> 798
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2860
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 ttccggggggc gcagagccat tctgatcgat cttcccggta gcggttacag tgacaaacct 240
 gacaactacc gttatcgcac gagcgaacag gcgcagggtg tggttgaact gttaaacct 300
 ctoggcctgg atagtctatg gctctatggt catagcatgg gggggagtat cgcgatcgaa 360
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 gcgggtggcg ggtgtttcag ccgggcaatt gcggcccaaa cggaacaaca ttttctggct 480
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 ctgctgatg acgattttta tcgtctgcaa caaaacggcg ttgctgtaaa aattatccct 720
 gatgcggggc attcaatgtc ctgggaaaac ccgtcagcgt tggctcaggc tttgtctggc 780
 ttcataaacg gctcatga 798

<210> 2861
 <211> 1689
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2861
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 tactgtcccg aggcgtcgcc ggagtcgttt aaccgcgaga tcgccagctc tggaccttcg 240
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 tttaacgctg atgacgttat tttctccgtt atgcgtcaga aagaccctaa gcacccctat 480

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<210> 2862

<211> 714

<212> DNA

<213> Enterobacter cloacae

<400> 2862

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gcgttaatta	cgggctcatt	aaaacctggg	gctcgactca	tcacgaaaga	gattgcggat	180
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aacgaaatta	acgccatccg	aaaacagctt	gagccgatgg	ccgttgccgc	ggcatgtcag	360
aatatgaccg	agaccaaact	gggtgcatta	cgcgcgctgt	cagataactt	cagcacccgc	420
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tatgccgac	tgctttctgc	gcttgagcaa	agggaagtg	cggccagtcg	ggaagcgatc	660
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<210> 2863

<211> 693

<212> DNA

<213> Enterobacter cloacae

<400> 2863

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aatattgtga	caaaaccata	ctactatagt	gaacaacaca	gccagagggt	aacctgatt	180
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cactcggttt	acgttcatcc	cgatcatcag	ggcaaggcca	ttggctgact	gctaattgacg	480
gaattaatta	aggaagcccg	ccagataggt	aaacatgtga	tgggttgcgg	tattgaggcg	540
cagaaccagg	cgtcgattca	tctgcatgaa	acctggggt	ttattaccac	cggaaatatg	600
cagcaggtag	gaaccaaatt	cggctcgctg	ctggatttaa	cctttatgca	actccagctc	660
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<210> 2864

<211> 351
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2864
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 ctgggctatg ctgatgaatt tacctctgag cctgacacgc agctcgtcat tgaagcgggt 240
 cgtttcggcg ttttcccgcc agagagatgg caccacattg aggtgatgac cgacgacacc 300
 ctgttcaata ttgaattctt tgttgaacct gaagtgccta agtcccttta a 351

<210> 2865
 <211> 381
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2865
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 cgctcgacgc cgttctggaa taaagagacc gcccaaaaag cgctttttac ccatacacaac 120
 accaaagccg gcgtgtacgg tcggttgctc gtcattgcagg gtgcgggtgcg ttactttggc 180
 tttgccgatg gcgacgccac cgagcccgat ctggaagtgg tcattgaggc cggttctttt 240
 ggcattctcc caccgcaaaa atggcaccgc attgagcttc tgaccgacga cacctatttt 300
 aatatcgact ttttcgcgga tctgcccgtc acgctcagcg gtgcgggcat cggtaaagtg 360
 gtcaacacgc ataaggagta a 381

<210> 2866
 <211> 186
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2866
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 gattatgaaa cagaagcgcc aatggagctg ttgatcccg acgtcgcggc agatgtcgtg 120
 aaggatctgg tgaacaccgt tcgcgcctac gatacggaaa atgaacacga ggtatgtggc 180
 tggtaa 186

<210> 2867
 <211> 1023
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 2867
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 acgttgatgt atatcgtgat ggacggtttt gatctgggga taggcatcct gtttcgggca 120
 acgccgaatg cggacgaccg cgacgtgatg gtcaacagcg tggctcccgt ctgggatggc 180
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 cgtggggctc ccttcgaatt tcgcttcaag gccactccgg cgcaccgccc gttctgggat 360
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 gtcattccagg ggttcagcgt caccggctcg gcttacagcg gtggtccgtt tgactgggtt 480
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 caaccgcca ttgctgcgcg ctggtttact ctgccgaatc tgttttatct cgtgcctggt 720
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 gcccaaagcc agggctttat gttagtgggt gcactgttga tcattcccgt gattctgggtc 960
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<210> 2868
 <211> 243
 <212> DNA
 <213> Enterobacter cloacae

<400> 2868
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 tttttaccgg tagccgcaaa cccgtctttt atcgctaacc agatggggca cgtaaatgcg 180
 cagatggtgt atgaaatcta tgctacatgg atagaagaga tgaacacgaa gctgacgctt 240
 tga 243

<210> 2869
 <211> 387
 <212> DNA
 <213> Enterobacter cloacae

<400> 2869
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 attgcccgtg atatggggta tgcgtcggtt ggctgggagc ctgaggaagg ctggtacgcg 120
 ggggcagatg cccgctacat gagcgacgtg atggcaaacg acaccaatac cgccaaagcg 180
 cccctcttata ccgtggtcgg tctgaatacc gggataaaac tcaattacgg caaatgggga 240
 atggacatct ttggtcgcgt cgataacctg ttcgataaag agtaacgtcg ttcagagatt 300
 gtaaaccgac gctacaatcg ctattacgaa cccgcccctg gccgtaacta tggcgtgggc 360
 ctgtcgggtct cttatcgctt tgagtaa 387

<210> 2870
 <211> 1452
 <212> DNA
 <213> Enterobacter cloacae

<400> 2870
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<210> 2871
 <211> 441

<212> DNA

<213> *Enterobacter cloacae*

<400> 2871

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<210> 2872

<211> 474

<212> DNA

<213> *Enterobacter cloacae*

<400> 2872

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<210> 2873

<211> 3537

<212> DNA

<213> *Enterobacter cloacae*

<400> 2873

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<211> 1155

<212> DNA

<213> Enterobacter cloacae

<400> 2874

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<211> 567
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 <213> Enterobacter cloacae

<400> 2875

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<210> 2876

<211> 837

<212> DNA

<213> Enterobacter cloacae

<400> 2876

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<210> 2877

<211> 1896

<212> DNA

<213> Enterobacter cloacae

<400> 2877

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<211> 2277

<212> DNA

<213> Enterobacter cloacae

<400> 2878

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<211> 768
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2881
 <211> 702
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2882
 <211> 1359
 <212> DNA
 <213> Enterobacter cloacae

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<210> 2883

<211> 303

<212> DNA

<213> Enterobacter cloacae

<400> 2883

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cacgccttcg	aagaactgat	ctttctcggg	gaaggcttcc	agcggcgcggt	tccaggtcag	240
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<210> 2884

<211> 417

<212> DNA

<213> Enterobacter cloacae

<400> 2884

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gtcggccccc	aggaagtctt	gcacttcggc	cttcacgtcg	taatcgctgt	ccgcgcgcac	180
gaccttaaca	tcattgtcgg	cgtcgcgcag	gaaaccatcc	gcgacctcgg	tcagggtgtc	240
attgagctgg	ccttttagagt	gcgcaaatcc	tttcgcgcgg	ttgataatca	gaatgttgct	300
cattattttg	cctcgatgat	gagagtatgc	cgggtattct	acgcgcgagg	acggagcgga	360
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<210> 2885

<211> 1539

<212> DNA

<213> Enterobacter cloacae

<400> 2885

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gcttatatgt	cactcagtcg	gcgtcagttt	attcaggctt	cgggtatcgc	cctttgtgog	180
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ttgtggtatc	acgccaacac	cccgaaccgc	accgcccgag	aggtctacaa	cggcctggcc	600

ggaatgtggc	tgattgaaga	tgaggctcagt	aaaacgctgc	cgatcccga	tcactacggc	660
gtcgatgatt	tcccgatcat	tattcaggac	aagcggtgg	ataacttcgg	cacgccggag	720
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ccttcctggc	cgcacttccc	gttctgttgc	cacagccaga	cgctggagat	gatggacagg	1500
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<210> 2886

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 2886

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gaatttggtg	ccgtccagca	cggaaaccgc	gcccaccgccc	agcaggaagg	tgatctgctc	180
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gccgaactcg	cgcacgtcca	gaccttccag	agcgtctgtac	acctgatcca	gtacgcgggt	300
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gcgcaggtca	gcgatagcgt	ttttaccaaa	cagaatgcgg	ggtgggggat	gaagattaaa	420
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gatgctgctc	attgtggcgg	gcaggcgcta	tcctctcaat	gcacattcct	gccgatgtct	540
tgcccatttc	tacagcgcg	tgagaaaacg	gtaagaaaat	gcgcacactg	tcagcgctcg	600
aaaccgtacc	cggagtaa					618

<210> 2887

<211> 906

<212> DNA

<213> Enterobacter cloacae

<400> 2887

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cccggaaacg	gcaccccggg	gatgtatcag	cccggcatcg	tgtttctctt	ttctggccat	180
aagattggct	atatcaatga	gcgcgtgttc	cgttacgaca	ccaatgaata	tctgcttctg	240
acagtacctt	tacctttcga	atgtgaaaact	ttcgcgacag	aggaggtgcc	gctggccggg	300
atccgcgtca	acgtcgacat	cctccagtgg	caggagctgc	tgatggatat	tggggaggac	360
gaacttttcc	ggcgcgtgat	ggcggcaagc	ggtatcaact	ccgcgacct	atcggaggaa	420
attctctgcg	cgattgaacg	cctgttagac	gtgatggaaa	ggccgctgga	tgccgcgtatt	480
ctcgggaagc	agattatccg	cgaaattctt	taccatgtgc	tgctcggggc	ggcgggcggg	540
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cgcattgaga	gccagtacac	ggaaaacctc	agcgttgacc	agctggcggc	ggaagccaat	660
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gccagcgccg	cggcgatgcg	ggttgggtat	gaaagcgctg	cgcagtttag	tcggggagttt	840
aagcgctact	tcggcgctac	gccgggggaa	gatgcgtcgc	gcacagaaac	gatgcagggc	900
gcttag						906

<210> 2888

<211> 726

<212> DNA

<213> Enterobacter cloacae

<400> 2888

gccgcactgc	gccaaacttta	cgctggatac	catcgcaccg	ggctggcgct	ggctggagct	60
gcatgccgat	ggctcgtgta	ccaccgaagt	ttgccgtctg	gccggggcac	aattccgccc	120
ggataccgct	tccgaaggct	attgatgtcg	acgcttctct	atctgcatgg	gtttaacagc	180
tcaccgcgtt	cggcgaaagc	gacgcagctt	cgccagtggc	tgagcgcgca	tcatccccac	240
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tcgctagtgc	tggaaacacg	cggcgaatcg	tttgccgttg	tcgggtcgtc	gctcggcggc	360
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caacaatatg	tgctagagtc	acgccatatt	tacgatctca	aagttatgca	ggtcgacccg	540
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cgccaggcag	tggcgtatta	cgcatcctgc	cgccagactg	tagaagaggg	cggtaaccat	660
gctttcacgg	gctttgaaga	tcatttcacc	cagattgtcg	atcttcttgg	actgcacagc	720
cactga						726

<210> 2889

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 2889

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ttcgtctgcaa	ttgctgccat	catgatgatg	accacggccc	ctgtctttgc	tgcacagggg	120
ggcttctctg	gcccattctgc	gacacagaat	cagacgcaaa	cccagcaggg	tggttttgtc	180
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gaaagcggca	cgggtggtgg	ggagatcgac	cacaagcgct	ggaacggcgt	gacggtgacg	360
ccgcaggata	aagtcgaact	ccagggtaaa	atcgataaag	actggaacga	gtttgaaatc	420
gacgtgaagc	aggttatcaa	gctgaacaaa	taa			453

<210> 2890

<211> 2265

<212> DNA

<213> Enterobacter cloacae

<400> 2890

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cctttttgtct	atttttttctt	cggaagcatt	atgagcgcta	tttccctgat	ccagccggat	120
cgcgacctct	tctcctggcc	ccagtactgg	gcagcctgct	ttggaccggc	gccgttccctg	180
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ccgaaagggg	ataaacagcg	ccgtctgcat	aaagcgctgc	tcgcctatca	cgatccgaaa	2040
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cgctgtgatt	gcctggtgcc	tcgcccaacg	ctggaagaga	tcgcggaagc	gcgcgccag	2160
aaccgcaaca	cgcgcccgcc	gctgaccaa	cataccccga	ttgcgcatca	gcgttcgaat	2220
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<210> 2891

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 2891

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tccgtgatca	cctgggctat	cttcttcagc	aagagcgccg	aacttctttc	acaaaaacgc	180
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gcgcaggttc	tgtgtctgca	aagccgcgat	ctggacctga	acgccagcgc	cgttaaaccg	720
gttcatgcgg	cgtccaaact	gcgcgtaggt	tga			753

<210> 2892

<211> 1347

<212> DNA

<213> Enterobacter cloacae

<400> 2892

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ttgataatat	tttctgctta	ttcgataagc	atccggatgc	acattctgac	aatcggtgta	120
gtctggacgt	ccagacgtat	aaaaataggg	ttagcgaaca	tgactaaaaa	gcagcttgag	180
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atccagcgcg	cctcctcgct	ggtgtttgat	accgttgaag	ataaaaaaat	cgctacgcgt	300
aatcgcgcca	agggcgggct	gttttacggt	cgctgtggca	cgttaaacca	tttctcggtg	360
caggaagcca	tgtgcgaact	ggaggcgccg	gcgggctgcg	cgctgttccc	gtgcggcgcg	420
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acgcgcgttg	tgttctctgga	atctcccggg	tccatcacca	tggaagtgca	tgacgtcccg	660
gccatcgtag	aggcggtgcg	cagcatagcg	ccggaagcga	tcacatcatg	cgacaacacc	720
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gggaccttaa	tccgcctgca	tatcgggctg	gaaaatgtgg	acgatttaat	cgcgatttta	1320
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<210> 2893

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 2893

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cgtgggttca	cgcagctgca	tcgggttcac	ctcaccacagc	cccttaaagc	gctgaacgtt	180
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gatgtgcagg	ccatcggagt	ccgcacccgc	gagaatgcag	atcttgccgt	agcgcaactg	420
gctcagatcg	tcgctgtccg	gatcgatacc	gatcgcaacc	gagatgtcgt	gtacttccctg	480
cgaggccagc	acttcacacg	acgagacctc	ccaggtgttg	aggatcttac	ccttgagcgg	540
catgatcgcc	tgatattcac	gatcccgccg	ctgcttggcc	gatccgcctg	ccgagtcctc	600
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acgctgggca	ctggagatcg	ccatttcagc	cagcatttcc	gcggcctgaa	cgttctgggtt	780
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<210> 2894

<211> 378

<212> DNA

<213> Enterobacter cloacae

<400> 2894

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ctcttcgggg	tgatatacta	ccggcatgcc	gcggccgtcg	tcgatgaact	ccagcgactg	180
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gttatcaatt	acttcctggc	ccaggtgggt	tgggcgcgct	gtatcgggtg	acatccccgg	300
gcggcgggcga	accggctcaa	gcccggtgag	tacctcaatg	gcacacgcgt	tatagggttg	360
cgtcatgatt	taagctag					378

<210> 2895

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 2895

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ataaacggcg	tcacgttgat	ctcatgcatt	tcacogttat	cgtccagatt	ttcattaaga	180
cgcattgccca	tacaatcaac	ctacgcgcag	tttggaacgc	gcatagaaccg	gtttaacggc	240
gctggcggtt	aggtccagat	cgcggctttg	cagcagcaga	acctgcgcgg	caacgtcacc	300
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accgcggccc	atatgacgac	ccacggccgc	aacgcgacgc	tccagacgga	agccggtacg	600
ctctttaatg	ccttcggttat	cttcactgcc	tgcgagaggt	tccagctcgt	tctgcgcttc	660
gttcactaa						669

<210> 2896

<211> 690

<212> DNA

<213> *Enterobacter cloacae*

<400> 2896

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ttcctgatgg	tgctgccgat	attcctgctg	gttgccggcc	tggtcggcac	aatcgcggtg	660
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<210> 2897

<211> 1353

<212> DNA

<213> *Enterobacter cloacae*

<400> 2897

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aacgacggcg	aaaacggggc	cgacatacct	tacctctacc	gccgggacgg	gtttgatgac	360
ggtcgggttg	aggatgacaa	cgacgaatgg	cgttctctgt	ggctgacttc	tcgggacggg	420
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<210> 2898

<211> 453

<212> DNA

<213> *Enterobacter cloacae*

<400> 2898

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attcccggtt	ccgataaagt	tcaggttaac	gtcaccgacg	gcaaagccag	cgtaacgggc	180
gacgggctaa	cgcaggagca	gaaagaaaaa	atccaggctc	ccgtcggcaa	catcgcgggc	240
gtcagcgagg	tggagaacaa	tatcaccgcg	acagacgccca	aagatgaagc	aacctactat	300
acggtgaaat	ccggcgatac	cctgagcgcc	atctctaaaa	ccgtgtacgg	cgatgccaat	360
cagtacaaca	agatctttga	ggcgaaccgc	ccgatgctct	ccagcccgga	taaaatttat	420
ccgggccaga	cgtgcgtat	tcctaaggca	taa			453

<210> 2899
 <211> 900
 <212> DNA
 <213> Enterobacter cloacae

<400> 2899
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 gcctcggttca gccgcctggt tgccaatacg gtgcgctacc atcactggca tcagtgtctg 180
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 atgcgccccg gacgactggt tttcttcccc ccttttaacg tgcacaaggt catggtggac 300
 gaacaggcgg aggcaattta ccgcgcgacc attattcatc tcgaccagca cgcggtgctg 360
 aagatcctgc gggatttttc ccagaccggg cagcgcttgg agcggctgtc acgccgtggc 420
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 atgatctggc tcgacgagca ttatcaggag aaatttcgtc tggatgcgct ggctgcagag 660
 ctgggtaaat cgcgcagtta cgtatcgcgga agattccatg cggaaacagg cgaaaaaatt 720
 cagcactacc tgaacacgct aagggttgcgt aaggcgtgcg agtgtttact ccacactgat 780
 tcgagcgtgc gtgacattgc cgcacaggcg ggattttccg acgtgacgtg gttttatcagc 840
 gcgttttaaaa aggggattgg cgagacgccg ttgcagtacc ggaaaaacca ttcactogtga 900

<210> 2900
 <211> 1242
 <212> DNA
 <213> Enterobacter cloacae

<400> 2900
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 ggtaaaaaac ctatcgctga cctgcgcgcg caaatcccgga cggacgcccg cgtcctgatt 180
 acctacggcg gcggcagcgt gaaaaaaacc ggcgtactgg atcaggtgta cagcgtctctg 240
 gaaggtctgg acgtgcgcga gttcgggcgg atcgagccta acccgtctta tgaaacgctg 300
 atgaacgcgg taaaaatcgc ccgcgaggag cagatcacct tcctgctggc ggtgggcggc 360
 ggttcctgtc tggacggcac caaattcatc gcggcgggcg cccattacgc tgacggcatc 420
 gaccctggc atattctgga aacggggcgg agcgacatca gcagtgcgat cccgatgggc 480
 tccgtgctga cgtgcgcggc caccggatca gagtccaaca aaggcgcggg catctcccgt 540
 aaaaccaccg gtgacaagca ggcttttatg aacgaacacg ttcagcccgt gttcgcgatc 600
 ctcgatccgg tttacacctt taccctgcct gcgcgtcagg tggcgaacgg cgtggtcgac 660
 gcctttgttc acaccgttga gcagtacgtt acttaccggg taaacgccaa aattcaggat 720
 cgtttcgcgg aaggcattct gctgacgctg attgaagaag gtccgaaagc gctgaaagag 780
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 gccctgctgg cgaaactgga agcacacggt atgacgcaga tcggcgagca tggcgacatc 1200
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<210> 2901
 <211> 846
 <212> DNA
 <213> Enterobacter cloacae

<400> 2901
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 cataaagccc tggaagtcgg ctatcggtcc atcgataccg ccgccgccta taaaaacgag 180
 gacggcgtgg gaaaagcgtc tgccagcgcc ggcgttcccc gggatgagct tttcatcacc 240

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cattacgttg	atgcctggaa	agggatgatt	gaactgcaaa	aagaggggct	gataaaaagc	420
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ggggtgtttg	accagaaaat	catccgtgaa	ctggcgagata	agtaacggtaa	aaccccggcg	660
cagatcgta	ttcgctggca	tctggatagc	ggctctgggtg	tgatcccga	atcggtcacg	720
ccatcgcgta	tcgccgagaa	cttcgacgtc	tgggatttcc	gcctggataa	agacgagctg	780
ggtgaaattg	cgaagctgga	tcagggcaag	cggcttgggc	cggacccgga	tcagtttggc	840
gggtaa						846

<210> 2902

<211> 678

<212> DNA

<213> Enterobacter cloacae

<400> 2902

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ggcatcaaa	cgggcttaag	caaaatgggc	tttaacgtgg	actgggttac	cgacgggaaa	120
accgggcagg	cggccctgta	caccgcgcgc	tatgatgccc	tggtgcttga	tctgacgctg	180
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gtgctgatcc	tgaccgcgcg	ggatgcgctg	aatcagcgcg	tcgaaggttt	acgcctgggg	300
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catcatttac	gccgcaagct	cggcagcgac	tttatccgca	ccgtgcacgg	catcggttat	660
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<210> 2903

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 2903

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agcaacattc	tgattatcaa	cggcgcgaaa	gaatttgccg	actctaaagg	ccagctcaat	180
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tcagatgcgt	ctaaaaaata	cggttctggc	ggtctgattc	agggcaaaaa	atatatgctc	480
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gtgggcgtag	acggcgcgta	tctgccgttc	cacaaggcga	atcagttcct	gggaatggag	600
ccgctgccga	cctttatcgt	caacgacgta	attaaaatgc	cggacgtccc	gcgctatata	660
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<210> 2904

<211> 327

<212> DNA

<213> Enterobacter cloacae

<400> 2904

aaggagttaa	ttatgcttac	cgttattgct	gaaatccgta	cgcgtcctgg	ccaacatcac	60
cgccaggcag	tactggatga	gttcgcgaag	atcatcccga	ccgttctgaa	agaagaaggc	120
tgccacggct	acgcgcggat	ggtagacgcc	gccaccagcg	caagcttcca	ggcgaccgcg	180
ccagactcca	tcatcatggt	ggagcagtg	gaaaccgtcg	cacatcttga	agccattttg	240
cagaccgcgc	atatgaaagc	gtggagcgac	gcagtgaaag	gggacgttct	ggaaacccac	300

atccgtatttc tggagcaagg ggttttaa

327

<210> 2905

<211> 1239

<212> DNA

<213> Enterobacter cloacae

<400> 2905

ccgcacacga	cgaatgagga	acatcttatg	aacacaacta	ccaccggggc	cgtaagccgc	60
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cagcctctgc	tgccgctgat	gggctcagac	ctgaacctga	gtatcgaagg	catgggcatg	180
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<210> 2906

<211> 714

<212> DNA

<213> Enterobacter cloacae

<400> 2906

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actttttaaac	gtggcctggc	ggcgacccta	ctgcttttga	gccctctggt	gcaggctgag	120
gggttagagg	accagctcaa	tgcattcttt	gcgcagaagc	tgcccggttt	cagcgatgac	180
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aaagcgggac	aacaggtgat	ggtggctcgcc	aatggcgaag	gctttagtat	caacagcgaa	600
ggaaaagcgc	tgaataatgc	cgcagtggcg	caaaatgccc	gggtcagaat	gtcctcaggc	660
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<210> 2907

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 2907

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cagtcgaagc	tgatgcagcc	aggcagcagc	gatataca	tggaacgtgt	tgaagcgtg	240
aaaacggcta	tccgtaacgg	cgaactgaaa	atggatacca	gcaaaatcgc	tgatgcgctg	300
attcaggacg	cacagagttt	cctccagagt	aactaa			336

<210> 2908
 <211> 621
 <212> DNA
 <213> Enterobacter cloacae

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 cagcttacgc agtacaccgt cagtgcagcag gaaattaatc aggcgctgga aaaacataat 180
 aacttttcaa aagatatcgg cgtgcccggc cttgcggatg cgcatacgt cctgacgaat 240
 ctgcgccagcc agattggctg cgaggagcct aacaaagtca ccttttcggg cgatgccagc 300
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 atcatccctt tcaccgacta a 621

<210> 2909
 <211> 360
 <212> DNA
 <213> Enterobacter cloacae

<400> 2909
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 aatggggttg gtttttgccg ttcatcaggc agttcccaa agaccatgtc cgctcggac 180
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<210> 2910
 <211> 3123
 <212> DNA
 <213> Enterobacter cloacae

<400> 2910
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 gcgaacattht acaaaggcaa aatcaccgca attgaaccaa gccttgaaag tgcatttgct 180
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<210> 2911

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 2911

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<210> 2912

<211> 1632

<212> DNA

<213> Enterobacter cloacae

<400> 2912

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<210> 2913

<211> 357

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (341)

<400> 2913

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gca	aaccatc	ttt	ccgtcat	cgg	cggtg	aa	agaagaca	a	gaacgc	cat	cagcgaaatt	300
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<210> 2914

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 2914

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<210> 2915

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 2915

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<210> 2916

<211> 1068

<212> DNA

<213> Enterobacter cloacae

<400> 2916

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<210> 2917

<211> 1620

<212> DNA

<213> Enterobacter cloacae

<400> 2917

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<210> 2918

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 2918

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<210> 2919

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 2919

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<210> 2920

<211> 756

<212> DNA

<213> *Enterobacter cloacae*

<400> 2920

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<210> 2921

<211> 1101

<212> DNA

<213> *Enterobacter cloacae*

<400> 2921

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ggcctgggtg	tggggctgga	tgggaacggg	gaccagacga	cccagacgcc	gttcaccacc	180
caagccctga	acaacatgct	ctcgcagctc	ggtattaccg	taccggccgg	gaccaacatg	240
cagctgaaaa	acgtggcggc	cgtgatgggt	accgcgtctt	atccggcctt	tgcgcgtcag	300
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<210> 2922

<211> 954

<212> DNA

<213> *Enterobacter cloacae*

<400> 2922

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accactaccg	aatatgaaaa	cggtgcggca	gtgaagggtga	aagccaaatt	ccgcgtctac	720
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tacgcgaccg	atccaaacta	tgcacgcaag	ctgaccagca	tgatccagca	gctgaaatcc	900
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<210> 2923

<211> 1683

<212> DNA

<213> Enterobacter cloacae

<400> 2923

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tcaagctaca	acgtggcagg	ttataccccc	cagaccacca	ttttgggggc	atcaaacagc	180
accctgaccg	gtggtggctg	ggtgggtaac	ggggctctatg	tctccggcgt	tcagcgtgaa	240
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tctgccaaacc	tccaggattt	ctttaaaggc	ctgcaaaccg	tggtgagtaa	cgcagaagat	420
ccggctgcac	gccagacggg	gctcggtaag	gcggatggtc	tggtaaacca	gtttaaaacc	480
aacgatcaat	atctccgcga	tcaggatgcg	caggtcaata	cggcgatttc	taccagcgtt	540
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tccgggggta	acctggatga	agagtatggc	aacctgcaac	gctatcagca	gtactatctg	1620
gcgaatgcgc	agggtgctgca	aacggcgagc	acgctgtttg	atgcattgat	caatatccgc	1680
taa						1683

<210> 2924

<211> 195

<212> DNA

<213> Enterobacter cloacae

<400> 2924

aagatcaata	cgtcttaacgc	cattgctgcg	tgatgatcg	gtcagacaaa	attggtoatt	60
ccgtcgacat	ccttacaaaa	cccggattta	acgcggaaaa	cggattcatt	attccactgc	120
tcgcggggtt	atagcaagat	gacttttacc	aattatcacc	cggttactca	cagttttctt	180
acttcaacgg	ggtga					195

<210> 2925

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 2925

tatgcgcgcc	ctatgcaaaa	ggtaaaatta	cccctgactc	ttgatccggt	tcgtacggct	60
caaaaacgcc	tcgattacga	aggaatctat	tcttccgatc	aggctgagcg	tattgccgaa	120

tctgtagtca	gtgtggacag	tgatgtagaa	tgctccatgt	cgttcgctat	cgacaaccag	180
cgtctcgccg	tgtaaaccgg	tgatgcaaag	gtgacggtaa	cgctcgaatg	tcagcggttg	240
gggaaaccgt	ttgtacagca	tgttcacaca	acgtattgtt	ttagtccggg	tcgttctgac	300
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atcgatcttc	tggcgtctgg	tgaagatgaa	gtcactctct	ccctgccagt	cgttccgggtg	420
catgattctg	aacactgtga	agtgtccgag	gcgacatgg	tctttgggga	actgcctgat	480
gaagcgcaaa	aaccaaacc	atttgccgta	ttagccagct	taaagcgtaa	gtaa	534

<210> 2926

<211> 621

<212> DNA

<213> Enterobacter cloacae

<400> 2926

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ccaaaagtgc	gtctgacgac	ggacaggctg	gtcgttcgtc	tgggtgatga	gcgtgatgcc	120
tggcgtctgg	cggattatta	cgccgagaat	cgccagtttt	taaaaccctg	ggaaccggtt	180
cgggacgaga	gccactgcta	ccctctggc	tggcaggcgc	gcctcagtat	gattgcgga	240
tttcataaac	agggaagtgc	gttttatttc	gcgcttctcg	atccggaaga	gaaagagatc	300
gttggcattg	ccaatttttc	aaacgttgta	cgcggttcgt	ttcacgcctg	ctatctcggg	360
tattccatcg	gccagaaatg	gcagggacag	gggctcatgt	ttgaggcgct	gacggcggcg	420
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aataagcgca	gcggcgatct	gctggccccg	ctgggggtttg	agaaagaagg	ctatgccaaa	540
gattatctgc	tgattgacgg	cgagtggcgg	gaccatgtgc	tcaccgcgct	caccacgcag	600
gagtggaccg	cgggtcgtta	a				621

<210> 2927

<211> 660

<212> DNA

<213> Enterobacter cloacae

<400> 2927

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gaaaagcagg	tcaccacgcc	ggaacagtat	cctctgtccg	tgaatgccgt	cacgatggcc	120
tgcaaccaga	agacgaaccg	tgagccgggtg	atgaaccttg	gcgagcacga	ggtgcaggat	180
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gcgggaagtgg	ctgttatcac	caogttgctg	ctgcgcgggg	cgacagcgcc	gggggaactg	360
cgcgcaacgc	cctcccgcat	gcatgagttt	caggatatgc	aggacgttga	acagacgctg	420
gagggattag	cctcacgcga	ggacgggtccc	tacgtggtgc	gtctgccccg	cgaaccgggc	480
aagcgtgaaa	gcgctacat	gcacctgttt	agcggtgacg	tggagccctc	tgcgtggcc	540
gtcgtatccg	acacgccagc	atcaaacgaa	agcctgaccg	cgcgctggc	agccctggaa	600
gacgaggttg	cggggtgaa	gcagcgtctg	gatgcgttac	tcgcacatct	gggagattaa	660

<210> 2928

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 2928

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gcggataccc	ccgggtatca	ggcgcgcgat	attgattttt	ccagtgaact	caaaaaagtg	180
atggagcgtg	gacgtgccga	aggaaacggg	gtctcactgg	ccctgacatc	ctcacgtcat	240
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ccctcgcttg	atggtaacac	cgtcgacatg	gaccgggagc	gcacacagtt	tgccgataac	360
agcctgcaat	accagacagg	cctgacgcta	ctcggcgggc	aaattaaagg	catgatgacc	420
gtcctacagg	ggggcaatta	g				441

<210> 2929

<211> 405

<212> DNA

<213> *Enterobacter cloacae*

<400> 2929

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ccgtatcgcg	ctaaacaggt	tgtcttccag	gttgatgctg	caccgggtgc	ggcaacgggc	180
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ggcaaccgcg	tcgcggatgc	cagcggctac	gtgaaaatgc	cgaacgtgga	tgtggtcggg	300
gagatgggtg	actccatgtc	cgcgtcgcgc	agctaccagg	caaacgtcga	agtgtttaat	360
accgtgaaga	gcatgatgct	caaaacactc	actctcggcc	agtaa		405

<210> 2930

<211> 768

<212> DNA

<213> *Enterobacter cloacae*

<400> 2930

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cagctcaacg	cgctgcgtgc	ggcgccggta	gaagggtgtg	cattgcccac	gcgtacgctg	180
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atgaccgaca	tgatcgccag	cgcgcgcgcg	ttcgaaaatgc	agatgaaaat	tatcagcagc	720
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<210> 2931

<211> 957

<212> DNA

<213> *Enterobacter cloacae*

<400> 2931

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tctgacgata	cgattgcgcg	ttcgcaggcc	gttgtgtctt	ctcaggcaca	aacgcaaaac	180
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gacgtggact	ggaactcggg	gatttcgtcc	tacaccatgc	agcaggcggc	gttgcaggcc	900
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<210> 2932

<211> 957

<212> DNA

<213> *Enterobacter cloacae*

<400> 2932

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<210> 2933

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 2933

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cgttcccac	acgcgtgac	cgcagttacc	agcctgtctg	tagacaagac	ttctgggtgag	120
aaacacctgc	gtcaccacat	caccgctgac	ggtttctacc	gcggccgcaa	ggttatcact	180
aagtaa						186

<210> 2934

<211> 321

<212> DNA

<213> Enterobacter cloacae

<400> 2934

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gattttggcc	ctaccgtgac	agtggctgca	gcattgcagg	cactgaattc	taattcgcaa	180
ctcaaacttc	ttttattcgg	taatcccgac	accatcacgc	cattacttgg	caaaactgac	240
ttggatcaac	gttcgcgtcc	gcagattatc	cctgggcaat	cacgtatgcc	aatgatgccc	300
ggcctcgcac	gctttcccta	a				321

<210> 2935

<211> 1212

<212> DNA

<213> Enterobacter cloacae

<400> 2935

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aacggtttct	tccgtatggt	ggatgccaac	ggttccgtat	tctacagccg	caacggccag	300
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ccggttgccg	gcacgcgcgc	tacgggtgca	accggtgcga	atccgcaggc	gatctccatc	420
ccaacgacgc	tgatggcggc	gaagtccacc	accacggcct	ctcagcagat	caacctgaac	480
tccaccgata	ctgcaccaac	cgtcgccttc	gaccggcca	accctgactc	ttacaacaag	540
aaaggcaccg	tgacgggtgtt	tgacagccag	ggtaatgcgc	acaacatgaa	cctgttctat	600
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ggagatgcag	cgaaactggc	aaccacgctg	acctttaatg	cgacggcgct	gctgacgggt	720
ggcgatgata	tcaagatcac	aacgggcacc	gttcggggcg	cgacgccagc	cacgtttgac	780
atgagtttctg	ccaactccat	gcaacagaat	accggtgcga	acaacatcgt	ggcgacgagc	840

cagaacgggtt	ataagccggg	cgatctgggtg	agctaccaga	tcaacgatga	cggtaccggt	900
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gccacaacg	aaggcctgaa	atccgaagg	gacaacgtct	ggtctgccac	gcagtcttcc	1020
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ctggaagcct	ctaacgtcga	tctgagtaaa	gagctgggtga	acatgatcgt	cgcgcaacgt	1140
aactaccagt	ccaacgcgca	gaccatcaaa	acccaggatc	agatccttaa	cacgctggtt	1200
aacctgcgtt	aa					1212

<210> 2936

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 2936

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<210> 2937

<211> 969

<212> DNA

<213> Enterobacter cloacae

<400> 2937

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<211> 1218

<212> DNA

<213> Enterobacter cloacae

<400> 2938

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<210> 2939

<211> 1206

<212> DNA

<213> Enterobacter cloacae

<400> 2939

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<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 2940

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<210> 2941

<211> 1506

<212> DNA

<213> Enterobacter cloacae

<400> 2941

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<210> 2942

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 2942

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<211> 1008

<212> DNA

<213> *Enterobacter cloacae*

<400> 2943

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<210> 2944

<211> 552

<212> DNA

<213> *Enterobacter cloacae*

<400> 2944

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<210> 2945

<211> 1182

<212> DNA

<213> *Enterobacter cloacae*

<400> 2945

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<210> 2946

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 2946

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<210> 2947

<211> 2805

<212> DNA

<213> Enterobacter cloacae

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<210> 2948

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 2948

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<210> 2949

<211> 213

<212> DNA

<213> Enterobacter cloacae

<400> 2949

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<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 2950

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<210> 2951

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 2951

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<210> 2952

<211> 648

<212> DNA

<213> Enterobacter cloacae

<400> 2952

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<210> 2953

<211> 1179

<212> DNA

<213> Enterobacter cloacae

<400> 2953

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<211> 1644

<212> DNA

<213> Enterobacter cloacae

<400> 2954

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<211> 1455

<212> DNA

<213> Enterobacter cloacae

<400> 2955

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<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 2956

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<211> 837

<212> DNA

<213> Enterobacter cloacae

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<211> 1752

<212> DNA

<213> Enterobacter cloacae

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<210> 2959

<211> 705

<212> DNA

<213> Enterobacter cloacae

<400> 2959

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<210> 2960

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 2960

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555

<210> 2961

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 2961

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<210> 2962

<211> 1569

<212> DNA

<213> Enterobacter cloacae

<400> 2962

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<210> 2963

<211> 1329

<212> DNA

<213> *Enterobacter cloacae*

<400> 2963

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<210> 2964

<211> 1908

<212> DNA

<213> *Enterobacter cloacae*

<400> 2964

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<210> 2965

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 2965

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<210> 2966

<211> 735

<212> DNA

<213> Enterobacter cloacae

<400> 2966

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<210> 2967

<211> 1695

<212> DNA

<213> Enterobacter cloacae

<400> 2967

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<210> 2968

<211> 960

<212> DNA

<213> Enterobacter cloacae

<400> 2968

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<210> 2969

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 2969

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<210> 2970

<211> 1221

<212> DNA

<213> Enterobacter cloacae

<400> 2970

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gcggaagaac	aaaaggaaga	agatattgtg	gtctccgccca	gccgggcaca	tcgcagcgtg	180
gcagagatgg	cgcaaaccac	ctgggttatt	gagcgggcgg	aaattgagca	gcaggttcag	240

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<210> 2971

<211> 714

<212> DNA

<213> Enterobacter cloacae

<400> 2971

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<210> 2972

<211> 207

<212> DNA

<213> Enterobacter cloacae

<400> 2972

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gaggagggac	gggtcattat	cgagcatgac	ggccagcact	acctgctgcg	ccagaccaat	180
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<210> 2973

<211> 1197

<212> DNA

<213> Enterobacter cloacae

<400> 2973

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ttatcaatgg	taattccctt	cggggcaacg	attcagaagg	ataagattat	gggtcactac	180
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<210> 2974

<211> 684

<212> DNA

<213> Enterobacter cloacae

<400> 2974

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<210> 2975

<211> 2067

<212> DNA

<213> Enterobacter cloacae

<400> 2975

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<210> 2976

<211> 1071

<212> DNA

<213> Enterobacter cloacae

<400> 2976

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<210> 2977

<211> 1176

<212> DNA

<213> Enterobacter cloacae

<400> 2977

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<210> 2978

<211> 1059

<212> DNA

<213> Enterobacter cloacae

<400> 2978

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<210> 2979

<211> 1071

<212> DNA

<213> Enterobacter cloacae

<400> 2979

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<210> 2980

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 2980

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<210> 2981

<211> 972

<212> DNA

<213> Enterobacter cloacae

<400> 2981

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<210> 2982

<211> 1071

<212> DNA

<213> Enterobacter cloacae

<400> 2982

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<210> 2983

<211> 1074

<212> DNA

<213> Enterobacter cloacae

<400> 2983

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<210> 2984

<211> 561

<212> DNA

<213> Enterobacter cloacae

<400> 2984

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<210> 2985

<211> 2433

<212> DNA

<213> Enterobacter cloacae

<400> 2985

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<210> 2986

<211> 1485

<212> DNA

<213> Enterobacter cloacae

<400> 2986

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<210> 2987

<211> 2379

<212> DNA

<213> Enterobacter cloacae

<400> 2987

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<210> 2988

<211> 2280

<212> DNA

<213> Enterobacter cloacae

<400> 2988

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<210> 2989

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 2989

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<210> 2990

<211> 453

<212> DNA

<213> Enterobacter cloacae

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<210> 2991

<211> 312

<212> DNA

<213> Enterobacter cloacae

<400> 2991

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<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 2992

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<210> 2993

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 2993

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<210> 2994

<211> 1584

<212> DNA

<213> *Enterobacter cloacae*

<400> 2994

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<210> 2995

<211> 3129

<212> DNA

<213> *Enterobacter cloacae*

<400> 2995

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<211> 231

<212> DNA

<213> Enterobacter cloacae

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<213> Enterobacter cloacae

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<211> 1884

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<213> *Enterobacter cloacae*

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<210> 2999

<211> 678

<212> DNA

<213> *Enterobacter cloacae*

<400> 2999

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<210> 3000

<211> 1131

<212> DNA

<213> *Enterobacter cloacae*

<400> 3000

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<210> 3001

<211> 870

<212> DNA

<213> Enterobacter cloacae

<400> 3001

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<210> 3002

<211> 1686

<212> DNA

<213> Enterobacter cloacae

<400> 3002

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<210> 3003

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 3003

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atgatcgccc	gccgtctgga	catcaccgag	agcacggcca	aagtgcattg	caaacacatg	600
ctgaaaaaaa	tgaagttaaa	atcccgcgtc	gaagccgcgc	tctgggtgca	tcaggagcgc	660
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<210> 3004

<211> 246

<212> DNA

<213> Enterobacter cloacae

<400> 3004

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tatgggcaaa	cgggttggtg	tccgtctcct	gcataccctc	agataccacg	accagcgggc	180
aggccgccag	agcctggcac	accgcgtggc	tgctcggaag	cgacaaggca	gggttggtgc	240
ccatga						246

<210> 3005

<211> 1899

<212> DNA

<213> Enterobacter cloacae

<400> 3005

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cagaacgccg	agcttgttgt	acagtctgct	gcggcgccca	gcgcgctgca	aagccaggcg	1860
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<210> 3006

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 3006

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tgttcctgtt	atcagccgaa	aggcccgggc	aaaagccctg	actcacgcga	gtggcgccag	180
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<210> 3007

<211> 588

<212> DNA

<213> Enterobacter cloacae

<400> 3007

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<210> 3008

<211> 1107
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3008

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<210> 3009
 <211> 1017
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3009

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<210> 3010
 <211> 279
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3010

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<210> 3011
 <211> 1116
 <212> DNA
 <213> Enterobacter cloacae

<400> 3011
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<210> 3012
 <211> 888
 <212> DNA
 <213> Enterobacter cloacae

<400> 3012
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<210> 3013
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 <212> DNA
 <213> Enterobacter cloacae

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<210> 3014

<211> 1365

<212> DNA

<213> Enterobacter cloacae

<400> 3014

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<210> 3015

<211> 1440

<212> DNA

<213> Enterobacter cloacae

<400> 3015

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<210> 3016

<211> 1164

<212> DNA

<213> Enterobacter cloacae

<400> 3016

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<210> 3017

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 3017

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<210> 3018

<211> 1227

<212> DNA

<213> Enterobacter cloacae

<400> 3018

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<210> 3019

<211> 2505

<212> DNA

<213> Enterobacter cloacae

<400> 3019

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<210> 3020

<211> 1419

<212> DNA

<213> *Enterobacter cloacae*

<400> 3020

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<210> 3021

<211> 1302

<212> DNA

<213> *Enterobacter cloacae*

<400> 3021

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1302

<210> 3022

<211> 417

<212> DNA

<213> *Enterobacter cloacae*

<400> 3022

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<210> 3023

<211> 813

<212> DNA

<213> *Enterobacter cloacae*

<400> 3023

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<210> 3024

<211> 864

<212> DNA

<213> *Enterobacter cloacae*

<400> 3024

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<210> 3025

<211> 891

<212> DNA

<213> *Enterobacter cloacae*

<400> 3025

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<210> 3026

<211> 798

<212> DNA

<213> *Enterobacter cloacae*

<400> 3026

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<210> 3027

<211> 3996

<212> DNA

<213> *Enterobacter cloacae*

<400> 3027

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<210> 3028

<211> 582

<212> DNA

<213> Enterobacter cloacae

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<211> 918

<212> DNA

<213> Enterobacter cloacae

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<211> 765

<212> DNA

<213> Enterobacter cloacae

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<210> 3031

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 3031

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acatggcaac	tgcagttcac	ttacaccgct	tctcaaccgg	gtacgcacca	gaaaatcatt	180
gatatggcca	tgaatggcgt	tggatgccgg	gcaaccgccc	gcattatggg	cgttggcctc	240
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<210> 3032

<211> 219

<212> DNA

<213> Enterobacter cloacae

<400> 3032

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gattacaaaa	tcaacctcgt	ggatgacagc	cagttcacca	aagatgccaa	agtggctacc	180
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<210> 3033

<211> 1473

<212> DNA

<213> Enterobacter cloacae

<400> 3033

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<210> 3034

<211> 1590

<212> DNA

<213> Enterobacter cloacae

<400> 3034

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<210> 3035

<211> 234

<212> DNA

<213> Enterobacter cloacae

<400> 3035

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<210> 3036

<211> 345

<212> DNA

<213> Enterobacter cloacae

<400> 3036

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<210> 3037

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 3037

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<210> 3038

<211> 1599

<212> DNA

<213> *Enterobacter cloacae*

<400> 3038

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<210> 3039

<211> 996

<212> DNA

<213> *Enterobacter cloacae*

<400> 3039

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996

<210> 3040

<211> 3783

<212> DNA

<213> Enterobacter cloacae

<400> 3040

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<210> 3041

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 3041

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ttccgcgtgc	atctggtgct	ggggatgacg	atcttcttta	tcttcccggt	caccgcctg	660
gtgcacgtgt	ggagcgcgcc	gtttgagtat	tttaccgctc	gctatcagg	tgtgagatcg	720
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<210> 3042

<211> 525

<212> DNA

<213> Enterobacter cloacae

<400> 3042

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ggcagtgacg	tcatcgctctg	cgcggaaatg	gacgaacagt	ggggatacgt	cggggctaaa	180
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gtattcggtg	aacgcactat	ggcgacgctg	ggcgctctta	tgagcctgct	gtcacccttt	300
gacgtggtga	tatggatgac	ggatggctgg	ccgctgtatg	aatcccgcct	gaagggaag	360
ctgcacgtaa	tcagcaagcg	atatacgcag	cgaattgagc	ggcataacct	gaatctgagg	420
cagcacctgg	cacggctggg	acggaaagtcg	ctgctgttct	caaaatcggt	ggagctgcat	480
gacaaagtca	tcgggcatta	tctgaacata	aaacactatc	aataa		525

<210> 3043

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 3043

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ataaccaaac	atctcagcca	gcgggacgtc	agcgcggaata	atctggctgc	cgtactgctc	180
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cogtgccccc	tctttgaagc	cgaggatcgc	cgccatgcgg	aaggccatct	ccgaggagtc	360
aacgtcatgg	taagaaccaa	acgtcagggg	cgctttcaca	tccaccaccg	gatagcccgc	420

cagcacaccc	gtattcatgg	cttctcgcaa	ccctttttcc	accgacggga	tgtactcccg	480
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<210> 3044

<211> 270

<212> DNA

<213> Enterobacter cloacae

<400> 3044

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accaatgttc	gcctcaacgc	caaactcgcg	cttcatgcgg	tcgacgatga	tctccagatg	180
cagctcgccc	atcccgga	taatcgtctg	accggactct	tcgtccgtgt	gcaggcgga	240
cgacggatct	tccgcgcga	ggcgtgtag				270

<210> 3045

<211> 954

<212> DNA

<213> Enterobacter cloacae

<400> 3045

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cttcaccggg	ttgtacaccg	cgtcgccttt	acgcagtatg	cgggaataga	cgcgatgaa	300
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gaagaaatct	gcgcccgggc	ggtccatttt	gttgacgaat	gccagacgcg	gaacatggta	900
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<210> 3046

<211> 402

<212> DNA

<213> Enterobacter cloacae

<400> 3046

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gcgaccgtca	cctttgaacc	cggcgcaacgt	accgcctggc	atacgcatcc	tcttgacaaa	180
acgtgatcg	tgacgcaggg	gcgcggctgg	ttacaggagt	gggggaaaga	ggcggaaccg	240
ctgaatcagg	gggatatcgc	ctggatccca	cccggcgtga	agcaactggca	cggcgcaagc	300
gcgcagacgg	cgatgaccca	tatcgccatc	gcagaagcgg	tcgaaggag	tccggtggcg	360
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<210> 3047

<211> 1020

<212> DNA

<213> Enterobacter cloacae

<400> 3047

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gaacacgaaa	cagccgcgga	tgcgctggcg	cgaaccttag	cactggcgca	gcaggcagaa	120
acgtgggtt	atcaccgctt	ctggattgcc	gaacaccaca	ataccccgca	gcttgccagc	180

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catcagcagt	gggggattga	cgaattttat	atcgacacgc	cggtcgctga	tggcgcaacg	960
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<210> 3048

<211> 1329

<212> DNA

<213> Enterobacter cloacae

<400> 3048

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gatttctgta	aagaaacggc	tttaaaagca	gaagagggca	agctcgactt	tatatattgtg	180
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cgcgcgtttg	ttgaccagg	ggtgcccggt	ttacaggcgc	gtggcctgtt	cgcacccgac	1260
tatcccggca	ccacgctgcg	cgaaggtctg	ggcttagacg	agcccaaaaa	tcagttcaca	1320
caacaataa						1329

<210> 3049

<211> 837

<212> DNA

<213> Enterobacter cloacae

<400> 3049

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cgacataaag	cgctcgataa	cgtcacgctt	gagatcccgc	cgggctccgt	gacgggtgatc	180
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gtggttgga	tgcgcgataa	agccgatgcc	tggctcgctc	acctctccgg	cggccagcag	540
cagcgtatcg	ccattgcccg	cgcgctggcg	ctgcgcccgc	gcgtgatgct	gtttgatgaa	600

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gcggaccagg	tggtatattat	ggtagacggg	aaaattgtgg	agcagggcag	cagcgatgac	780
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<210> 3050

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 3050

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gcgaaaatcc	cggcgaacta	taaatttgg	gagccgggta	ccctcacggg	ggcgatttca	180
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gacgcctcag	gcaatcttta	tattcagtcg	ggcagggcgg	atgtgttctt	tggaccgcag	660
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<210> 3051

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 3051

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gaagcgatcg	cccgccactt	gaacagcaaa	gatcgctcaa	tctccgtggc	gcttcaggag	180
gttcaggaag	ctgactggaa	ggcgcaggtc	tgggataccg	agatcggccc	gaaactggat	240
gaactgatta	agaagcccgg	ctattcgatg	ttaa			273

<210> 3052

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<400> 3052

aaggataatt	tttccatgac	aaaattacct	cagttttcac	tcgcctttat	tcatacctcgt	60
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<210> 3053

<211> 882

<212> DNA

<213> Enterobacter cloacae

<400> 3053

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<210> 3054

<211> 2112

<212> DNA

<213> Enterobacter cloacae

<400> 3054

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<210> 3055

<211> 1074

<212> DNA

<213> Enterobacter cloacae

<400> 3055

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<210> 3056

<211> 576

<212> DNA

<213> Enterobacter cloacae

<400> 3056

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<210> 3057

<211> 1137

<212> DNA

<213> Enterobacter cloacae

<400> 3057

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<210> 3058

<211> 1062

<212> DNA

<213> Enterobacter cloacae

<400> 3058

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<210> 3059

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 3059

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ctcaaccgcg	accggaaga	gtacagccag	ccgcggttcg	acggtcggct	gcgtttcacc	480
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<210> 3060

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 3060

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<210> 3061

<211> 627

<212> DNA

<213> Enterobacter cloacae

<400> 3061

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aacacgccta	attttaccgc	cgtcgcggat	gcgctctgcg	cgtgcgcgga	actgcacaag	600
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<210> 3062

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 3062

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<210> 3063

<211> 1395

<212> DNA

<213> Enterobacter cloacae

<400> 3063

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<210> 3064

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 3064

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<210> 3065

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 3065

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<210> 3066

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 3066

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429

<210> 3067

<211> 1011

<212> DNA

<213> Enterobacter cloacae

<400> 3067

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<210> 3068

<211> 1743

<212> DNA

<213> Enterobacter cloacae

<400> 3068

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taa

1743

<210> 3069

<211> 1347

<212> DNA

<213> Enterobacter cloacae

<400> 3069

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<210> 3070

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 3070

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<210> 3071

<211> 1317

<212> DNA

<213> Enterobacter cloacae

<400> 3071

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<210> 3072

<211> 441

<212> DNA

<213> Enterobacter cloacae

<400> 3072

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<210> 3073

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 3073

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<210> 3074

<211> 792

<212> DNA

<213> *Enterobacter cloacae*

<400> 3074

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<210> 3075

<211> 465

<212> DNA

<213> *Enterobacter cloacae*

<400> 3075

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<210> 3076

<211> 1431

<212> DNA

<213> *Enterobacter cloacae*

<400> 3076

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<210> 3077

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 3077

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<210> 3078

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 3078

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<210> 3079

<211> 2076

<212> DNA

<213> Enterobacter cloacae

<400> 3079

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<210> 3080

<211> 573

<212> DNA

<213> Enterobacter cloacae

<400> 3080

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<210> 3081

<211> 1635

<212> DNA

<213> Enterobacter cloacae

<400> 3081

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<210> 3082

<211> 1059

<212> DNA

<213> Enterobacter cloacae

<400> 3082

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gccatcaata	tgagtggcgt	aagcgaagtg	gtcgatctta	gccaggtaag	ccagcagatg	1020
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<210> 3083

<211> 720

<212> DNA

<213> Enterobacter cloacae

<400> 3083

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gactacgtcg	tgcagatgac	cgcgcaggcg	gccgagcgtg	cgctgaacag	cgttgaagcc	300
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<210> 3084
 <211> 1173
 <212> DNA
 <213> Enterobacter cloacae

<400> 3084
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 attgcgaaaa tgttctccgc gcaaacccgg gctgagcttc ttaaagcgat cctgaaatcg 480
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 gattttttga acgagaagga cactgatggc taa 1173

<210> 3085
 <211> 432
 <212> DNA
 <213> Enterobacter cloacae

<400> 3085
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 ggcaccaccc aggccttcaa cggggtgtct gctcaggagc ctttacgctt tatctgggaa 360
 gtgccaggcg gtggacgtct gatcccgcg ctgaaagtcc agcgcaacga ggtgctcgtc 420
 aactaccgct aa 432

<210> 3086
 <211> 1599
 <212> DNA
 <213> Enterobacter cloacae

<400> 3086
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<210> 3087

<211> 564

<212> DNA

<213> Enterobacter cloacae

<400> 3087

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<210> 3088

<211> 765

<212> DNA

<213> Enterobacter cloacae

<400> 3088

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<210> 3089

<211> 462

<212> DNA

<213> Enterobacter cloacae

<400> 3089

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tccgagttgc	taaaacatat	ttatgacatc	aatttgcgt	atttattgct	cgcgacgcgt	180

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gtggacgac	tgcaacaaat	ccacaccggt	attcttctct	ccaccgtct	gctcaacgaa	420
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<210> 3090

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 3090

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gcgtcgcgg	agcgtatgct	aattctgggt	aattattgaga	agctgctgaa	cagtgaagag	480
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<210> 3091

<211> 609

<212> DNA

<213> Enterobacter cloacae

<400> 3091

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<210> 3092

<211> 2400

<212> DNA

<213> Enterobacter cloacae

<400> 3092

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<210> 3093

<211> 1773

<212> DNA

<213> Enterobacter cloacae

<400> 3093

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1773

<210> 3094

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 3094

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<210> 3095

<211> 2094

<212> DNA

<213> Enterobacter cloacae

<400> 3095

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<210> 3096

<211> 1167

<212> DNA

<213> Enterobacter cloacae

<400> 3096

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<210> 3097

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 3097

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<210> 3098

<211> 621

<212> DNA

<213> Enterobacter cloacae

<400> 3098

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621

<210> 3099

<211> 3147

<212> DNA

<213> Enterobacter cloacae

<400> 3099

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<210> 3100
 <211> 942
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3101
 <211> 822
 <212> DNA
 <213> Enterobacter cloacae

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 gcgcaggaag tggctcaggt ggcgatatt gtctttggcg ccgttaagcc gaatatcatg 240
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<210> 3102
 <211> 900
 <212> DNA
 <213> Enterobacter cloacae

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 cgcaacaagt ccggtcgcca gagcacctgg tatatgggtc tgggtacaga cattgagact 480
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atcgcggtcca	gccacatcct	ggcgctgaac	tacgatcact	ggcactactc	tggtgttgcg	780
cgttactggc	acaacgggtg	tcagtggaa	gacgacgcca	gcctgaactt	cggcaacggc	840
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<210> 3103

<211> 1323

<212> DNA

<213> Enterobacter cloacae

<400> 3103

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accaccgtgg	tggccagcgc	cgggcacgcg	ccgcagatcc	tgaaaaaacg	cgaaggcacg	480
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<210> 3104

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 3104

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tcattggcatg	acctggatga	acattacgat	gcgctggaag	cccgtttctg	gcagttctac	600
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<210> 3105

<211> 273

<212> DNA

<213> Enterobacter cloacae

<400> 3105

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gaagagtcga	aagagctggt	tgcccaggtc	gagggcgctg	aaatcgttgt	gacggcgctg	120
ctgcgacaga	tggcaaaacc	agagcaggag	gcgttgatcg	acaacgttga	aggcgcgctg	180
gaaaaagctc	gccctgattc	acagggtccc	gcagaggatg	cggagctgct	tcagcaatac	240
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<210> 3106

<211> 195

<212> DNA

<213> Enterobacter cloacae

<400> 3106

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ctgatcagcg	aacatgaaac	cgaacaggaa	gcgctggatg	cgaacacggcg	ctatgaggat	180
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<210> 3107

<211> 1107

<212> DNA

<213> Enterobacter cloacae

<400> 3107

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<210> 3108

<211> 717

<212> DNA

<213> Enterobacter cloacae

<400> 3108

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<210> 3109
 <211> 1299
 <212> DNA
 <213> Enterobacter cloacae

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 acgggattgc tegtctggca ttctggaat ttactgcgtc ttctctgggt gctgtgggtc 180
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<210> 3110
 <211> 1326
 <212> DNA
 <213> Enterobacter cloacae

<400> 3110
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 aacgttatcg cgctggcgaa agtcgggtgc ggtgtggaca gctcagcac cccgattggc 240
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<210> 3111
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<212> DNA

<213> *Enterobacter cloacae*

<400> 3111

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<210> 3112

<211> 1845

<212> DNA

<213> *Enterobacter cloacae*

<400> 3112

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<210> 3113

<211> 474

<212> DNA

<213> Enterobacter cloacae

<400> 3113

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ctggctgtgg	cagaaaatcg	cgctgccggg	cagctgggca	ttgctggccg	gtgggttgct	180
gttctggtta	gtggcggtgc	tgggcgcgtc	gcagtgttgc	ctgaagcagg	agttatcgct	240
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<210> 3114

<211> 1107

<212> DNA

<213> Enterobacter cloacae

<400> 3114

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gaacaaaaat	atcgcttttt	tagctacggg	gacgcgatgt	ttatcacgta	caatccgcag	1080
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<210> 3115

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 3115

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ccacagcaga	agcgtactaa	agagcaca	aacctgatga	actccatcgc	gaaggcgat	180
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attgctatcg	ccctcaacga	caccactgaa	gtggttatca	aacgtgactt	cgtagctgcc	300
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<210> 3116
 <211> 1875
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3117
 <211> 384
 <212> DNA
 <213> Enterobacter cloacae

<400> 3117
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 ctggaactgc cgcaaggcat tggcactata gccctgttta ccgacagcga aggtaatcgc 360
 gtcggcctcc atcaaccggt atga 384

<210> 3118
 <211> 471
 <212> DNA
 <213> Enterobacter cloacae

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ccgctggctg	ccgacgtgct	ggcgaagggg	gccgcggcgc	ttaaccgcgc	cggcgagcgg	300
tactctccgg	caacgatccg	ggagaagctc	accatgcgtg	attttatgga	tacggttgcgt	360
tccagcggcg	tgcaaacccg	tgggcccggac	agcctgtcgc	agcgcgatcg	ccagcagttt	420
gccgcgcgagc	tggataaatg	gctgctggaa	gtgaagcgcc	gcccgcgcta	g	471

<210> 3119

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 3119

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agcgagggtcc	tcgccgaacg	cgatgcactg	taccgcgagg	cggcacacca	cgttgtggat	600
gcgtcggcgt	cacccgaaaa	agttgcgatt	cagattatta	ccgccctgcg	tttggtttgc	660
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<210> 3120

<211> 321

<212> DNA

<213> Enterobacter cloacae

<400> 3120

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ggcgcgctga	acgtcctgct	gccgggtgaa	acggagtggg	aagtatatag	tgccgggcag	240
gtcttcaacg	tgccgggcca	cagcgagttc	catttacagg	ttgcagagcc	aacctcttat	300
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<210> 3121

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 3121

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cgcgagcatc tgatccagca gaaagtcgag aaagaagggg cggatcagcc gtccattctg 1020
ccgtaa 1026

<210> 3122

<211> 744

<212> DNA

<213> Enterobacter cloacae

<400> 3122

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<210> 3123

<211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 3123

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<210> 3124

<211> 363

<212> DNA

<213> Enterobacter cloacae

<400> 3124

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<210> 3125

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 3125

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<212> DNA

<213> Enterobacter cloacae

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<211> 1197

<212> DNA

<213> Enterobacter cloacae

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<211> 1419

<212> DNA

<213> Enterobacter cloacae

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<210> 3129

<211> 1164

<212> DNA

<213> Enterobacter cloacae

<400> 3129

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<211> 2523

<212> DNA

<213> Enterobacter cloacae

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<212> DNA

<213> Enterobacter cloacae

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<211> 912

<212> DNA

<213> Enterobacter cloacae

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<211> 1179

<212> DNA

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<211> 732

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<213> Enterobacter cloacae

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<211> 1116

<212> DNA

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<210> 3136

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 3136

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<211> 885

<212> DNA

<213> Enterobacter cloacae

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 <212> DNA
 <213> Enterobacter cloacae

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 <213> Enterobacter cloacae

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339

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<213> Enterobacter cloacae

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<211> 420

<212> DNA

<213> Enterobacter cloacae

<400> 3141

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<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 3142

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<210> 3143

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 3143

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<210> 3144

<211> 1419

<212> DNA

<213> Enterobacter cloacae

<400> 3144

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<210> 3145

<211> 807

<212> DNA

<213> Enterobacter cloacae

<400> 3145

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<210> 3146

<211> 378

<212> DNA

<213> Enterobacter cloacae

<400> 3146

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<210> 3147

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 3147

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<210> 3148

<211> 894

<212> DNA

<213> Enterobacter cloacae

<400> 3148

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<210> 3149

<211> 2202

<212> DNA

<213> Enterobacter cloacae

<400> 3149

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<210> 3150

<211> 1131

<212> DNA

<213> Enterobacter cloacae

<400> 3150

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<210> 3151

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 3151

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<210> 3152

<211> 1890

<212> DNA

<213> *Enterobacter cloacae*

<400> 3152

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<210> 3153

<211> 984

<212> DNA

<213> *Enterobacter cloacae*

<400> 3153

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ctgtcgatta	tggggctgtc	gctggcagta	cgttacgcac	gtgaacgcac	agtagcctgg	840
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gttctgatac	gtttcgccac	ggtcctgttc	ctgacggtga	tccccgtcag	cgtcgccggc	960
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<210> 3154

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 3154

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ggttttacaa	aaggtatgat	caccggaaacg	gtaccgatgc	tggcagtcgt	gttcttttgc	180
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gagaatggaa	ttcagactgg	cttcttcgcc	ggattatccg	ttctggccat	tgtctcagca	360
atggatatga	ccaacggcgg	tctctatgcc	agcctgatga	atcaatatgg	caccaaagaa	420
gaatcgggcg	cgttcgtgct	gatgtccctg	gagtcgggtc	cactgatgac	gatgttgatt	480
ctgggttctg	ctggccttgc	ctcctttgaa	ctacaccatt	ttgtcggggc	gacccctgcc	540
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gccaccccg	tactgatccc	gttcttcggc	ttcgcgttgg	gcaataccat	caacctgaac	660
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acggcaattc	tggtccctat	catcacggca	ctgtacgcca	gacgctttgg	gcatgtgcct	960
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<210> 3155

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 3155

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tctttcgccg	gcaactgtgc	ggaggcgacg	gccttctatc	agcaggccgt	cggcgcagaa	180
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agcgatatca	tgatgagcga	tggtctgcca	cccggtagca	gcacgcagta	cgcgggattt	360
acgctggtgc	tcgacacgca	ggacgtggat	gaaggcaaac	gctggttcga	caacctctct	420
gatggcggca	atgtcgaaat	ggcctggcag	gagactttct	gggcgcacgg	attcgggaaa	480
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<210> 3156

<211> 1029

<212> DNA

<213> Enterobacter cloacae

<400> 3156

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atcatttcga	cagaatcaca	gcaaaacctg	aaaccccagt	gggaaccgtt	cctgaaagat	180
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gaagcggtag	atcgcgcgaa	cggccagggtg	ttcgcccgaga	ccgttgccgc	agacggctct	360
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gttgctacca	acaacactga	aaacctcgac	aagctgaaga	cctccgcgcc	ggacaagctg	660
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gatttgcaac	tgggtccgat	tgcgcagctg	gcgctgttca	agcagatgca	ggcgtgaag	900
gacaacaaag	gcctgaagga	cgaagagaag	accagcaaag	tgtcggaaat	tcaggcgcag	960
ctggacgata	tcgaccgcct	gaccgccgcg	ctcggcgcca	tgaccagcgt	gaataaagcg	1020
gtgcagtaa						1029

<210> 3157

<211> 669

<212> DNA

<213> Enterobacter cloacae

<400> 3157

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gatgcccaac	agagtttccg	tcgactgctg	aaagccatga	gcgagccggg	cgtcattgtc	180
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ctgccggagt	gcatacttca	tgagctgacc	gagcgcccg	atccgttccc	gctcgggtatc	600
gacctgatcc	tgacctgcgg	cgagcgccctg	ctggcgatcc	cgagaaccac	tcacgtggag	660
gtgtgctga						669

<210> 3158

<211> 870

<212> DNA

<213> Enterobacter cloacae

<400> 3158

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taccaggtgc	cgttcggcgg	ccgcgaaatg	ccgatgccct	acggctgggg	caaccggcgg	180
attcagatca	ccgccagcgt	gatcggcgaa	gcggacgtgc	tgaaggtcat	cgaccagggg	240
gcagacgaca	ccaccaacgc	cgtgtcgatc	cgcaacttct	ttaagcgcgt	aacgggcggt	300
aacaccactg	aaaaaaccca	agacgcgacg	ctgatccaga	cccgtcaccg	cattccggag	360
accccgctga	ctgaagatca	gattttgatt	ttccaggtgc	cgatcccggg	gccactgcgt	420
tttatcgagc	cgcgggaaac	cgaaaccgcg	accatgcacg	ccctggaaga	gtacgggata	480
atgcaggtca	aactgtatga	ggacatcgcc	cgttcgggcc	atatcgccac	cacctacgcc	540
tatccggtga	aggtgaacgg	ccgctacgtg	atggaccgct	cgcgcgaccc	gaaattcgat	600
aaccggaaga	tggacatgat	gcccgccttg	caactttttg	gtgccggacg	ggaaaaacgc	660
atctacgccg	taccgcctga	caccgcgtgtg	gagagcctgg	atcttgacga	tcaccggttt	720
acggtgcagg	agtgggacga	gccgtgcgcc	atctgcggtt	cgaagcatag	ctatctggat	780
gaagtgtgtc	tggacgacac	gggcaaacgg	atgtttgtct	gctccgacac	cgattactgc	840
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<210> 3159

<211> 648

<212> DNA

<213> Enterobacter cloacae

<400> 3159

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atgggcccgt	ccggctccgg	gaaggacagc	ctgctgtcgg	cgttacggca	gcgggaacat	180
tcacagctgc	tggtagcgca	ccgctacatt	acccgcgcgg	caaacgcggg	gagtgaaaac	240
catatcgccc	tgagcgagca	ggagtttttt	acccgcaccc	ggcaaaacct	gctggcgcgt	300

agctggcatg	ccaacggtta	ctactatggc	gtcggcatcg	agatcgacct	ctggctgcac	360
gcgggctttg	acgtgctggt	caacggctcg	cgggcgcate	tcccgcaggc	tcgcgcccgg	420
tacgaagcgg	cgctgctccc	ggtctgtttg	caggtttccc	cggacgttct	gcgtagccgg	480
ctgcaaaagc	gggggcgcga	aaacgcgcgc	gagatcgacc	agcggctgga	acgggcggcg	540
cgttacaccc	cgtcgggttg	ccatctcctc	aataacgacg	gaagtttgct	acagtcagtc	600
gagacctttc	tatcccttat	ccgccagaag	gagaaacagc	atgcctga		648

<210> 3160

<211> 1080

<212> DNA

<213> *Enterobacter cloacae*

<400> 3160

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ctaattgctg	gtatggtact	ggggtgttgc	aacggcgcg	tggtggcctt	cgccggactt	480
ccgccattta	tcgtcacgct	cggcacctac	acggcgctgc	gcggcgcggc	ctacctgtcg	540
gcggacggca	cgacggtcat	taactccaac	atcaacttcg	agtggatcgg	caataactac	600
ctcggcccga	tcccctggct	ggttgtgagc	gccctggcgg	tgattgtggg	gtgctggttt	660
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aacaacggca	tgacgctgat	gggcgtctcc	tacttctggc	agctggtgat	caaaggggcg	1020
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<210> 3161

<211> 864

<212> DNA

<213> *Enterobacter cloacae*

<400> 3161

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caggaaacgt	cgccgttcat	catcaacatc	gcgaagtg	attttaagta	cgtgtctctg	180
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aacctcgacc	acgggctgca	ttttgaggcc	gtcgtgcggc	ccctgcgctt	agggttcagc	300
tcggtgatgt	tcgacggctc	gacgctgagc	tatgaggaaa	atatccgcca	gacgcgggaa	360
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cgccgcgcca	tcgagctggg	cattcataaa	atcaactttt	ataccggcat	gtcgcaggcc	720
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gaactgctgc	tgggcattga	agaggccatt	accgatacgg	ttgcggaaca	gatgcgcate	840
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<210> 3162

<211> 492

<212> DNA

<213> *Enterobacter cloacae*

<400> 3162

gaatccatga	aaatcctttt	tctgatgttg	ttatttttta	ccgcgtttgc	ccatgccgat	60
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gagataggca	gccagtataa	aaagcaggct	gaagcgggcg	atgcgcgcgc	gcagtattat	120
ctcgccgata	cctgggttcag	ttccggcgac	agcgcgcagg	cggcgctgtg	ggcggaaaaa	180
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caggccatcg	cattgctgca	atcggcgacc	gaagacatcg	atagcgactc	ggcggtagac	420
gcgcaacagc	tggtggggct	gatttatgcc	aacggcggtg	aagttcctca	ggatgacgtg	480
caggccgcat	ag					492

<210> 3163

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 3163

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ctgttcaggc	aggggtgaaa	aggctttatc	acaccgaata	agcagaaagc	gctttactgg	120
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ggggagtaa						189

<210> 3164

<211> 492

<212> DNA

<213> Enterobacter cloacae

<400> 3164

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aagtggggat	ttgcgtttata	ctcgctgcct	ttttcggcac	actgccgtca	tttagctggc	120
gttttccagc	gtgttaacac	ttttgaggat	acccacatgc	aacttccaca	ctgcccga	180
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agctcctcca	tgctgaagat	cggcactaaa	gttaaaaata	tccgtcttgt	tgaaggcgat	420
cataatatcg	actgcaaaat	tgacggcttc	ggtccgatga	aactgaaatc	tgagttcgtg	480
aaaaagaact	ga					492

<210> 3165

<211> 759

<212> DNA

<213> Enterobacter cloacae

<400> 3165

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<210> 3166

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 3166
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 gctgaccgcg ccgcacgcct tgccgcgcgt caggccgaag taaataccag ccgggtcgac 420
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<210> 3167

<211> 1266

<212> DNA

<213> Enterobacter cloacae

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<210> 3168

<211> 774

<212> DNA

<213> Enterobacter cloacae

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 gcaggcgccg agctgaccga gctttccacc agcgtgaagc gcgtggacgc gcaccgtttt 720
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<210> 3169

<211> 768

<212> DNA

<213> *Enterobacter cloacae*

<400> 3169

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catatggatc	acgttcaggg	gctgtttcct	ctgcgctggg	gcgtgggggc	gaccattccg	300
gtttacggtc	cgccggacga	cgcaggctgt	gacgacctgt	taaaacatcc	gggccttctg	360
gatttcagcc	acacggtgga	gccgtttgtg	acgtttgaac	ttcagggcct	gcgggtgacg	420
ccgctgccgc	tcaaccattc	aaaactcacg	tttggtatc	tgctggagtc	cgcccacagc	480
cgcgtggcgt	ggctttctga	taccgcggga	ctgcgggata	aaacggtgac	gtttctgcta	540
aacaatcagc	cgcaggcgat	gattgtcgac	tgtagccatg	aaccgcgccc	ggagacgccg	600
cgcaaccatt	gtgatttgaa	tacggtgggt	gcgctgaacg	aggtgattgg	ctgtccgcag	660
gtgatcctga	cgcataatcag	ccatcagttt	gacgtgtgga	tgatggataa	cccgtgcgcg	720
tccggcattg	aagcggggta	tgacgggatg	gtgatggtgc	tggattag		768

<210> 3170

<211> 1548

<212> DNA

<213> *Enterobacter cloacae*

<400> 3170

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<210> 3171

<211> 1008

<212> DNA

<213> *Enterobacter cloacae*

<400> 3171

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accccgtttg	cgcaggcaaa	agatctgaaa	tccatcggcg	tgacggtggg	cgacctggct	180
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gacaacgtca	aggtgacgct	ggtctccagc	gggtacgata	tgggccagca	ggtgtcgcag	300
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gggatcgcc	cggcgtaaaa	acgcgccaaa	gaggcgggga	tcgtggtcgt	ggcggttgac	420
gtggcgggcg	aaggagccga	tgcgaccatc	acctccgata	acaccaggc	gggggaaatg	480
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ccgatatca	aagtgtcttc	ggataaccag	aacgccaaaag	gcagccgtga	aggcgggctg	660
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tttgtggcga	cgcagcgca	ggatccgcag	gtgatggcgg	cgaaggcggg	ggagatcggc	900
tatgacattc	ttcagggcaa	acctgcgcgc	aaagagcccg	tgtgatccc	ggtgacgatg	960
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<210> 3172

<211> 816

<212> DNA

<213> Enterobacter cloacae

<400> 3172

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atggtggcgc	tgttggggcc	gtctggttca	ggtaaatacca	cccttcttcg	tcacttgagc	180
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gaagccttac	aggcgctgac	ccgcgtcggc	atggcgcatc	tcgcccacca	gcgcgtctcc	480
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<210> 3173

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 3173

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tgggctgttc	tgttgccggg	gctcggttata	tcctggaagg	gcgcggagat	ggatccgctg	180
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gtgccatggg	gggtttacca	gccgatgcgc	cgcctgatgg	acgcctgtcg	cgccatcaac	420
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<210> 3174

<211> 1170

<212> DNA

<213> Enterobacter cloacae

<400> 3174

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aaagggggcg	agaaggcgat	cgccgcccgc	catgccttgc	aggagcacag	acgccggggg	180
gatgacgcct	tacccgagct	gagcgctcgcc	cagattgaac	agcagttaaa	cctggccgctc	240
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caggccagcg	gcgataacgt	ggaagccatc	ttcctgctgc	gcgcttacog	cactacgctt	360
gcgaagctgg	cggtaagcga	gccggtgaaa	acggcgga	tgcgtttaga	gcgcgctatt	420
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gtctcgaccc	tcaagctgcc	gcactacgtc	gatttccagg	ccgaactgga	actgctgaaa	1140
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<210> 3175

<211> 840

<212> DNA

<213> Enterobacter cloacae

<400> 3175

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gaccgcctgc	tggtgatgaa	gcagggtcag	gtggtgga	gtgggctgac	cgatcggtg	780
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<210> 3176

<211> 690

<212> DNA

<213> Enterobacter cloacae

<400> 3176

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gtcaacatcg	cccgcggttt	tatcgtcgat	tacccgattt	tactcctgga	tgaacccacc	540
gcctcgctcg	acagtaaaaa	cagcgcagcg	gtgatagaac	tgatcgaaca	ggccaaagcg	600
cgcggcgcg	cgatcgctcg	gatcttccac	gacgacgcc	tacgccatcg	cgtggcgga	660

agactgcacc cgatggggac aaacgtatga

690

<210> 3177

<211> 1083

<212> DNA

<213> Enterobacter cloacae

<400> 3177

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<210> 3178

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 3178

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gggaatgaaa	ccaactatgt	gatgcaaaaa	ttcgcgcgcg	ccgttattgg	taccaataac	420
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<210> 3179

<211> 1728

<212> DNA

<213> Enterobacter cloacae

<400> 3179

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<210> 3180

<211> 189

<212> DNA

<213> Enterobacter cloacae

<400> 3180

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<210> 3181

<211> 2310

<212> DNA

<213> Enterobacter cloacae

<400> 3181

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<210> 3182

<211> 237

<212> DNA

<213> Enterobacter cloacae

<400> 3182

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<210> 3183

<211> 417

<212> DNA

<213> Enterobacter cloacae

<400> 3183

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<210> 3184

<211> 909

<212> DNA

<213> Enterobacter cloacae

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<210> 3185
 <211> 1587
 <212> DNA
 <213> Enterobacter cloacae

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 cgcgatgtca ccattattga tgacgcgaaa ctgcgcaaa cgcattacagc ggccctcgctc 180
 ggtaatgcga tggagtgggt cgatttttgggt gtttacggct ttgtggccta tgcacttgggt 240
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 <211> 744
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3187
 <211> 240
 <212> DNA
 <213> Enterobacter cloacae

<400> 3187

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cctgaaactc	cccgcgggcc	agtcgtccat	cagggtgtga	ataccgcgt	ccagcaagg	180
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<210> 3188

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 3188

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<210> 3189

<211> 2370

<212> DNA

<213> Enterobacter cloacae

<400> 3189

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<210> 3190

<211> 891

<212> DNA

<213> Enterobacter cloacae

<400> 3190

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<210> 3191

<211> 1350

<212> DNA

<213> Enterobacter cloacae

<400> 3191

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<210> 3192

<211> 891

<212> DNA

<213> Enterobacter cloacae

<400> 3192

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<210> 3193

<211> 1119

<212> DNA

<213> Enterobacter cloacae

<400> 3193

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ccgcatcagg	agcgcgcgaa	ggcaggcagc	acgctgtggc	tgcatatgcc	ggaaaatcac	1080
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<210> 3194

<211> 1083

<212> DNA

<213> Enterobacter cloacae

<400> 3194

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<210> 3195

<211> 549

<212> DNA

<213> Enterobacter cloacae

<400> 3195

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gttgatatcg	atcagccgct	ggaagggtgt	gttgccagca	ccatcgaggt	tattaataaa	540
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<210> 3196

<211> 1344

<212> DNA

<213> Enterobacter cloacae

<400> 3196

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<210> 3197

<211> 2049

<212> DNA

<213> Enterobacter cloacae

<400> 3197

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<210> 3198

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 3198

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gaaaaagact	tctccgcgct	gatcgcccg	ctgcaaaaag	agaatatcga	cttcgtttac	480
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<210> 3199

<211> 1362

<212> DNA

<213> Enterobacter cloacae

<400> 3199

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<210> 3200

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 3200

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<210> 3201

<211> 2205
 <212> DNA
 <213> Enterobacter cloacae

<400> 3201
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<210> 3202
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 <212> DNA
 <213> Enterobacter cloacae

<400> 3202
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<210> 3203

<211> 2466

<212> DNA

<213> Enterobacter cloacae

<400> 3203

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<211> 939

<212> DNA

<213> Enterobacter cloacae

<400> 3204

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<210> 3205

<211> 858

<212> DNA

<213> Enterobacter cloacae

<400> 3205

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<210> 3206

<211> 756

<212> DNA

<213> Enterobacter cloacae

<400> 3206

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aacaaacccc	agcgtgcagc	cgagctgctg	cgctggggcg	tggaacagcat	ctgtaccgat	720
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<210> 3207

<211> 1782

<212> DNA

<213> Enterobacter cloacae

<400> 3207

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<210> 3208

<211> 1041

<212> DNA

<213> Enterobacter cloacae

<400> 3208

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<210> 3209

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 3209

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<210> 3210

<211> 1173

<212> DNA

<213> Enterobacter cloacae

<400> 3210

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<210> 3211

<211> 1374

<212> DNA

<213> Enterobacter cloacae

<400> 3211

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<210> 3212

<211> 258

<212> DNA

<213> Enterobacter cloacae

<400> 3212

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ttgatgccac	cgcctatcac	aatcagatct	ttggtttcca	taacaccctc	atgcactttc	180
gttaaagctc	aaaaatgttc	gatatcgctc	ataatagcaa	aggaacgcgc	ttttggtaac	240
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<210> 3213

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 3213

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cagcagcacc	tgcaaaacca	gatgaatacc	aacaccacgc	gcgtacagca	gggccagatg	360
cttgaacagc	cgctgcctaa	tacaaacggt	gggatgttag	gaggcggagt	atcgcaaaagc	420
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<210> 3214

<211> 318

<212> DNA

<213> Enterobacter cloacae

<400> 3214

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agcgttaatg	tactcaaaaac	ttactgcctt	ttattaataa	cctcgatggg	gctggcaaca	300
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<210> 3215

<211> 507

<212> DNA

<213> Enterobacter cloacae

<400> 3215

ctgactgagg	cacaaggaat	gagtgcagata	gtgatacgcc	acgctgaaac	gaaagattac	60
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cgcatcgagt	taacgggtgtt	tgtggataac	gaaccggcaa	tcgcggtgta	caaaaagcac	420
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<210> 3216

<211> 1536

<212> DNA

<213> Enterobacter cloacae

<400> 3216

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<210> 3217

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 3217

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<210> 3218

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 3218

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aataccaata	cgggcgcgca	gtgcagcatg	atcgaacata	tcatgcagtc	catgcagttc	600
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<210> 3219

<211> 1665

<212> DNA

<213> Enterobacter cloacae

<400> 3219

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<210> 3220
 <211> 303
 <212> DNA
 <213> Enterobacter cloacae

<400> 3220
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 tga 303

<210> 3221
 <211> 1125
 <212> DNA
 <213> Enterobacter cloacae

<400> 3221
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<210> 3222
 <211> 501
 <212> DNA
 <213> Enterobacter cloacae

<400> 3222
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 aatgtgaaaa aacaaagacc tgtcaatctg gatctcaaaa cgatccgatt ccctgtaaca 180
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<210> 3223
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 <212> DNA

<213> Enterobacter cloacae

<400> 3223

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<210> 3224

<211> 657

<212> DNA

<213> Enterobacter cloacae

<400> 3224

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<210> 3225

<211> 792

<212> DNA

<213> Enterobacter cloacae

<400> 3225

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<210> 3226

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 3226

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<210> 3227

<211> 1860

<212> DNA

<213> Enterobacter cloacae

<400> 3227

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 gctgttggtga ttggtgcggg tggcgaggt atgcgcgcgc cactgcaaat tcccagagc 180
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<210> 3228

<211> 732

<212> DNA

<213> Enterobacter cloacae

<400> 3228

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<210> 3229

<211> 1260

<212> DNA

<213> Enterobacter cloacae

<400> 3229

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<210> 3230

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 3230

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ggcttcaccg	gtagccaggg	gactttccac	tccgaacagg	caattgccta	cgttacgcag	180

atggttaggcg	gcgtaacgcc	aggtaaaggc	ggcaccaccc	acctgggcct	gccggtgttc	240
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<210> 3231

<211> 1686

<212> DNA

<213> Enterobacter cloacae

<400> 3231

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<210> 3232

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 3232

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<210> 3233

<211> 399

<212> DNA

<213> Enterobacter cloacae

<400> 3233

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<210> 3234

<211> 2817

<212> DNA

<213> Enterobacter cloacae

<400> 3234

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<212> DNA

<213> Enterobacter cloacae

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<211> 1929

<212> DNA

<213> Enterobacter cloacae

<400> 3236

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<211> 1695

<212> DNA

<213> Enterobacter cloacae

<400> 3237

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<211> 2067

<212> DNA

<213> *Enterobacter cloacae*

<400> 3238

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<211> 588

<212> DNA

<213> *Enterobacter cloacae*

<400> 3239

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<210> 3240

<211> 2688

<212> DNA

<213> *Enterobacter cloacae*

<400> 3240

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<210> 3241

<211> 195

<212> DNA

<213> *Enterobacter cloacae*

<400> 3241

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<210> 3242

<211> 2214

<212> DNA

<213> *Enterobacter cloacae*

<400> 3242

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<210> 3243

<211> 750

<212> DNA

<213> *Enterobacter cloacae*

<400> 3243

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<210> 3244
 <211> 1221
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3244
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<210> 3245
 <211> 693
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3245
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<210> 3246
 <211> 1389
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3247

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 3247

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acaaaatgga	cgatggggag	aatgatctca	tttaatacat	cttcgcctta	tgctaacgct	480
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<210> 3248

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 3248

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<210> 3249

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 3249

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atcatccogt	tacaggcccc	aaaaagtgc	catcgctccc	gttatctgtg	gttgtaacggc	240

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 tgtcagcgcc agtga 315

<210> 3250

<211> 807

<212> DNA

<213> *Enterobacter cloacae*

<400> 3250

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<210> 3251

<211> 1200

<212> DNA

<213> *Enterobacter cloacae*

<400> 3251

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<210> 3252

<211> 333

<212> DNA

<213> *Enterobacter cloacae*

<400> 3252

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ttgctgagaa tcaagtcgag aggataccgg aacaaagagc gcttcaaaat cgcagtgatg 300
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<210> 3253

<211> 597

<212> DNA

<213> Enterobacter cloacae

<400> 3253

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<210> 3254

<211> 2112

<212> DNA

<213> Enterobacter cloacae

<400> 3254

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2112

<210> 3255

<211> 2025

<212> DNA

<213> Enterobacter cloacae

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<210> 3256

<211> 579

<212> DNA

<213> Enterobacter cloacae

<400> 3256

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<210> 3257

<211> 1482

<212> DNA

<213> Enterobacter cloacae

<400> 3257

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<210> 3258

<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 3258

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<210> 3259

<211> 1518

<212> DNA

<213> Enterobacter cloacae

<400> 3259

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<211> 327

<212> DNA

<213> Enterobacter cloacae

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<210> 3261

<211> 1428

<212> DNA

<213> Enterobacter cloacae

<400> 3261

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<210> 3262

<211> 1695

<212> DNA

<213> *Enterobacter cloacae*

<400> 3262

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<210> 3263

<211> 483

<212> DNA

<213> *Enterobacter cloacae*

<400> 3263

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<210> 3264

<211> 588

<212> DNA

<213> *Enterobacter cloacae*

<400> 3264

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<210> 3265

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3265

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cttgccctggt	tcgtaaaactg	ccgtaaacaa	atattcgcat	tgctaaaaact	caaactgata	420
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<210> 3266

<211> 567

<212> DNA

<213> Enterobacter cloacae

<400> 3266

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<210> 3267

<211> 2073

<212> DNA

<213> Enterobacter cloacae

<400> 3267

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<210> 3268

<211> 2151

<212> DNA

<213> Enterobacter cloacae

<400> 3268

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<210> 3269
 <211> 1050
 <212> DNA
 <213> Enterobacter cloacae

<400> 3269
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<210> 3270
 <211> 630
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3271
 <211> 672
 <212> DNA
 <213> Enterobacter cloacae

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672

<210> 3272

<211> 1341

<212> DNA

<213> Enterobacter cloacae

<400> 3272

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<210> 3273

<211> 225

<212> DNA

<213> Enterobacter cloacae

<400> 3273

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gataagggca	aaatccttat	cccgaagtg	aaggacaaac	agcacttgtc	tgtgatgtcc	180
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<210> 3274

<211> 2940

<212> DNA

<213> Enterobacter cloacae

<400> 3274

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<210> 3275

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 3275

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<210> 3276

<211> 1053

<212> DNA

<213> *Enterobacter cloacae*

<400> 3276

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<210> 3277

<211> 1209

<212> DNA

<213> *Enterobacter cloacae*

<400> 3277

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<210> 3278

<211> 774

<212> DNA

<213> *Enterobacter cloacae*

<400> 3278

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<210> 3279

<211> 1860

<212> DNA

<213> Enterobacter cloacae

<400> 3279

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<210> 3280

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 3280

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<210> 3281

<211> 1623

<212> DNA

<213> Enterobacter cloacae

<400> 3281

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<210> 3282

<211> 1377

<212> DNA

<213> Enterobacter cloacae

<400> 3282

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<210> 3283

<211> 1176

<212> DNA

<213> Enterobacter cloacae

<400> 3283

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<210> 3284

<211> 1923

<212> DNA

<213> Enterobacter cloacae

<400> 3284

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<210> 3285

<211> 354

<212> DNA

<213> Enterobacter cloacae

<400> 3285

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ctggggccact	atccaggcgc	agttccgggg	aacggaacgg	tacagggtga	ggtttatcgt	180
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cgccagttga	tccagacgcc	ttacggcagt	gcattggatg	acgtgtacca	acgttcggtc	300
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<210> 3286

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 3286

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aataacctac	cctacgagga	cgttcataatg	tggaaagcgt	tacttcttgt	tacagcagtt	180
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<210> 3287
 <211> 1614
 <212> DNA
 <213> Enterobacter cloacae

<400> 3287
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 gaacaacacc aggaaatcct tcgcacagag ggctgagta aatttttccc tggcgtaag 180
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<210> 3288
 <211> 1434
 <212> DNA
 <213> Enterobacter cloacae

<400> 3288
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 gatggcgccg aagtggcggt cagcaaaaacc accggcatta gcgtgagcac ccgctatggc 240
 gaagtggaga atgtagaatt taatagcgat ggcgcgctgg ggatcaccgt gtatcaccag 300
 aatcgcaaa gacgcgcgtc gtctaccgat ctacgccgg atgccatgc ccgtacgggtg 360
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aacctcaagg	acatgtggcg	caatattgtt	acggtcggta	acgatattga	aacacgcagc	1380
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<210> 3289

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 3289

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aagaaaaccg	acaatgcggc	ggaaatgaaa	gacgcactga	cgaagatgcg	tgaagctgcg	180
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atgaaagact	accgccacgg	ctttgacgtg	ctggtcggcc	agattgacgg	cgcgctgaag	300
ctggcgaacg	aaggcaaagt	gaaggaagcc	caggcggcag	ccgatcagtt	tgcggcgacc	360
cgcaacgcgt	atcacaagaa	gtatcggtta				390

<210> 3290

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 3290

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caggcggcga	tgaacggcat	gaatcactat	ttcgagatga	aggagctggt	caataaaacc	180
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<210> 3291

<211> 789

<212> DNA

<213> Enterobacter cloacae

<400> 3291

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<210> 3292

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 3292

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<210> 3293

<211> 756

<212> DNA

<213> Enterobacter cloacae

<400> 3293

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gattccggcc	tggctgaaaa	aagctatctg	cgacatccgg	ggctgaacga	ctatcgccgg	720
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<210> 3294

<211> 249

<212> DNA

<213> Enterobacter cloacae

<400> 3294

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ggctcatcgt	tccagggtgt	gcgcgttgcg	ccgttggggc	atcctgttca	tatcgaaacc	180
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<210> 3295

<211> 2349

<212> DNA

<213> Enterobacter cloacae

<400> 3295

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caggtcacgc	tggttgattt	accggggacc	tattcactca	ccacgatttc	atcccagacc	240
tcactcgatg	agcaaattgc	ctgccactat	attctgagcg	gcgacgcgga	tctgctcatc	300

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<210> 3296

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 3296

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gatggctctg	caatcctgca	attcggcggc	ggctgtaacg	gctgctccat	ggtcgatgta	480
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<210> 3297

<211> 747

<212> DNA

<213> Enterobacter cloacae

<400> 3297

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tgctgggcaa	aaaagcgcag	actacatccg	agccgggttg	gaaagaaaaa	tggggatatg	180
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<210> 3298

<211> 2469

<212> DNA

<213> Enterobacter cloacae

<400> 3298

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 <211> 183
 <212> DNA
 <213> Enterobacter cloacae

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 ctgcatccgg cgatctccat ttcgaagatc atcggcggtt gcggcccggc ggcacagcag 180
 taa 183

<210> 3300
 <211> 2625
 <212> DNA
 <213> Enterobacter cloacae

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 <211> 351
 <212> DNA
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<210> 3302
 <211> 1383
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3303
 <211> 2151
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<210> 3304

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 3304

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<210> 3305

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 3305

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<210> 3306

<211> 1677

<212> DNA

<213> Enterobacter cloacae

<400> 3306

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<210> 3307

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 3307

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<210> 3308

<211> 654

<212> DNA

<213> Enterobacter cloacae

<400> 3308

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<210> 3309

<211> 2418

<212> DNA

<213> Enterobacter cloacae

<400> 3309

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<210> 3310

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 3310

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<210> 3311

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 3311

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<210> 3312

<211> 1350

<212> DNA

<213> Enterobacter cloacae

<400> 3312

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<210> 3313

<211> 486

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (350)

<400> 3313

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agcaacaaac	gcgtaaagag	caggagcggg	cccagcgtct	gctcgacgcc	ccgctgcaact	420
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<210> 3314

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 3314

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<210> 3315

<211> 1104

<212> DNA

<213> Enterobacter cloacae

<400> 3315

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caggcgatgc tggtcaccaa cgagacgctg gctccgcttt atctcgaccg tgtacgtcac 180
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<210> 3316

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 3316

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<210> 3317

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 3317

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catttcgacg ttatggataa ccactacgtt cccaacctga ccatcggtcc gatgggtgctt 180
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gatatgttcg	tcgcaggctc	cgccatcttc	gatcaaccgg	attacaaaaa	agtcattgat	660
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<210> 3318

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 3318

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cagcggccag	attatgccag	tccagctcgc	tgccggtttt	caggtggccc	gtcaccaggc	180
gcacgctctg	ggcatagtcg	cgatgggtta	acggaatgcc	ggaataggca	gaacagccgg	240
atgccgccgt	aa					252

<210> 3319

<211> 786

<212> DNA

<213> Enterobacter cloacae

<400> 3319

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ccctga						786

<210> 3320

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 3320

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<210> 3321

<211> 591

<212> DNA

<213> Enterobacter cloacae

<400> 3321

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ccgctggctc	atctgatgga	tttgctggaa	gatcctgact	ttaacgaggc	acgcaacgtg	540
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<210> 3322

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 3322

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<210> 3323

<211> 456

<212> DNA

<213> Enterobacter cloacae

<400> 3323

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<210> 3324

<211> 315

<212> DNA

<213> Enterobacter cloacae

<400> 3324

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<210> 3325

<211> 765

<212> DNA

<213> *Enterobacter cloacae*

<400> 3325

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<210> 3326

<211> 501

<212> DNA

<213> *Enterobacter cloacae*

<400> 3326

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<210> 3327

<211> 1761

<212> DNA

<213> *Enterobacter cloacae*

<400> 3327

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gcattgacca	gaggagaact	tgaccgcgca	ttaaggcaga	ggaaagtga	atctgtcggtg	1680
aagccctggg	cggatattga	gatttttggg	gagcgtgtcg	atatgagcta	cgacagttac	1740
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<210> 3328

<211> 777

<212> DNA

<213> Enterobacter cloacae

<400> 3328

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tccgacggcg	ttatcgggga	aggcaaaata	cttaagccag	aagagctggt	taacgcatta	180
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cgcgttctgc	aacgcgcgtt	gccccgtcca	tccgttacct	tgcgtgacag	cgaacagctc	300
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gatgccgggtg	cgctggctaa	tctctctctc	gctgttgccc	ccgcccggtg	cgctgcctgg	540
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gaagcggcga	cgggtgaatga	actggcggcg	ctgcttgccg	tttcttcttc	tgatacgcgc	660
gtgtttgatg	ctgccgcgca	tccttgggaa	gcggtgacgc	tgtgccagcc	gccgctgcgc	720
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<210> 3329

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3329

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cgggatccct	tctctgtgcc	ggaagagcgt	tgtcagcccg	ggcagctcag	ccagtggcgg	180
tatcagggga	tagtcagcgg	cagcagggat	atcgccctta	tgcaggacgg	gcagaaacgc	240
tggcaccggg	taaaaacgca	gatgcggtta	ccgacaggct	ggcgggtgag	cgcgatagat	300
agacaacaac	tgaccgttga	tgtcggcgat	atgtgcgagc	cgaagcgatg	gacatggcaa	360
cgagaaggaa	cgaaaaaaag	tgaagataag	gatagggctg	ttactggcgg	tactcagcca	420
gcccctgtgg	gccgcgacgc	caaaaccggt	caccctgctg	gtggatga		468

<210> 3330

<211> 1149

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (195)

<400> 3330

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gcttcagacg	gtagtgaaca	gcgcggggct	ggtattgcgg	aagaggcgcg	cattttttat	180
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<210> 3331

<211> 1290

<212> DNA

<213> Enterobacter cloacae

<400> 3331

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gcaggcaaca	ccagcaccgg	tcaggatatc	tctctgcgcg	ctgtctcttc	taccccgact	540
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cgtaacggtc	aaccgtggta	tgtgctggtg	agtggtatct	atgcttccaa	agatgaagca	1200
aaacgtgccg	tttccacgct	gccagccgac	gtgcaggcga	aaaaccctgt	ggcgaagccg	1260
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<210> 3332

<211> 1008

<212> DNA

<213> Enterobacter cloacae

<400> 3332

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tgcacgtggt	atttgcattg	tatcaccgcg	cgtcaggatc	ccgagaagct	tcgcaaagca	180
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<210> 3333

<211> 1638

<212> DNA

<213> Enterobacter cloacae

<400> 3333

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<210> 3334

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 3334

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ggcgacatgt	gggacagcca	gctgaactac	ctggccgagc	gcggctttcg	cgccatcgcc	180
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ccgcaggggtg	tgagctagag	cgtgttcgag	ggcattcgcg	acgggctgcg	taaagatcgc	480
gccagtttca	tcagcgactt	cgccaccocg	ttctacggta	tcaatgcggg	gcagacggtt	540
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ggcttcgcgc tgacccacca ggaccagctc aacgaagatc tgctggcggt tgtgaagtcg 840
ctgtaa 846

<210> 3335

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<400> 3335

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tacaacaaag	caccagcggt	gaataaacc	ttacttgttc	tgtacgttct	ttcccagtac	180
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<210> 3336

<211> 858

<212> DNA

<213> Enterobacter cloacae

<400> 3336

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<210> 3337

<211> 1179

<212> DNA

<213> Enterobacter cloacae

<400> 3337

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<210> 3338

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 3338

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<210> 3339

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 3339

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accggtcacg	gcaccatccc	tatgtccgtc	cgggcgatca	aaggcggagc	ctacgaattt	300
ctcactaagc	ccgttgaaatc	cagcgcgctc	atcggctcca	tccaatccgc	gctcagactg	360
gcacagcaca	acgcgcgccg	cgtcaaagag	cactacgccc	tgaagcagcg	ccacatgtcc	420
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atcgccgcgc	agctgggcgt	cagtgcagatc	acggtgaaag	tgcacgcgcg	ccgggtaattg	540
gagaaaatgc	aggtccgctc	cgtggccgaa	ctggtcaggg	ccgtcgagcg	cctgacccaa	600
catcaaccag	tggataa					618

<210> 3340

<211> 1884

<212> DNA

<213> *Enterobacter cloacae*

<400> 3340

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gactttgccc	gcacgtcagc	gatgccggta	tccgacgata	acgtttctctg	gggggcgctg	1860
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<210> 3341

<211> 2028

<212> DNA

<213> *Enterobacter cloacae*

<400> 3341

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cgctcgctta	ccgttaccaa	ccgaagaaat	atcgacgcca	gcctggcaaa	actgataggc	360
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<210> 3342

<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 3342

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cgcgataaca	tccccgaagt	gctggccgac	tacctcgccg	ccggtatcga	cccgaaacctg	240
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gacatcaccc	cgtttaaggc	cgagtgcgtg	cccgtcggcg	acgaccagtt	gccgatgatt	480
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<210> 3343

<211> 370

<212> DNA

<213> Enterobacter cloacae

<400> 3343

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cttaatccag	ccgggcaatc	caacgcacaa	cggattttatt	gagagcttta	acggacgatt	180
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taatgactgg	cggcaggatt	ataacgaatg	ccgcccgcac	tccacgctga	attatcagac	300
accgtctgaa	tttgacgcgg	gctggagaaa	gggtcattct	gagaatgaag	attccgacgt	360
tactaactga						370

<210> 3344

<211> 414

<212> DNA

<213> Enterobacter cloacae

<400> 3344

agaagaccca	accagccgc	tcacgtctg	cgcgtggcgc	ctgccgccgg	aagaggaggg	60
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cgagacgttc	ttccagcctc	cgctggacca	gaccgcgctg	gcgctctcgg	acgtgggtgag	120
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caaaacccag	acgtggctgc	cgtggccggt	ggtgatgaag	gagtccacgg	actactgccg	360
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<210> 3345

<211> 1155

<212> DNA

<213> Enterobacter cloacae

<400> 3345

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aattttgtcg	acccatttac	ccctgatgaa	ctggcgggtc	tgccgatgga	gccggaagtc	180
gatagccgcc	tggttaagcca	cgctaaccgc	aagtggcagg	cgagcaatgg	cccgtttgag	240
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<210> 3346

<211> 516

<212> DNA

<213> Enterobacter cloacae

<400> 3346

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ttacaacata	accttagcct	accaacagac	tcggcaacgg	gcaaggtoac	cggcactcgc	180
caacattcgc	cgtttcagtt	taccaaggaa	ctggatagct	cttcgcccta	tctgttcaaa	240
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tttaattatg	agaagattac	ccatttgtac	aaggacggtg	acttgtttagc	gcacgacgcg	480
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<210> 3347

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 3347

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gacgtgttcg	aggagaacgg	tatcccgctt	tcacgcgctg	aaatcgcgct	gatgaagaag	1080
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<210> 3348

<211> 1434

<212> DNA

<213> Enterobacter cloacae

<400> 3348

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<210> 3349

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3349

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gacgaacgct	ctggtcgcag	cgggctcagt	aacctgctgc	aatccgaagg	gtatgctacc	180
gataccttcg	attccgcaga	ggtgttcttg	agccaccctc	tcgccctgtc	cggcgcgtcg	240
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<211> 630

<212> DNA

<213> Enterobacter cloacae

<400> 3351

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<212> DNA

<213> Enterobacter cloacae

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<210> 3354

<211> 477

<212> DNA

<213> Enterobacter cloacae

<400> 3354

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<210> 3355

<211> 612

<212> DNA

<213> Enterobacter cloacae

<400> 3355

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<212> DNA

<213> Enterobacter cloacae

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<212> DNA

<213> Enterobacter cloacae

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<211> 1143

<212> DNA

<213> Enterobacter cloacae

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<210> 3359

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 3359

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gcaccgttta	tcgacctcag	cgggccgaaa	gacgaagtea	gcgcggcgct	ggatcgcgctc	240
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cttcgtccgg	gaatgatgat	tggtgcgttg	agcttcgaac	cgctgaccgg	ccgggcagac	540
cgtccttata	accgcgctca	ggacgcaaaa	tatcgcgacc	agcagggtgc	ggttgccagt	600
cgtatcgata	aagactga					618

<210> 3360

<211> 2235

<212> DNA

<213> Enterobacter cloacae

<400> 3360

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gaaatcgata	tcggtcgcct	ggtcgggacc	gttattgaag	cgaaatggtg	ggtgctgggt	180
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<210> 3361

<211> 510

<212> DNA

<213> Enterobacter cloacae

<400> 3361

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cgggcttcgg gggaaataat gtttctggaa gattgtcgcg ctaacagctg gagcctgcgc 60
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aatgtgctga acaatatctg gccgcgcgca gtgctgggtg tgtaccgcat catcaccgaa 180
tgcttttttg gctatgaaat tcaggccgct gccaccattg gccgcgcgtt taccattcat 240
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aacgtcgagc tgggcgccaac cgtgggtgat atcggggaca ttaccgtggg taataacgtg 420
acgattggcg caggcagcgt ggtgctggac agcattccgg acaacgcgct ggtgggtggc 480
gagaaagccc gcgtgaaggt gataaaatga 510

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<210> 3362

<211> 1116

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1113)

<400> 3362

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gacgccagca	aatatgtcac	ctccaccatg	ctgtttgttt	atatacgttat	cattattggc	480
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tcgtcctatt	atcgcatcat	tggtccactg	gtgatgggtg	gttattcctt	aaccaccta	1080
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<210> 3363

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 3363

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gtacagtccg	atggcaccat	gtttctatccc	tacattggca	aagtgcacgt	cgcgggcaaaa	420
acgcttgctg	agatccgtag	tgatattacc	ggccgccttg	cgcagtacat	tgctgacccg	480
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gatatgtccg	acgcgacgct	gctggctcatg	gcaacgtcgt	tccgtctcca	gccgtacgat	1020
gtggtctatg	tcaccaccgc	gccggtccgc	cgttggaacc	gtctgatcaa	ccagttgctg	1080
cctaccatca	gtggcggttcg	ctacatgacg	gatacggcga	gcgacgttca	taactggtaa	1140

<210> 3364

<211> 450

<212> DNA

<213> Enterobacter cloacae

<400> 3364

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<210> 3365
 <211> 852
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3366
 <211> 1020
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3367
 <211> 534
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3367
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 ggccagcagc gccacacca ccgcgccgt gcgagtgtag tagcgttttt cgaggctgta 480
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<210> 3368
 <211> 693
 <212> DNA
 <213> Enterobacter cloacae

<400> 3368
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 aaacaatacg ccgatattat cgtgcctcgt ggcggtaaaa accgtattgc cattgatata 660
 ttaaaagcga aaatcagtcg gttttttgaa taa 693

<210> 3369
 <211> 1881
 <212> DNA
 <213> Enterobacter cloacae

<400> 3369
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 cgtcggtgta atgactgggc ggaccgcaat aaagagcttc agtcaggtaa ggacgtgaaa 1860
 aaactgctcg ataagctgtg a 1881

<210> 3370
 <211> 1308

<212> DNA

<213> *Enterobacter cloacae*

<400> 3370

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<213> *Enterobacter cloacae*

<400> 3371

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<210> 3375

<211> 1416
 <212> DNA
 <213> Enterobacter cloacae

<400> 3375
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 ctgcccggtc agtccggccc gctgcttggc ccggcgctgg ggggattctt ggtggagtat 480
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<210> 3376
 <211> 357
 <212> DNA
 <213> Enterobacter cloacae

<400> 3376
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 ccgcgctgga caccgcagc caggatgaac tgggcaagct ggccgaggac ttcaaccagc 180
 tcgcagcagc gctggaaaaa aaccagcaga tgcgcgcgga ttttatggcc gacatttcgc 240
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<210> 3377
 <211> 1386
 <212> DNA
 <213> Enterobacter cloacae

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 aacatcgtgc ataaacacga gccgatcccg gtcaccaacg ttgagccaac gctgggtatc 720

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<210> 3378

<211> 1629

<212> DNA

<213> Enterobacter cloacae

<400> 3378

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gataacctgg	tgtttatcgc	catccttgcc	gataaattac	ccccctcaca	acgcgaccgc	180
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gaggtgtag						1629

<210> 3379

<211> 1452

<212> DNA

<213> Enterobacter cloacae

<400> 3379

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<210> 3380

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 3380

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caggacagtc	agacgggtgg	gatcagcgcc	gggctgtccg	caggcgaccg	cgtcgtaacc	1140
gacggtattg	accggtcgac	cgaagggggc	caggctcagg	tgggtggaagc	gcagaataca	1200
ggagcaaaaag	cctga					1215

<210> 3381

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 3381

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ctgatcgact	atttgccgcg	tgcgagttac	gcgccaacgc	ttatcagcca	cggcgaccag	180
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cgcgcgtgta	agccgcagcg	tgaattgcag	gtgctggatg	cgcaaagccc	gctgatcgctc	480

gacgaaagcc	gtttccaggc	gagctggcgc	agcaaaacttt	tggatctcac	ccccgcagag	540
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aaaaacctgc	gccgcaagct	ggaggcgtg	gacgccgacc	agtcgtttat	tcgcgcgggtg	720
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<210> 3382

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 3382

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cgcattcacg	tcggggtgac	ctttgaaaaa	ggcgatgcgg	cgcgtatat	cgatgaaggt	180
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<210> 3383

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 3383

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attcccgtaa	gaatcgcaat	tcttctaat	caagataatt	atgatcttct	tgtatctggt	240
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<210> 3384

<211> 1392

<212> DNA

<213> Enterobacter cloacae

<400> 3384

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<210> 3385

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 3385

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gtcgttccgc	aaaagctgga	acgcacgcca	cctgacacct	gtcgcgctgg	cggtcacccg	180
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<210> 3386

<211> 1200

<212> DNA

<213> Enterobacter cloacae

<400> 3386

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ggcgagccgt	actggtgtga	agatgcttac	tataagctca	cgcttgctca	ggtcaaaaag	180
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<210> 3387

<211> 2532

<212> DNA

<213> Enterobacter cloacae

<400> 3387

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gcgtccctgt	taatgacgat	agttgcctct	gccactgaat	ttaataataaa	cgccatcgat	180
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gccgccagac	cagacatcaa	atttactttt	gagcaaggca	gccagaccct	gaaagtaacg	480
atcccccagg	cgtggctgca	ataccgtgcg	gttgactgga	tgcgccatc	cacctgggac	540
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<210> 3388

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 3388

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aaggccagca	gcctgaaagt	ggacaaccag	agcaaggcgc	tgccttatct	ggcgtctctc	180
tggattgaag	atgaaaagg	gcaaaaagaa	gatgtgcact	ttatggcgct	tccccccatt	240
caacgtatcg	aagcggggcg	ctcgtcgcag	gtaagaattg	ttaaacaagc	cgctaccgcg	300
cagttgccaa	aagacaggga	atcgtgtgtt	tatttcaacc	tgcgtgaagt	accgcctaaa	360
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<210> 3389

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 3389

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cagtcctga	cgcgcgatca	ggtgatggag	ggcgtaccgc	agatgatccc	ggatattcag	540
gtggaagcca	ccttcccggg	cggatccaag	ctcgtcaccc	tccacaacct	gacgtgttaa	600

<210> 3390

<211> 255

<212> DNA

<213> Enterobacter cloacae

<400> 3390

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gttctggctg	aagttcgtcg	tctgtagttt	tatgaaaaac	caacgaccga	acgtaagcgc	180
gctaaagctt	ccgctgtgaa	acgtcacgcg	aagaaactgg	ctcgcgaaaa	cgcacgcgcg	240
actcgtctgt	actaa					255

<210> 3391

<211> 1980

<212> DNA

<213> Enterobacter cloacae

<400> 3391

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tgtggatacc	gtcttatgga	gcaaaaaccg	cagtcacagc	tgaaacttct	tgtccaacgc	180
ggtaaggagc	aaggctatct	gacctatgcc	gaggccaatg	accatctgcc	ggaagatata	240
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gaagatgcgg	aagaagctgc	tgcacaggte	ctgtccagcg	tggaatctga	aatcgggcgt	420
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gaagtgggta	aacagtttga	cgtgacccgc	gaacgtatcc	gtcagatcga	agcgaaggcg	1920
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<210> 3392

<211> 1203

<212> DNA

<213> Enterobacter cloacae

<400> 3392

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<210> 3393

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 3393

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<210> 3394

<211> 375

<212> DNA

<213> Enterobacter cloacae

<400> 3394

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aaagaagcgc	tggcgctcaa	ctgctatctg	ggtggatctg	gcggcccggt	cgaggagaca	180
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<210> 3395

<211> 1578

<212> DNA

<213> Enterobacter cloacae

<400> 3395

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atcacagatt	caactccctt	tccagcgcca	ggaaacaccc	cggatggcga	tatcaagtgg	180
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<210> 3396

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 3396

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acataa

846

<210> 3397

<211> 399

<212> DNA

<213> Enterobacter cloacae

<400> 3397

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cgcgaggcca	cccgaggcta	cgggctgaac	atcccggcgg	gcaccgctgt	gcgcttcgag	300
cccggccaga	agcgggaagt	gacgctgggt	cagggtgacgg	gcgcacagcg	cattttcggt	360
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<210> 3398

<211> 726

<212> DNA

<213> Enterobacter cloacae

<400> 3398

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<210> 3399

<211> 627

<212> DNA

<213> Enterobacter cloacae

<400> 3399

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<210> 3400

<211> 1812

<212> DNA

<213> Enterobacter cloacae

<400> 3400

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gggcatatgg ccggaagaat cccacgcgtt ttcataaatg acctgcttgc cagaaccgac 120
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gcgaagaat aa 1812

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<210> 3401

<211> 504

<212> DNA

<213> Enterobacter cloacae

<400> 3401

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ggaagaaaca tgcgacacga acacgacggc ggcggaacgc ggccacgatt ttttggtcat 60
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ctgatcaaaag agatcgagaa cctgacgcag ggacattaca cgccaagccc tggcgtgatc 180
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ctggagatct cccagctgga ttaa 504

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<210> 3402

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 3402

```

ggagaatgca tgtcagtacc gttgattttg accatacttg cgggcgcgcg aacctttatc 60
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ggtttcgcgc ccgggatcat gctgcttata tcgctgatgg agatgctgcc cgccgcgctt 180
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```



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gatgagctga tgccgctggc aaaagagatc gatcccaaca ataaccacaag ctacggcgtg 720
ctgtgtggaa tgtcagtgat ggggatgagc ctggttctgc tgcaaacggc aggtattggc 780
taa 783

```

<210> 3403

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 3403

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atgtatatgg gtaaaaaatt gctgttagcg gcagctatgg ctgccattgt atcgggttct 180
gcgtttgctg atgatcaagg ctacaggcaa atcaaattca aaggcgtggg tattgacgca 240
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cagccaaacg tgcttgatct gctggcgggt tcaaccacc agacgctgca tttcaaagcg 600
gttatggaag tcccaacagg taaaactcgc acggcaggcc aggttgaagc cagggctaac 660
tacgtcctga tgtacaaata a 681

```

<210> 3404

<211> 741

<212> DNA

<213> Enterobacter cloacae

<400> 3404

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gatgccacag gccagcccaa cggcgtggat acccgccagt gcctggacaa cgataacatc 60
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gaactttcac gggaagaagg gaaagcgatt cagtcggggc cgttcgaaac cgtggtactg 720
ttcaaaaatta actaccacta g 741

```

<210> 3405

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 3405

```

cacgctacaa taggcactaa caccttttca tcaagggaaa cgacaatgat tgacccaaag 60
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aagccagcgc cagctattcc accggtggat gaccaggcat aa 342

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<210> 3406

<211> 702

<212> DNA

<213> *Enterobacter cloacae*

<400> 3406

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<210> 3407

<211> 1302

<212> DNA

<213> *Enterobacter cloacae*

<400> 3407

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<210> 3408

<211> 735

<212> DNA

<213> *Enterobacter cloacae*

<400> 3408

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<210> 3409

<211> 1707

<212> DNA

<213> Enterobacter cloacae

<400> 3409

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<210> 3410

<211> 474

<212> DNA

<213> Enterobacter cloacae

<400> 3410

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ctgcgtcagt	tccggctgga	ggtgaccttc	gccagcctgc	cgtttgaacc	ggaagcgggg	420
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<210> 3411

<211> 888

<212> DNA

<213> Enterobacter cloacae

<400> 3411
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<210> 3412

<211> 1644

<212> DNA

<213> Enterobacter cloacae

<400> 3412
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<210> 3413

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 3413
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<210> 3414

<211> 390

<212> DNA

<213> Enterobacter cloacae

<400> 3414

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cgtggcacia	atctgaaagg	aaagatttaa				390

<210> 3415

<211> 822

<212> DNA

<213> Enterobacter cloacae

<400> 3415

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<210> 3416

<211> 1512

<212> DNA

<213> Enterobacter cloacae

<400> 3416

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<210> 3417

<211> 519

<212> DNA

<213> Enterobacter cloacae

<400> 3417

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<210> 3418

<211> 1323

<212> DNA

<213> Enterobacter cloacae

<400> 3418

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<210> 3419

<211> 2877

<212> DNA

<213> Enterobacter cloacae

<400> 3419

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<210> 3420

<211> 1032

<212> DNA

<213> *Enterobacter cloacae*

<400> 3420

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<210> 3421

<211> 1449

<212> DNA

<213> *Enterobacter cloacae*

<400> 3421

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<210> 3422

<211> 666

<212> DNA

<213> *Enterobacter cloacae*

<400> 3422


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<210> 3423

<211> 825

<212> DNA

<213> Enterobacter cloacae

<400> 3423

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<210> 3424

<211> 906

<212> DNA

<213> Enterobacter cloacae

<400> 3424

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<210> 3425

<211> 1386

<212> DNA

<213> Enterobacter cloacae

<400> 3425

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<210> 3426

<211> 1092

<212> DNA

<213> Enterobacter cloacae

<400> 3426

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<210> 3427

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 3427

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<210> 3428

<211> 849

<212> DNA

<213> Enterobacter cloacae

<400> 3428

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<210> 3429

<211> 1428

<212> DNA

<213> Enterobacter cloacae

<400> 3429

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<210> 3430

<211> 948

<212> DNA

<213> Enterobacter cloacae

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<210> 3431

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 3431

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<210> 3432

<211> 1464

<212> DNA

<213> Enterobacter cloacae

<400> 3432

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<210> 3433

<211> 963

<212> DNA

<213> Enterobacter cloacae

<400> 3433

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<210> 3434

<211> 1296

<212> DNA

<213> Enterobacter cloacae

<400> 3434

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<210> 3435

<211> 1326

<212> DNA

<213> Enterobacter cloacae

<400> 3435

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<210> 3436

<211> 1974

<212> DNA

<213> Enterobacter cloacae

<400> 3436

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<210> 3437

<211> 420

<212> DNA

<213> Enterobacter cloacae

<400> 3437

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<210> 3438

<211> 1128

<212> DNA

<213> Enterobacter cloacae

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<210> 3439
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<400> 3439

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<210> 3440
 <211> 681
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3440

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ccgaaagcct ctacacactt ccatactctt atgggcaaca cctcccacga ggcgctgctg    600
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<210> 3441
 <211> 825
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3441

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<210> 3442

<211> 1653

<212> DNA

<213> Enterobacter cloacae

<400> 3442

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tggcatagcc	tgatggacga	ggcgcaaaaa	tccctggcgg	cgtctcaaca	ggcatggcaa	420
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<210> 3443

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 3443

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acggtccagc	tgatcaccca	tcagcccgaa	aaccagccgc	accgtgctga	tgtcgcgaaa	300
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gaggcggttg	cgcggtgaaaa	agcgcttacg	gtgctggtgc	ttgatacctc	aaccggcagc	420
ggcgcgagaga	cggttttatca	gagagcgggc	tggcaaaagg	cgggggagat	ctcacgctac	480
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<210> 3444

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 3444

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gcggccacct	gggacagggc	gtcacagat	tcatcaccoc	tgttttgcog	ggtcgtggag	180
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gcgcccgttt	gctatctgga	agatctgttt	gttgacgctg	ccgaacgtgg	cgcaggggog	300
ggtaaagcgc	ttatcgacgc	cctgatcgat	gaaggcaagc	gggaagggtg	gtcaaaaactc	360
tactgggtaa	cccgcattgaa	caatccggcg	cgtaagctgt	atgatcacta	tggtgaagcc	420
gacgattacg	tccggtaccg	aatctcgctt	tag			453

<210> 3445

<211> 792

<212> DNA

<213> Enterobacter cloacae

<400> 3445

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ctcgtgaaat	ccggctacca	cgctctggc	gcggcgaaac	ggaaagagat	gcgcgtagt	180
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accgcgcgca	acgaggacac	ggaccggatc	ctgggactgg	agatggggcg	cgacgattat	360
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tttcgtacta	tgccgcctaa	tcttcagggt	accgaggcag	ggcgccctgg	ggtattcgg	480
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attgatctcc	tggtgagccg	cgtgcgacag	cgccctgaatg	aagatgcccg	cacgccggcc	720
tacattaaaa	ccgttcgcag	cgaaggctac	gtttttacca	tgccgggtgac	catcgctcag	780
gccaatgaat	ga					792

<210> 3446

<211> 1302

<212> DNA

<213> Enterobacter cloacae

<400> 3446

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attccgcaag	gcggttttct	gaccggcgca	ctgtttctga	aaagcgggtg	ttcgcttcgc	180
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gagtttgga	aaatttccgg	tgtggatggg	ttgcgctttc	aggatgtgca	ggtgactgcc	1260
gtagagaaca	cgcaagactg	taacgacagt	tatgaacggt	ga		1302

<210> 3447

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 3447

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ctgtcaaaac	tggcgaaga	gacgggcgtg	tcgaaagcga	tgcttgggca	aatcgaacgc	180
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tacgctgatt	ccggcgtgcg	ttttgcgggc	gataaacgcg	acgcgtaccg	caacagcagc	540
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<210> 3448

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 3448

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gccctcgcca	gccgggtaca	acaaccagat	ccgcggtttc	aagcagacgc	agatcgccgt	240
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cgccaaactc	aaagggtacat	aaaccgtcat	atgccagcac	gaccgcgcgc	ggcgagggat	420
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<210> 3449

<211> 810

<212> DNA

<213> Enterobacter cloacae

<400> 3449

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gtgctgcac	aagggcgcg	actggcgga	ggttcgcttc	gcgaggtaca	ggccaatgaa	780
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<210> 3450
 <211> 594
 <212> DNA
 <213> Enterobacter cloacae

<220>
 <221> unsure
 <222> (564)

<400> 3450
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 gatgaaccca cgggaaggtat tcagccgctg gtgattaaag agattgggca ggtgatccgc 540
 aacctggcga accgggggga tatngcgatc ctgctgggtg gagcaatttt atga 594

<210> 3451
 <211> 936
 <212> DNA
 <213> Enterobacter cloacae

<400> 3451
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 aacatgcctc cattgatgct ggcggtctg cgttccctgc tgggtggcgtt tccggcgctg 180
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<210> 3452
 <211> 513
 <212> DNA
 <213> Enterobacter cloacae

<400> 3452
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 gaccaaactg cttggacggt ccgtatactg atgtccacgt tagatcctct gttcgcgcgc 180
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<210> 3453

<211> 1074

<212> DNA

<213> *Enterobacter cloacae*

<400> 3453

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cagaaatag	acgcctacga	acaaaagctg	gctacgctgc	cgaatattac	ggtgccgacc	900
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aaattcacgg	gaaaatatga	gcaccgtact	ttcggcgcaa	cggttggcca	caaccgcgcg	1020
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<210> 3454

<211> 762

<212> DNA

<213> *Enterobacter cloacae*

<400> 3454

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<210> 3455

<211> 669

<212> DNA

<213> *Enterobacter cloacae*

<400> 3455

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gagggggaag	atatcgacgt	gctggaaatg	acgctggacg	acgcgcttca	gggcattgaa	600
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669

<210> 3456

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 3456

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<210> 3457

<211> 615

<212> DNA

<213> Enterobacter cloacae

<400> 3457

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<210> 3458

<211> 912

<212> DNA

<213> Enterobacter cloacae

<400> 3458

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<210> 3459

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 3459

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<210> 3460

<211> 1011

<212> DNA

<213> Enterobacter cloacae

<400> 3460

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<210> 3461

<211> 237

<212> DNA

<213> Enterobacter cloacae

<400> 3461

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cgtcatgaag	ctgacagcga	cgagttacgc	agcgcggctg	aggagtctgc	ggaggggttg	180
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<210> 3462

<211> 1206

<212> DNA

<213> Enterobacter cloacae

<400> 3462

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<210> 3463

<211> 476

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (32)

<400> 3463

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tactgaaacg	cgaacggatt	aagaaaagga	tctacggaac	gagagacgaa	gccagaagcg	360
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<210> 3464

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 3464

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<210> 3465

<211> 480

<212> DNA

<213> Enterobacter cloacae

<400> 3465

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<210> 3466

<211> 1266

<212> DNA

<213> Enterobacter cloacae

<400> 3466

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<210> 3467

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 3467

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<210> 3468

<211> 1248

<212> DNA

<213> *Enterobacter cloacae*

<400> 3468

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gccattggct atctcggggc gattccggcg ctgacgcgc tgatctggte ggtgcttata   1200
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<210> 3469

<211> 234

<212> DNA

<213> *Enterobacter cloacae*

<400> 3469

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accatgatta tgccgtccac gcaaaaccag tcgccctggg acttcaatca catgggcgt    180
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<210> 3470

<211> 489

<212> DNA

<213> *Enterobacter cloacae*

<400> 3470

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gtcgggctgg actcattgct ttcgatttgc ccaagcatcg ctttcgacac gcccgctctc    420
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aggtgttga
489

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<210> 3471

<211> 369

<212> DNA

<213> *Enterobacter cloacae*

<400> 3471

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catgcaaaag caaatccgc cagccagccc ctgttcctta tcccctcgga taacagggaa    60

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gtgctggtgt	tcagcgggtga	atacttcctt	gatgaacaag	gattacccac	cccaaaaagc	300
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<210> 3472

<211> 1584

<212> DNA

<213> Enterobacter cloacae

<400> 3472

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<210> 3473

<211> 1272

<212> DNA

<213> Enterobacter cloacae

<400> 3473

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<210> 3474

<211> 1050

<212> DNA

<213> *Enterobacter cloacae*

<400> 3474

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<210> 3475

<211> 465

<212> DNA

<213> *Enterobacter cloacae*

<400> 3475

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<210> 3476

<211> 2745

<212> DNA

<213> *Enterobacter cloacae*

<220>

<221> unsure

<222> (2733)

<400> 3476

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acctgcggtg	tgctgtcaga	agacgatact	ttcggcacca	tcaccatcgc	agaaccgatc	420
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<210> 3477

<211> 642

<212> DNA

<213> Enterobacter cloacae

<400> 3477

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642

<210> 3478

<211> 252

<212> DNA

<213> Enterobacter cloacae

<400> 3478

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<210> 3479

<211> 564

<212> DNA

<213> Enterobacter cloacae

<400> 3479

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<210> 3480

<211> 2052

<212> DNA

<213> Enterobacter cloacae

<400> 3480

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<210> 3481

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 3481

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<210> 3482

<211> 1512

<212> DNA

<213> Enterobacter cloacae

<400> 3482

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<210> 3483

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 3483

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<210> 3484

<211> 654

<212> DNA

<213> Enterobacter cloacae

<400> 3484

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<210> 3485

<211> 771

<212> DNA

<213> Enterobacter cloacae

<400> 3485

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<210> 3486

<211> 1653

<212> DNA

<213> Enterobacter cloacae

<400> 3486

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<210> 3487

<211> 1362

<212> DNA

<213> *Enterobacter cloacae*

<400> 3487

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<210> 3488

<211> 861

<212> DNA

<213> *Enterobacter cloacae*

<400> 3488

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<210> 3489

<211> 1227

<212> DNA

<213> Enterobacter cloacae

<400> 3489

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<210> 3490

<211> 435

<212> DNA

<213> Enterobacter cloacae

<400> 3490

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<211> 351

<212> DNA

<213> Enterobacter cloacae

<220>
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<210> 3492
 <211> 954
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3493
 <211> 921
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3494
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 <212> DNA

<213> Enterobacter cloacae

<400> 3494

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<210> 3495

<211> 471

<212> DNA

<213> Enterobacter cloacae

<400> 3495

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<210> 3496

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 3496

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<210> 3497

<211> 864

<212> DNA

<213> Enterobacter cloacae

<400> 3497

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<210> 3498

<211> 648

<212> DNA

<213> Enterobacter cloacae

<400> 3498

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<210> 3499

<211> 876

<212> DNA

<213> Enterobacter cloacae

<400> 3499

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<210> 3500

<211> 654

<212> DNA

<213> *Enterobacter cloacae*

<400> 3500

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<210> 3501

<211> 633

<212> DNA

<213> *Enterobacter cloacae*

<400> 3501

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<210> 3502

<211> 1062

<212> DNA

<213> *Enterobacter cloacae*

<400> 3502

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<210> 3503

<211> 2841

<212> DNA

<213> *Enterobacter cloacae*

<400> 3503

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<210> 3504

<211> 348

<212> DNA

<213> *Enterobacter cloacae*

<400> 3504

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<210> 3505

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 3505

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<210> 3506

<211> 1749

<212> DNA

<213> Enterobacter cloacae

<400> 3506

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<210> 3507

<211> 1050

<212> DNA

<213> Enterobacter cloacae

<400> 3507

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<210> 3508

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 3508

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<210> 3509

<211> 951

<212> DNA

<213> Enterobacter cloacae

<400> 3509

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<210> 3510

<211> 885

<212> DNA

<213> Enterobacter cloacae

<400> 3510

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<210> 3511

<211> 2610

<212> DNA

<213> Enterobacter cloacae

<400> 3511

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<210> 3512

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 3512

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<210> 3513

<211> 192

<212> DNA

<213> Enterobacter cloacae

<400> 3513

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<210> 3514

<211> 567

<212> DNA

<213> *Enterobacter cloacae*

<400> 3514

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<210> 3515

<211> 1653

<212> DNA

<213> *Enterobacter cloacae*

<400> 3515

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<210> 3516

<211> 435

<212> DNA

<213> *Enterobacter cloacae*

<400> 3516

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<210> 3517

<211> 573

<212> DNA

<213> Enterobacter cloacae

<400> 3517

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gcgctggacg	ccacaccgtg	ggcatttagc	ccgtggatgg	tgcaagaagc	gaacactgcg	540
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<210> 3518

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 3518

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<210> 3519

<211> 633

<212> DNA

<213> Enterobacter cloacae

<400> 3519

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<210> 3520

<211> 903

<212> DNA

<213> Enterobacter cloacae

<400> 3520

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<210> 3521

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<400> 3521

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<210> 3522

<211> 930

<212> DNA

<213> Enterobacter cloacae

<400> 3522

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<210> 3523

<211> 1527

<212> DNA

<213> Enterobacter cloacae

<400> 3523

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<210> 3524

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 3524

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<210> 3525

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 3525

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<210> 3526

<211> 534

<212> DNA

<213> Enterobacter cloacae

<400> 3526

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<210> 3527

<211> 1452

<212> DNA

<213> Enterobacter cloacae

<400> 3527

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<210> 3528

<211> 999

<212> DNA

<213> Enterobacter cloacae

<400> 3528

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<210> 3529

<211> 762

<212> DNA

<213> Enterobacter cloacae

<400> 3529

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<211> 375

<212> DNA

<213> Enterobacter cloacae

<400> 3530

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<210> 3531
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<210> 3532
 <211> 783
 <212> DNA
 <213> Enterobacter cloacae

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taa

783

<210> 3533

<211> 687

<212> DNA

<213> Enterobacter cloacae

<400> 3533

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<210> 3534

<211> 873

<212> DNA

<213> Enterobacter cloacae

<400> 3534

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<210> 3535

<211> 1077

<212> DNA

<213> Enterobacter cloacae

<400> 3535

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<210> 3536

<211> 1527

<212> DNA

<213> Enterobacter cloacae

<400> 3536

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<210> 3537

<211> 636

<212> DNA

<213> Enterobacter cloacae

<400> 3537

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<210> 3538

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 3538

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<210> 3539

<211> 297

<212> DNA

<213> Enterobacter cloacae

<400> 3539

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gatgtttact	tcaataccgg	gatctgcaaa	cactcgggca	actgcgtgcg	cggcagcgcg	180
gcgctgttcg	acctgaagcg	taaaccatgg	atcgcgcttg	atgaagtaga	tgagaaaacg	240
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<210> 3540

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 3540

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agcgatgaag	ataagcgctt	gtttgtccgt	ctgcttgagt	ctgacgatcc	ggatttatct	180
aactggctga	tgaatcacgg	caagcccggc	gacaccgagt	tgcaacggat	ggtgcaatta	240
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<210> 3541

<211> 771

<212> DNA

<213> Enterobacter cloacae

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<210> 3542

<211> 702

<212> DNA

<213> Enterobacter cloacae

<400> 3542

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<210> 3543

<211> 456

<212> DNA

<213> Enterobacter cloacae

<400> 3543

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gcccgcgaga	atcacgggat	tacagaattg	aaggagataa	aatacgctat	tcttgagcgt	420
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<210> 3544

<211> 279

<212> DNA

<213> Enterobacter cloacae

<400> 3544

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gatgtagatc	caagcctgaa	agggcagggt	gtgggtaagc	agctggtggc	gaaggtggta	180
gagaagatgc	gcggggagaa	ccgtaaaatt	atcccgtgtg	gtccgtttgc	gaagcatgag	240
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<210> 3545

<211> 2958

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (35)

<400> 3545

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<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 3546

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<210> 3547

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 3547

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<210> 3548

<211> 1743

<212> DNA

<213> Enterobacter cloacae

<400> 3548

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<210> 3549

<211> 1260

<212> DNA

<213> Enterobacter cloacae

<400> 3549

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<210> 3550

<211> 648

<212> DNA

<213> Enterobacter cloacae

<400> 3550

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<210> 3551

<211> 2034

<212> DNA

<213> Enterobacter cloacae

<400> 3551

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<210> 3552

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 3552

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<210> 3553

<211> 1092

<212> DNA

<213> Enterobacter cloacae

<400> 3553

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<210> 3554

<211> 1797

<212> DNA

<213> Enterobacter cloacae

<400> 3554

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<210> 3555

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 3555

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<210> 3556

<211> 942

<212> DNA

<213> Enterobacter cloacae

<400> 3556

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<210> 3557

<211> 1677

<212> DNA

<213> Enterobacter cloacae

<400> 3557

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<210> 3558

<211> 744

<212> DNA

<213> Enterobacter cloacae

<400> 3558

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<210> 3559

<211> 750

<212> DNA

<213> Enterobacter cloacae

<400> 3559

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<210> 3560

<211> 684

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (13)

<220>

<221> unsure

<222> (67)

<220>

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<222> (219)

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<210> 3561

<211> 219

<212> DNA

<213> Enterobacter cloacae

<400> 3561

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<210> 3562

<211> 288

<212> DNA

<213> Enterobacter cloacae

<400> 3562

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<210> 3563

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 3563

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990

<210> 3564

<211> 972

<212> DNA

<213> Enterobacter cloacae

<400> 3564

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<210> 3565

<211> 1011

<212> DNA

<213> Enterobacter cloacae

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<210> 3566

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<400> 3566

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<210> 3567

<211> 696

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (693)

<400> 3567

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<210> 3568

<211> 1776

<212> DNA

<213> Enterobacter cloacae

<400> 3568

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<210> 3569

<211> 750

<212> DNA

<213> Enterobacter cloacae

<400> 3569

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<210> 3570

<211> 1734

<212> DNA

<213> Enterobacter cloacae

<400> 3570

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<210> 3571

<211> 1476

<212> DNA

<213> Enterobacter cloacae

<400> 3571

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<210> 3572

<211> 1818

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (1710)

<400> 3572

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<210> 3573

<211> 540

<212> DNA

<213> Enterobacter cloacae

<400> 3573

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<210> 3574

<211> 675

<212> DNA

<213> Enterobacter cloacae

<400> 3574

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<210> 3575

<211> 1293

<212> DNA

<213> Enterobacter cloacae

<400> 3575

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<210> 3576

<211> 453

<212> DNA

<213> Enterobacter cloacae

<400> 3576

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<210> 3577

<211> 387

<212> DNA

<213> Enterobacter cloacae

<400> 3577

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<210> 3578

<211> 486

<212> DNA

<213> Enterobacter cloacae

<400> 3578

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<210> 3579

<211> 2721

<212> DNA

<213> Enterobacter cloacae

<400> 3579

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 <211> 1689
 <212> DNA
 <213> Enterobacter cloacae

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 <212> DNA
 <213> Enterobacter cloacae

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<210> 3582
 <211> 909
 <212> DNA
 <213> Enterobacter cloacae

<400> 3582
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<210> 3583

<211> 777

<212> DNA

<213> Enterobacter cloacae

<400> 3583

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<210> 3584

<211> 1500

<212> DNA

<213> Enterobacter cloacae

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 <211> 1116
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3586
 <211> 1140
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3587
 <211> 1845
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3588

<211> 1980

<212> DNA

<213> Enterobacter cloacae

<400> 3588

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<210> 3589

<211> 339

<212> DNA

<213> Enterobacter cloacae

<400> 3589

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aaagcgcgtg	acattgcgtt	taaggagctg	ggcgagcagg	ccaaagcgtc	ggcgcgcgat	240
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<210> 3590

<211> 1944

<212> DNA

<213> Enterobacter cloacae

<400> 3590

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<210> 3591
 <211> 498
 <212> DNA
 <213> Enterobacter cloacae

<400> 3591
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 gtagaaaacg atggctaa 498

<210> 3592
 <211> 708
 <212> DNA
 <213> Enterobacter cloacae

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<210> 3593
 <211> 849
 <212> DNA
 <213> Enterobacter cloacae

<400> 3593
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<210> 3594
 <211> 537
 <212> DNA

<213> Enterobacter cloacae

<400> 3594

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<210> 3595

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 3595

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<210> 3596

<211> 393

<212> DNA

<213> Enterobacter cloacae

<400> 3596

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<210> 3597

<211> 2304

<212> DNA

<213> Enterobacter cloacae

<400> 3597

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<210> 3598

<211> 618

<212> DNA

<213> Enterobacter cloacae

<400> 3598

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<210> 3599

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 3599

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<210> 3600

<211> 600

<212> DNA

<213> Enterobacter cloacae

<400> 3600

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<210> 3601

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 3601

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<210> 3602

<211> 1356

<212> DNA

<213> Enterobacter cloacae

<400> 3602

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<210> 3603

<211> 1728

<212> DNA

<213> Enterobacter cloacae

<400> 3603

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<210> 3604
 <211> 426
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3605
 <211> 1251
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3605
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<210> 3606
 <211> 330
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3606
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<210> 3607
 <211> 1242
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3607

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<210> 3608

<211> 432

<212> DNA

<213> Enterobacter cloacae

<400> 3608

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ggcgtgatgg	cggcgtttat	gcaggcggtta	gggtttacgg	cgcaggcgaa	cgggtgggag	420
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<210> 3609

<211> 408

<212> DNA

<213> Enterobacter cloacae

<400> 3609

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ctgattttta	ccgcgttcat	gcatgcctta	cagatggtga	tgctgaaaaa	cggactgccg	300
aaagatagcc	caccgatgac	cggctggcag	cagctgcggg	tgtttatttt	cggcgtattt	360
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<210> 3610

<211> 753

<212> DNA

<213> Enterobacter cloacae

<400> 3610

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gttaatatgc	tttggtcatt	tatcgctgtc	tgttttttcg	catggcttta	cgtcgatgcg	180
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<210> 3611

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 3611

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<210> 3612

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 3612

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cttattacgc	tgtttgaaat	cgccccggag	gatattaccc	ctgaggcacg	tcttttacgag	180
gatctggacc	tgcacagcat	tgatgcgcgt	gatatgggtg	tgcacctgca	aaagaaaacg	240
ggccataaaa	tcaagcctga	aaccttcaaa	gcggtgcgca	cgggtgcagga	cgctcgtggac	300
gttggtggaac	agcttcagcg	cgacgcgtaa				330

<210> 3613

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 3613

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attggccgcy	ctatcgccct	tcagcttgcg	gcggacgggt	tcaccgtcgg	cgtgcattac	180
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<210> 3614

<211> 798

<212> DNA

<213> Enterobacter cloacae

<400> 3614

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agcgtcgact	cgtgaataa	aggcattcag	gcgctacagc	aggtgggtgoc	tggcgtaacag	180
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gccacgcacg	tcgatattct	ggtgaataac	gccgggatct	atggccagca	ggatttttat	300
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cccagctcgg	ttattcagcg	cgcgcgaacg	gtagaagaag	tggcgaaat	ggtgggtgat	720
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<210> 3615

<211> 2244

<212> DNA

<213> Enterobacter cloacae

<400> 3615

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<210> 3616

<211> 291

<212> DNA

<213> Enterobacter cloacae

<400> 3616

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gccgcgctct ttggcgacgg cctcggtctg gactcaatcg acgcccttga gctggggctg 180
gcggtaaaaa atcagtacgg cgtagtgttt tctgcgaaa gtgacgagat gcgtcagcac 240
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<210> 3617

<211> 384

<212> DNA

<213> Enterobacter cloacae

<400> 3617

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cctgctgcaa cgcagccagg cgtgagtggt cgtaaaaggc ccgctggatg ccgccgggca 300
acaggcctgg ggagatttct tctggcagca ccgcaatggc ctggtcgatc cggccaccgc 360
cgcccgctcg caaaacggcg gtga 384

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<210> 3618

<211> 543

<212> DNA

<213> Enterobacter cloacae

<400> 3618

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tttggcagct tcgagtgcac cattcatgcg gatagtgtct ccctcgccac gggccgcgtg 480
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<210> 3619

<211> 609

<212> DNA

<213> Enterobacter cloacae

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gacagcaccg ccagtcgct cccggtcagt cagctacgct tcggctcgct gagcctggcg 540
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<210> 3620

<211> 927

<212> DNA

<213> Enterobacter cloacae

<400> 3620
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gaagagacct accgagcca gtccctcggtc agctataacc tgtcgctttt gcaggagcgg 180
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<210> 3621

<211> 318

<212> DNA

<213> Enterobacter cloacae

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gatctacca ataaatag 318

<210> 3622

<211> 468

<212> DNA

<213> Enterobacter cloacae

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gtaaataatg cacaggcacc tgcccaccag atgcagtcac ctgctgaaaa aagtgcatt 180
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atgatgaaag ctaaaccogg agctaccaac gaaacagcaa agtcattttc tgaaatgagc 360

gagcatgaga aggccgcagc tgtacatgag aaggcgaata atgggtcagtc ttccgttgtt 420
caccagcagc aggctgataa gcacgcagc agatcaccc agaattaa 468

<210> 3623

<211> 699

<212> DNA

<213> Enterobacter cloacae

<400> 3623

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<210> 3624

<211> 1344

<212> DNA

<213> Enterobacter cloacae

<400> 3624

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caggagcgcg cgttgaacga agggtgctg cttttgagct gcggcgttta cggcaacgtt 1260
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<210> 3625

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 3625

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tcgcatgccc ctatggcaga cgacattaaa gttgcggtag tgggggcgat gtccggccct 180

gttgcccagt	ggggtgacat	ggagttcaac	ggcgcgcgtc	aggccatcaa	agatatcaac	240
gccaaaggcg	ggatcaaagg	cgacaagctg	gtgggcgtgg	agtatgacga	cgccctgcgat	300
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<210> 3626

<211> 1098

<212> DNA

<213> Enterobacter cloacae

<400> 3626

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gtgggtgatgg	ccgttggggc	gatgtttatc	gacctcttca	tgcaccgtca	cgataaaccg	180
atctcgctga	aaagcgcggt	tatgtgggtcc	atcttctggg	tcatgatggc	gatggccttc	240
gccggatttt	tatacgtgca	ccacggcgcg	gagatggcca	gtctgttctt	gaccggctat	300
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ttcggcgctgc	cggatagata	tcgctaccgc	gtgctctact	ggggcggtgt	cggggcgatt	420
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ggaaaacgtg	aggcctga					1098

<210> 3627

<211> 546

<212> DNA

<213> Enterobacter cloacae

<400> 3627

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gaaatttacg	ttaaaaacga	aaacacccctg	gactacogta	ttcacagtgg	tctggttggc	180
aaccgttggg	tgaagatca	gcaggccctac	atcgctccgtg	ttggggagag	catctataaa	240
atttcctgga	cggagccaac	cggtaactgac	gtgagcttga	tcgtgaacct	gggcgaccgc	300
ctgttccacg	gcaccatctt	cttcccgcgc	tgggtcatga	ataatccgga	aaaaaccgtc	360
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ccaaccgaag	tgattgatga	atttgccgcg	atcaccttctg	tcgctgactg	cggtgcgaat	480
gacgatagcg	tgatcaattg	cgcgccacgc	gagctgcctg	caaacttccc	ggaaaattta	540
aaataa						546

<210> 3628

<211> 246

<212> DNA

<213> Enterobacter cloacae

<400> 3628

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gagcgcgacg	gcattcagcag	ggaaggaatg	cgcggcagca	tgctgagaaa	cagacgggta	180
tgatcaaacg	agatgcgcac	gttgtcttct	agggcatcga	aatgggatac	cccgtccggc	240
ggatag						246

<210> 3629

<211> 285

<212> DNA

<213> Enterobacter cloacae

<400> 3629

cggggcgtaa	actacagccg	tttttacctg	aacgagaaga	aaatgaccga	cctgttttcc	60
agcccagacc	acacgcttga	tgtctagggc	ctccgttgcc	cggagccggt	aatgatgggtg	120
cgtaaaaccg	tccgtaacat	gcagagtggc	gaaacgctgc	tgatcgtcgc	cgatgaccgc	180
gctaccaccc	gtgatatccc	cggcttttgt	accttcctgg	aacatgaact	ggtggcgag	240
caaaccgaga	ccttgccgta	cgggtatttg	attcgtaagg	ggtaa		285

<210> 3630

<211> 1002

<212> DNA

<213> Enterobacter cloacae

<400> 3630

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gacatcgata	aaacgggtgtt	tatcaaggcg	acagagccgg	tgcgcgcgca	gtatggcgat	960
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<210> 3631

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 3631

gccggagtac	gtatgtccga	actctacctg	aagtggatgg	accgtctgta	cctgctcgcc	60
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tctcgctatg	tgctcaatcg	cggcgaatcc	tgcccgagagc	cgatcgccat	tatctgcatg	180
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ctgcctgtcg	ggtcggccat	tttgatcctg	tttgtgcttg	aacgcctgct	gtttggctcg	480
caggaaaaacc	gtccgggtcgt	gctgatcggc	aatcacagtt	aa		522

<210> 3632

<211> 1467

<212> DNA

<213> Enterobacter cloacae

<400> 3632

tcgcagatgg	caaaacaaaa	aaaacgtggc	ttcttttctc	ggttggggtt	cggtgaaaaa	60
gagcaagaaa	cagaacagaa	aaccgaagaa	cagcaggttg	tagaagagca	gtcacagcct	120
gaaacgcctg	tcgaaaccgc	tgccggttg	gaagcggaag	agccagcgca	cagcaaaagaa	180
gagattgaat	cctttgctga	agaggtgggt	gaggtcactg	agcaggttca	ggagagcgag	240
aagccagagc	cggttatcgt	tgaaccctt	accgaagcgc	cgcaggccgc	tatcgaacac	300

gaagcgctgc	cgctgccgga	agagggttaa	gotgaagagg	tttctgccga	agagtggcag	360
gccgaagcgg	aaaccggtga	aattggtgag	gcggtggaag	aagaggcggc	acttgagcca	420
gagctgaccg	acgaagagct	ggaagcccag	gcgctggcgg	cggaagcggc	tgaagaagcg	480
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tacatcggtg	tgggcgagcg	tattgaggat	ttacgtccgt	ttaaagcgga	cgactttatt	1440
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<210> 3633

<211> 1083

<212> DNA

<213> Enterobacter cloacae

<400> 3633

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aatgcgccta	agcgtgccaa	agcgacaccg	aaaccgaact	cccgcaaaac	caacgtcttt	180
aacgagcagg	tgcggtatgc	cttccagggc	gcgttgccag	atctgaaaag	caaaccgctg	240
gcgacgttcc	tgacggtgat	ggtgattgcc	atctccctga	cgtgcccag	cgtctgctat	300
atggtttaca	aaaacgtaaa	ccaggcgggc	tcacgtaact	atccgtcgcc	gcagatcacc	360
gtttatctgg	ataaaaccct	cgacgataac	gcggcggttc	aggtgggtggg	gcagattcag	420
gccgagcagg	gcgtggagaa	ggtgaactat	ctttcccgcg	atgaagcgct	gggcgaattc	480
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ctttacggcg	gcgcgttatt	aggtttttct	ggtgcatttc	tttcattgat	tttgtcagaa	900
attttggtga	tgcgctgtc	gtcagccgtc	accgaggtgg	cgcaggtttt	cggaactaag	960
tttgatatca	gtggtttagg	tttcgatgag	tgcctgctgt	tactgctggt	gtgctccatg	1020
atcggtggg	tggcggcag	gctggcaacg	gttcaacatt	tacgccactt	tactccgcac	1080
taa						1083

<210> 3634

<211> 1290

<212> DNA

<213> Enterobacter cloacae

<400> 3634

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gaggcgctga	tgatccagat	caccagtggg	gtgaataaat	ttaccctgct	ggcgatcccg	180
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ttttacggta	tgttgctggt	ggtgctgggg	atggtagcgt	acatcccggc	gatttcattg	1260
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<210> 3635

<211> 369

<212> DNA

<213> Enterobacter cloacae

<400> 3635

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<210> 3636

<211> 858

<212> DNA

<213> Enterobacter cloacae

<400> 3636

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gccgctatcg	aagcgtaa					858

<210> 3637

<211> 1164

<212> DNA

<213> Enterobacter cloacae

<400> 3637

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gcggagattg	ccacctggct	gaaagcgaag	tcggtggaaa	ccgtgatggg	gccgctgtcc	1080
tgggatgaga	agggcgattt	gaagggtctc	gagttcggcg	tgtttgactg	gcatgccaat	1140
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<210> 3638

<211> 2394

<212> DNA

<213> Enterobacter cloacae

<400> 3638

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<210> 3639

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3639

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<210> 3640

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 3640

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<210> 3641

<211> 3330

<212> DNA

<213> Enterobacter cloacae

<400> 3641

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<211> 294

<212> DNA

<213> Enterobacter cloacae

<400> 3642

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<210> 3643

<211> 2775

<212> DNA

<213> Enterobacter cloacae

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<210> 3644

<211> 2025

<212> DNA

<213> Enterobacter cloacae

<400> 3644

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<210> 3645

<211> 1725

<212> DNA

<213> Enterobacter cloacae

<400> 3645

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<210> 3646

<211> 936

<212> DNA

<213> Enterobacter cloacae

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<210> 3647

<211> 489

<212> DNA

<213> *Enterobacter cloacae*

<400> 3647
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<210> 3648

<211> 222

<212> DNA

<213> *Enterobacter cloacae*

<400> 3648
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tctctatact gcgcgccgat acccaacttt ttacttaccg gaggccacat ggatcccgat 180
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<210> 3649

<211> 918

<212> DNA

<213> *Enterobacter cloacae*

<400> 3649
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<210> 3650

<211> 1413

<212> DNA

<213> Enterobacter cloacae

<400> 3650

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<210> 3651

<211> 186

<212> DNA

<213> Enterobacter cloacae

<400> 3651

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ttatccctgt	cgacctgccg	ctatgaggct	caccgtccgg	ctgctgatgc	gcatttatca	180
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<210> 3652

<211> 1488

<212> DNA

<213> Enterobacter cloacae

<400> 3652

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<210> 3653

<211> 951

<212> DNA

<213> Enterobacter cloacae

<400> 3653

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<210> 3654

<211> 1551

<212> DNA

<213> Enterobacter cloacae

<400> 3654

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<210> 3655

<211> 300

<212> DNA

<213> Enterobacter cloacae

<400> 3655

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<210> 3656

<211> 2466

<212> DNA

<213> Enterobacter cloacae

<400> 3656

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<210> 3657

<211> 915

<212> DNA

<213> Enterobacter cloacae

<400> 3657

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<210> 3658

<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 3658

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<210> 3659

<211> 993

<212> DNA

<213> Enterobacter cloacae

<400> 3659

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<210> 3660

<211> 474

<212> DNA

<213> Enterobacter cloacae

<400> 3660

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catgctgagc	cggtttccct	cagctttgca	gtgaaaaagc	gcgccaatga	catcgcactc	420
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<210> 3661

<211> 1794

<212> DNA

<213> Enterobacter cloacae

<400> 3661

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acggccgggc	gtggcagtaa	cggcaaaaat	gacctctatg	gcattaagaa	actgcgcgag	180
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<210> 3662

<211> 1038

<212> DNA

<213> Enterobacter cloacae

<400> 3662

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<210> 3663

<211> 213

<212> DNA

<213> Enterobacter cloacae

<400> 3663

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gcggtgccct	gcttatcgag	ctggccatcg	gcggtaaaaa	tggtggagac	agggggaatg	180
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<210> 3664

<211> 1275

<212> DNA

<213> Enterobacter cloacae

<400> 3664

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ttaagtctga	aacggttaac	ccctcaaac	tgtoaggagc	tgttatttga	tgacgtgctc	180

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<210> 3665

<211> 1026

<212> DNA

<213> Enterobacter cloacae

<400> 3665

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<210> 3666

<211> 708

<212> DNA

<213> Enterobacter cloacae

<400> 3666

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<210> 3667

<211> 408

<212> DNA

<213> Enterobacter cloacae

<400> 3667

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<210> 3668

<211> 1449

<212> DNA

<213> Enterobacter cloacae

<400> 3668

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<210> 3669

<211> 978

<212> DNA

<213> Enterobacter cloacae

<400> 3669

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<211> 1272

<212> DNA

<213> Enterobacter cloacae

<400> 3670

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<210> 3671

<211> 1206

<212> DNA

<213> Enterobacter cloacae

<400> 3671

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<210> 3672

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 3672

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<210> 3673

<211> 1896

<212> DNA

<213> Enterobacter cloacae

<400> 3673

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<210> 3674

<211> 4983

<212> DNA

<213> *Enterobacter cloacae*

<400> 3674

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<210> 3675

<211> 535

<212> DNA

<213> Enterobacter cloacae

<400> 3675

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<210> 3676

<211> 1008

<212> DNA

<213> Enterobacter cloacae

<400> 3676

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<210> 3677

<211> 537

<212> DNA

<213> Enterobacter cloacae

<400> 3677

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<210> 3678

<211> 363

<212> DNA

<213> Enterobacter cloacae

<400> 3678

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<210> 3679

<211> 2343

<212> DNA

<213> Enterobacter cloacae

<400> 3679

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<210> 3680

<211> 633

<212> DNA

<213> Enterobacter cloacae

<400> 3680

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<210> 3681

<211> 912

<212> DNA

<213> Enterobacter cloacae

<400> 3681

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<210> 3682

<211> 1170

<212> DNA

<213> Enterobacter cloacae

<400> 3682

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<210> 3683

<211> 1323

<212> DNA

<213> Enterobacter cloacae

<400> 3683

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<210> 3684

<211> 651

<212> DNA

<213> *Enterobacter cloacae*

<400> 3684

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<210> 3685

<211> 807

<212> DNA

<213> *Enterobacter cloacae*

<400> 3685

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<210> 3686

<211> 495

<212> DNA

<213> *Enterobacter cloacae*

<400> 3686

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<210> 3687

<211> 1320

<212> DNA

<213> *Enterobacter cloacae*

<400> 3687

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<210> 3688

<211> 411

<212> DNA

<213> Enterobacter cloacae

<400> 3688

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attgctgaag	aactcgaact	gccgcgggtg	aaaattcact	gctcaattct	ggcagaagac	360
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<210> 3689

<211> 264

<212> DNA

<213> Enterobacter cloacae

<400> 3689

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ccgatctc	atccgaagac	cgtacgatcc	accgacatgc	accagtggat	ctgcgattta	180
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<210> 3690

<211> 1308

<212> DNA

<213> Enterobacter cloacae

<400> 3690

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<210> 3691

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 3691

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<210> 3692

<211> 2418

<212> DNA

<213> Enterobacter cloacae

<400> 3692

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gccgccctgc	cgtttgtcgt	caaaaaccgg	aaagtacagg	cacaggacgc	ggcggtttca	180
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tgtgatattc	gtgctcacgt	cagtgtggc	gtgtgaccc	gaatttcaac	gcgaccggat	300
aacgcgctgg	atccgcagat	gccagtgtg	cgccctgcg	ttcggggtcg	ggcttatcgg	360
aaatttgttt	atcatcccga	tccgtttaa	tatccaatga	aacgcgtggg	taaacgtggc	420
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<210> 3693

<211> 819

<212> DNA

<213> Enterobacter cloacae

<400> 3693

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acgcaacgca	gcgtgctgct	gccggcagcc	ggagcggttg	tgtggcgag	cctggggctg	180
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<210> 3694

<211> 516

<212> DNA

<213> Enterobacter cloacae

<400> 3694

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aacgcgggtg	caaaaaacgt	tattggcagc	atcttcgctc	gctttgaatc	agcagggttt	180
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gtggtatccg	tactggaagg	cgaaaaacgcg	gtacagcgctc	accgcgatct	gctgggtgca	360
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gagaacggca	cccacgggtc	cgactctgtt	gaatctgctg	cgcgcgaaat	cgctttcttc	480
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<210> 3695
 <211> 1311
 <212> DNA
 <213> Enterobacter cloacae

<400> 3695
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<210> 3696
 <211> 1011
 <212> DNA
 <213> Enterobacter cloacae

<400> 3696
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 aaggtctcca ccgttcgcga tattgaagaa gataaggcac ccgcgatct ggcttcaacg 180
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<210> 3697
 <211> 678
 <212> DNA
 <213> Enterobacter cloacae

<400> 3697
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<210> 3698

<211> 951

<212> DNA

<213> Enterobacter cloacae

<400> 3698

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<210> 3699

<211> 1353

<212> DNA

<213> Enterobacter cloacae

<400> 3699

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<210> 3700

<211> 1572

<212> DNA

<213> Enterobacter cloacae

<400> 3700

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<210> 3701

<211> 1380

<212> DNA

<213> Enterobacter cloacae

<400> 3701

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<210> 3702

<211> 813

<212> DNA

<213> Enterobacter cloacae

<400> 3702

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gatttcgtga	cgaacgtcga	taaagccgca	gaagcgatta	ttatcgaaac	gatccgcaaa	180
tcttaccgcg	agcacaccat	catcacccga	gaaagcgggt	aacatgaagg	taccgatcag	240
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<210> 3703

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3703

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gcggtcctgc	caaatatgat	taacttctac	aaaaatgtga	gtatcgctgg	cgcattttatt	420
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<210> 3704

<211> 783

<212> DNA

<213> Enterobacter cloacae

<400> 3704

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cagaagctgg	ggtttagcgg	ctttagcgag	tttatctggc	actgcaagca	gctgctttct	240
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cggttcgttg	ccaactatca	gcagaccttc	cagtgggtca	ctcaggacaa	acgccagcag	360
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tga 783

<210> 3705

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 3705

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ccgcagccga	cgggggagcg	tttctgcgta	aattcggctt	ccatgagctt	taccgatgat	420
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<210> 3706

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 3706

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<210> 3707

<211> 1926

<212> DNA

<213> Enterobacter cloacae

<400> 3707

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<210> 3708

<211> 636

<212> DNA

<213> Enterobacter cloacae

<400> 3708

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<210> 3709

<211> 1251

<212> DNA

<213> Enterobacter cloacae

<400> 3709

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<210> 3710

<211> 516
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3710
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<210> 3711
 <211> 339
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3711
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 gtggtgattg aggcgtttcc ggaaacgctg gcgggcgaga agggccagac agcagacgtt 180
 attttactcg ggccgcaaat cgcttatatg ctgccagaaa ttcaacgtct gctacccaat 240
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 aaagctgccg ttgcggcgat taaaaaagct gctaattaa 339

<210> 3712
 <211> 1374
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3712
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 gaattatggc tgggtggatgt tgaagaaggt caggagaagc tgaatattat ttttgaactg 180
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<210> 3713
 <211> 570
 <212> DNA

<213> Enterobacter cloacae

<400> 3713

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cgccagaccc	gctttttacg	cgaagggttt	gaagatcagc	tgataactga	gaaggcgaaa	420
ggccctgacg	ggatgagccg	cgagcagatc	gaatcgcgca	ttgtcgttcc	gcgtcatacc	480
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<210> 3714

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 3714

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<210> 3715

<211> 1938

<212> DNA

<213> Enterobacter cloacae

<400> 3715

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gataaagagg	tggaagcagg	caaagttgcc	gttcgcaccc	gccgtggtaa	agacctgggg	1860
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<210> 3716

<211> 321

<212> DNA

<213> Enterobacter cloacae

<400> 3716

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agagaagcga	tcgaaaaggc	tgaagaagct	ggagtagatt	tagttgaaat	cagccctaac	180
gccgaaccgc	cagtttgtcg	tatcatggac	tacggcaagt	tcctttatga	aaagagtaag	240
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<210> 3717

<211> 705

<212> DNA

<213> Enterobacter cloacae

<400> 3717

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cccgggttaa	atcagctggc	cgcgcgcgtg	gataaacctg	ttatcacgcc	tgatggctta	180
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gcgcatttctg	cgctctttgc	atgggtgttt	ggcgcgttgt	gctggctgac	caccacaacg	660
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<210> 3718

<211> 1500

<212> DNA

<213> Enterobacter cloacae

<400> 3718

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gggcagggtt	agcaggcctg	tcaggctgca	cgccgcgcgt	ttccggcgtg	ggcgaaaacgg	180
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gccgagctga	ccgcctcat	tgcttgcgaa	accagtaagc	cgcgctggga	ggcaacaacc	300
gaagtcacgg	cgatgatcaa	caaaattgcg	atatcggtga	aggcgtacca	taccgcacc	360
ggcgagcagc	ataccgagat	gccagacggc	gcggccacgc	tgcgccaccg	tccgcacggg	420

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gtactggcgg  tgtttggccc  gtataaacttc  cccgggcate  tgccgaacgg  gcacattgtg  480
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<210> 3719

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 3719

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acaagaggac  ggaatatgaa  caagaacgta  gcaggaatth  taagcgcagc  ggcggtactg  60
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gtaaaagacg  tcaaaaaagg  catgacgcgt  tcccagggtg  cagccattgc  cggtaaaccct  180
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cgtgatggta  aggcagagac  ctactttgtc  gccctggatg  atacgggtca  cgtgatcaat  300
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<210> 3720

<211> 291

<212> DNA

<213> Enterobacter cloacae

<400> 3720

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cagcacatga  ccatcgacac  taacggtcag  atggtgatga  aaagcaagcg  cgagttgaaa  240
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<210> 3721

<211> 1056

<212> DNA

<213> Enterobacter cloacae

<400> 3721

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gccaatatcg	acggcgtgaa	ggccatgacc	gacgtgaccg	gatttgggtct	gctggggcac	720
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gttcaggcga	cggctgccga	gtttggcatc	accctgacgg	ccattggtga	gctggtgacc	1020
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<210> 3722

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 3722

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caggctgata	gcattcgccc	ggatgtcgag	gttaacgtgc	cgccagaggt	ctttagcgc	180
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gaaggcgcag	tggtcagggc	ggatggcgtg	ctgttgacgt	gccagcgtga	tgaacgcacc	300
ctcagtacaa	accgcgtggt	ctggcgtcgc	gtaaaaagaat	aa		342

<210> 3723

<211> 1140

<212> DNA

<213> Enterobacter cloacae

<400> 3723

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<210> 3724

<211> 1359

<212> DNA

<213> Enterobacter cloacae

<400> 3724

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<210> 3725

<211> 975

<212> DNA

<213> Enterobacter cloacae

<400> 3725

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<210> 3726

<211> 708

<212> DNA

<213> Enterobacter cloacae

<400> 3726

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<210> 3727

<211> 1371

<212> DNA

<213> *Enterobacter cloacae*

<400> 3727

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cggttgacat tagccggggc aatgttcggt ttaattaaca acgtttttct gagctttgga 180
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<210> 3728

<211> 351

<212> DNA

<213> *Enterobacter cloacae*

<400> 3728

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aagcaggcta agcaggcgca cttcgttgcc gcgaaaacca tgatggagca gtcccgtacg 180
gcgttaaacc aagcgcactc ggtgcagacg aagcttatcg aaagcgacca gggcgaaggg 240
aagatgaaag tgagtctggt gctggtacat gcgcaggatc atctgatgac ctccatgctg 300
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<210> 3729

<211> 834

<212> DNA

<213> *Enterobacter cloacae*

<400> 3729

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tactacgagt tcacgattgt tctgacggcg cgtactatc aggagatcaa cggtaagcgc 180
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gatatcgctt acgaatcggg ttacagcagt cccagtctgt ttattaaaac ctttaaaaaa 780
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<210> 3730
 <211> 786
 <212> DNA
 <213> Enterobacter cloacae

<400> 3730
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<210> 3731
 <211> 267
 <212> DNA
 <213> Enterobacter cloacae

<400> 3731
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 tttcgcgatg tctggatgtt acggggtaaa tacgttgctt tcgtgctgat tggcagacac 180
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<210> 3732
 <211> 294
 <212> DNA
 <213> Enterobacter cloacae

<400> 3732
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 acggacgatg agggcaatat tcacgatctc ggctcactgg catttggcct gataagcccg 180
 ctgagtcagg aagaggtgaa ggcgctggcc agtagcctgg tggaaagcgt gactgacaaa 240
 gccacggaaa ttgatgtgga tagctgggaa aactggcata aaaaagaaca ataa 294

<210> 3733
 <211> 888
 <212> DNA
 <213> Enterobacter cloacae

<400> 3733
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<210> 3734

<211> 615

<212> DNA

<213> *Enterobacter cloacae*

<400> 3734

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<210> 3735

<211> 2283

<212> DNA

<213> *Enterobacter cloacae*

<400> 3735

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<210> 3736

<211> 951

<212> DNA

<213> Enterobacter cloacae

<400> 3736

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<210> 3737

<211> 483

<212> DNA

<213> Enterobacter cloacae

<400> 3737

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<210> 3738

<211> 1545

<212> DNA

<213> Enterobacter cloacae

<400> 3738

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cagttttacc	ggatctgtac	agtctgttcg	ccgcagcttg	accgctacgg	tatcgggctt	420
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<210> 3739

<211> 1404

<212> DNA

<213> Enterobacter cloacae

<400> 3739

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gcgctggccc	tgatctgcgg	cctgcctcca	ctctcctcca	cggcggctga	tatgcccac	180
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gagcgcggaa	cgctgcaaaa	cgtgaagcca	gccctgatt	ttggcgcgcc	gatcccgggc	960
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<210> 3740

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 3740

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ggcggaag	ttgaagccgg	tgagaccacg	ccggaagcgc	tgatccgcga	actgcgcgaa	180

gagctcggca	ttgaagctgt	gcccgcgcgg	tatgtggcaa	gccaccagcg	ggaggtgtcg	240
cagcggctga	ttcacctcca	cgcttggcat	gtgcctgaat	ttagcgggtga	gctgaaggcg	300
cattatcact	cggcgctggt	atgggtgtacg	ccagaagacg	cgttcacgta	tgattttagcc	360
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<210> 3741

<211> 924

<212> DNA

<213> Enterobacter cloacae

<400> 3741

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tcttacgtgc	agaatgacaa	taacctgact	tctgaggcgc	gtatgatact	ggatgctttt	180
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gccattgccc	tcgccgaagc	aggatgcgat	atcgtggggg	ttaaccgcaa	ggttcctgac	300
gaaacggcag	cgcgcgttac	ggcgcgtggga	cgacgcttta	tcgcgattcg	cgccgatctt	360
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<210> 3742

<211> 1407

<212> DNA

<213> Enterobacter cloacae

<400> 3742

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<210> 3743

<211> 882
 <212> DNA
 <213> Enterobacter cloacae

<400> 3743
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<210> 3744
 <211> 690
 <212> DNA
 <213> Enterobacter cloacae

<400> 3744
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<210> 3745
 <211> 1176
 <212> DNA
 <213> Enterobacter cloacae

<400> 3745
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<210> 3746

<211> 1359

<212> DNA

<213> Enterobacter cloacae

<400> 3746

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tatggcggcg	aggcgtctca	gaccaactac	gtgcgcgggg	cgaatatcgc	cgggttcgtg	1320
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<210> 3747

<211> 1128

<212> DNA

<213> Enterobacter cloacae

<400> 3747

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ctgcgttcag	acgggcagat	caacctgctt	aactccctgt	acgtggccgc	taattacccg	540
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gcgcacgcgc	atggctttga	cgtttttgcc	tcacctaaac	tgcaaccgct	gctggaagcg	660
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gttcatccga	tcaccccgca	gccgattggc	gtggtgacga	tttatccggg	gatctccgcc	780
gacgtgggtg	gcaacctcct	gcgcagccgc	gtgaaagcgc	tgatcctgcg	ctcctatggt	840
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gggattgtgg	tgggtcaacct	cacccagtggt	atgtccggca	aggtcaatat	gggcgggtac	960
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<210> 3748
 <211> 651
 <212> DNA
 <213> Enterobacter cloacae

<400> 3748
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 <213> Enterobacter cloacae

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 <212> DNA
 <213> Enterobacter cloacae

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<211> 684

<212> DNA

<213> Enterobacter cloacae

<400> 3751

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<210> 3752

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 3752

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<210> 3753

<211> 1143

<212> DNA

<213> Enterobacter cloacae

<400> 3753

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<210> 3754

<211> 261

<212> DNA

<213> Enterobacter cloacae

<400> 3754

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gacgcggcat acgccccac cagcgagtgg ggttcagcac cgcgccgaag tgtttttct 240
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<210> 3755

<211> 1866

<212> DNA

<213> Enterobacter cloacae

<400> 3755

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<211> 1575

<212> DNA

<213> Enterobacter cloacae

<400> 3756

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<211> 1521

<212> DNA

<213> Enterobacter cloacae

<400> 3757

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<211> 2919

<212> DNA

<213> Enterobacter cloacae

<400> 3758

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<210> 3759

<211> 499

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (471)

<400> 3759

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<210> 3760

<211> 1413

<212> DNA

<213> Enterobacter cloacae

<400> 3760

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<210> 3761
 <211> 1611
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3762
 <211> 1116
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3763

<211> 621
 <212> DNA
 <213> Enterobacter cloacae

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 cagcctgctt ttatgggtta a 621

<210> 3764
 <211> 1680
 <212> DNA
 <213> Enterobacter cloacae

<400> 3764
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 gtaccgttga ttcaccactg gctgctgata cagggccagc gcagcatgag cggcctgccc 1620
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<210> 3765
 <211> 1047
 <212> DNA
 <213> Enterobacter cloacae

<400> 3765
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<210> 3766

<211> 921

<212> DNA

<213> Enterobacter cloacae

<400> 3766

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<210> 3767

<211> 1770

<212> DNA

<213> Enterobacter cloacae

<400> 3767

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<210> 3768

<211> 828

<212> DNA

<213> Enterobacter cloacae

<400> 3768

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<210> 3769

<211> 2514

<212> DNA

<213> Enterobacter cloacae

<400> 3769

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<210> 3770

<211> 804

<212> DNA

<213> Enterobacter cloacae

<400> 3770

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<210> 3771

<211> 1263

<212> DNA

<213> Enterobacter cloacae

<400> 3771

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<210> 3772

<211> 513

<212> DNA

<213> Enterobacter cloacae

<400> 3772

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<210> 3773

<211> 399

<212> DNA

<213> Enterobacter cloacae

<400> 3773

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gcgctcggcg	atcacagccg	ggttgaacgg	atcgcaacgg	aaaaactgca	attacagcat	360
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<210> 3774

<211> 1782

<212> DNA

<213> Enterobacter cloacae

<400> 3774

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<210> 3775

<211> 1437

<212> DNA

<213> Enterobacter cloacae

<400> 3775

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<210> 3776

<211> 1278

<212> DNA

<213> Enterobacter cloacae

<400> 3776

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<210> 3777

<211> 564

<212> DNA

<213> Enterobacter cloacae

<400> 3777

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<210> 3778

<211> 1011

<212> DNA

<213> Enterobacter cloacae

<400> 3778

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<210> 3779

<211> 987

<212> DNA

<213> *Enterobacter cloacae*

<400> 3779

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<210> 3780

<211> 1509

<212> DNA

<213> *Enterobacter cloacae*

<400> 3780

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<210> 3781

<211> 1416

<212> DNA

<213> *Enterobacter cloacae*

<400> 3781

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<210> 3782

<211> 1479

<212> DNA

<213> Enterobacter cloacae

<400> 3782

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<210> 3783

<211> 1023

<212> DNA

<213> Enterobacter cloacae

<400> 3783
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<210> 3784

<211> 1755

<212> DNA

<213> *Enterobacter cloacae*

<400> 3784
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<210> 3785

<211> 1014

<212> DNA

<213> *Enterobacter cloacae*

<400> 3785

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<210> 3786

<211> 513

<212> DNA

<213> *Enterobacter cloacae*

<400> 3786

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gaatgtcaga	tggatagcgc	cgggcgatta	ttgattgcgc	ctgtgttgcg	gcaacatgcc	360
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<210> 3787

<211> 1128

<212> DNA

<213> *Enterobacter cloacae*

<400> 3787

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1128

<210> 3788

<211> 1107

<212> DNA

<213> Enterobacter cloacae

<400> 3788

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catttaatgg	aacagggctg	gcagggtacg	tggctgggaa	ccgcagaccg	catggaagcc	180
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gagatggcgc	aacgcgcacg	cgcgaccgct	atcccggtat	caacggaacg	ggtggcaaaa	1080
gaagtgaagc	tggcagccca	ggcataa				1107

<210> 3789

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 3789

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gaaggtggcg	tggacgcgca	tcgggttgat	ccgaaagagg	tggacgtcac	gcagctgaaa	180
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<210> 3790

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 3790

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accctactga	gcggccagcg	ggcggagcaa	gacttcaaaa	aatcattcca	ggaaaataag	180
aaccgaaaaa	cggaagagga	gcaccagcgc	aggcaggaag	cggtcgaaaa	acatccgacc	240

acctcgcagc	agcaccgcga	ggagcgaacg	catccggaga	ccggaaagca	ggcgcagaaa	300
gagaaagaag	ggaaaaccac	gcgaatcgag	gacgaagcgg	agaaagagag	cgaggcgcag	360
ctcggcaacc	agaaagcgca	aatcacgaaa	cccgagaatc	aggagcgcag	gcgcaggcag	420
gagaacgata	aggcgatcag	ggataaccgc	gtcacgcagc	attaa		465

<210> 3791

<211> 729

<212> DNA

<213> Enterobacter cloacae

<400> 3791

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aagaaagtca	cactgacgtt	acgcctcgcg	ccggccaata	ccgggggtcat	ctatcgtcgc	120
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caatcccgcg	gcctgtgcct	gggcggcagc	ttcgattgtg	ccatcgttgt	tgacgattat	660
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gacgcgatac						729

<210> 3792

<211> 846

<212> DNA

<213> Enterobacter cloacae

<400> 3792

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gccgcgcgac	gcgaaaaagg	cgtgaacgtg	gtgctcacca	ccggacgccc	gtatgccggg	180
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<210> 3793

<211> 978

<212> DNA

<213> Enterobacter cloacae

<400> 3793

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cgggatgttg	ctgcgggtgga	aggcgacacg	gcatttcagg	caggcataag	gagcatcgct	960
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<210> 3794

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 3794

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ccgggcggtg	gagtacggca	tgaccgtttg	cccgggttgc	gccacggcta	cagaagcctt	120
tgccgccttc	gatgcaggcg	cacagtctct	caaaattttc	ccgtcgtcgg	cctttggtcc	180
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cggcgctcag	ccggaaaacc	tggtgcagtg	gataaaagcg	ggctgtgtgg	gcgccgggct	300
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<210> 3795

<211> 1203

<212> DNA

<213> Enterobacter cloacae

<400> 3795

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gacgaaggcg	tggttggtcg	gggcgagccg	gtgattgaag	gccgtgcgcg	caccgttgaa	180
gcgcgcgttc	acgagctggg	cgaataacctg	attggccagg	atccggcgcg	catcaacgac	240
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ttaacgaagc	cgggccttgg	cgtggagatc	gacgaagcca	aagtcattga	gctgagtaaa	1140
agtgcgcggg	actggcgtaa	cccactgtgg	cgtcatgaag	acggttccgt	agccgagtg	1200
taa						1203

<210> 3796

<211> 1398

<212> DNA

<213> Enterobacter cloacae

<400> 3796

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<210> 3797

<211> 1281

<212> DNA

<213> Enterobacter cloacae

<400> 3797

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<210> 3798

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 3798

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<210> 3799

<211> 1851

<212> DNA

<213> Enterobacter cloacae

<400> 3799

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<210> 3800

<211> 1674

<212> DNA

<213> Enterobacter cloacae

<400> 3800

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<210> 3801

<211> 711

<212> DNA

<213> Enterobacter cloacae

<400> 3801

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<210> 3802

<211> 954

<212> DNA

<213> Enterobacter cloacae

<400> 3802

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tcgatcgccc	agtgtgtggc	ggcgccgatg	ctgggggatt	ttaccgcgcg	ctaccgctcg	420
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<210> 3803

<211> 1116

<212> DNA

<213> Enterobacter cloacae

<400> 3803

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<210> 3804

<211> 462

<212> DNA

<213> Enterobacter cloacae

<400> 3804

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<210> 3805

<211> 1233

<212> DNA

<213> Enterobacter cloacae

<400> 3805

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<210> 3806

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 3806

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<210> 3807

<211> 1038

<212> DNA

<213> Enterobacter cloacae

<400> 3807

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<210> 3808

<211> 717

<212> DNA

<213> Enterobacter cloacae

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<210> 3809

<211> 630

<212> DNA

<213> Enterobacter cloacae

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<210> 3810

<211> 378

<212> DNA

<213> Enterobacter cloacae

<400> 3810
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<210> 3811

<211> 459

<212> DNA

<213> Enterobacter cloacae

<400> 3811
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<210> 3812
 <211> 429
 <212> DNA
 <213> Enterobacter cloacae

<400> 3812
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 tttaaggatg aaattggtag taaatcgatg gtttcacggg ttctgaatgg tcagagacag 360
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 attgagtga 429

<210> 3813
 <211> 1731
 <212> DNA
 <213> Enterobacter cloacae

<400> 3813
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<210> 3814
 <211> 291
 <212> DNA
 <213> Enterobacter cloacae

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 cgtctggagc agatgatagc gcagatcgac aagctggaag acgtcaccaa agtggcgcg 240

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291

<210> 3815

<211> 1515

<212> DNA

<213> Enterobacter cloacae

<400> 3815

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<210> 3816

<211> 1017

<212> DNA

<213> Enterobacter cloacae

<400> 3816

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<210> 3817

<211> 531

<212> DNA

<213> Enterobacter cloacae

<400> 3817

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aacgacacta	cactgtggcc	gaactactac	agcaacgccg	aagatattcg	ttttcacgac	180
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cctgcacagg	aacttgctcg	caccgtgccg	aatccgatga	tcaacgggca	ccaggagtgg	480
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<210> 3818

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<400> 3818

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<210> 3819

<211> 2430

<212> DNA

<213> Enterobacter cloacae

<400> 3819

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<210> 3820

<211> 429

<212> DNA

<213> Enterobacter cloacae

<400> 3820

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<210> 3821

<211> 1479

<212> DNA

<213> Enterobacter cloacae

<400> 3821

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ccgctgaccg	tgggtgatat	tccgcacttc	cagaaaggac	tcatgagcca	gcagggtggcg	1320
gtggaaaaac	tgggtggtgga	cgctggggag	cagcgctcgt	atcagaaact	ctggcaggcg	1380
attacactgt	cgaaaaccgt	accgagcgca	tcggtggcga	aagcgattct	ggacgatctg	1440
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<210> 3822

<211> 363

<212> DNA

<213> Enterobacter cloacae

<400> 3822

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gctcttgcca	ttaagcacia	ctggcaccgc	acggggcgcg	cattctggat	ctccattggt	180
gtgctggcgc	tggtagccat	catttttatg	cgctacaccc	gcagccgtaa	cctgatggac	240
gtgtcgcaga	acgactttgc	gcagccgaaa	gcggtgcggg	ataagttcct	catcgccctg	300
gccgtgctgt	cgttgtcact	gctgtttgcg	gtaaccacaa	ttcaacaaat	tttgcacctg	360
tag						363

<210> 3823

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 3823

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gcggtaaagg	agttcccgc	acacagagaa	gagcttctct	ttttaggacg	agttattgaa	120
aagagccact	gcccgaacgc	cgctgcactg	agaaaaactt	tcccaacgc	ggataacttc	180
aagtatcttg	ataagcatta	tgttattgat	attgcaaata	acaatctcag	agtagtggct	240
ctcatcttct	ttgaaagcca	aaagttttat	gtgcgcgatg	tttttactca	taaggaatat	300
gaccgtttta	cggagaaaaca	tcgcactaag	gggaagaaat	ga		342

<210> 3824

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 3824

cgcagatcga	caagctggaa	gacgtcacca	aagtggcgcg	caaccagtcc	gatccaccca	60
tgtttaacaa	aattgcgggtg	ttcttogaat	agatcgctta	aggtaagcgt	ctttcgctct	120
tgtaggccgg	ataagcgcag	cgccatccgg	ctttttcaga	ccgcaggaa	acacatgacc	180
accatcgccc	ttattgacga	ccaccttacc	gtccgctctg	gctttgcccc	gcttctcaac	240
ctcgaaccgg	atttccagggt	cgtggccgag	tttggctccg	gtcgcgaggg	gctggcgggc	300
ctgccggggc	gcgggggtgca	ggtctgtacc	tgcgatattc	caatgccgga	tctctccggg	360
cttgagctgt	taagccagct	gccgaaagga	atggcgacca	ttatgctctc	ggtccacgac	420
agcccgggcg	tggctcgagca	ggcgctcaac	gcggggggcg	gcgggttcc	ctcaaaacgc	480
tgtagcccg	atgagctgat	cgcgcgcgtg	cgcaactgtc	ccaccggcgg	ctgctacctg	540
acgcgcgata	tgcctatcaa	gctggcggcg	ggacggcagg	atccactcac	cagacgcgag	600
cgtcagggtg	cagagaaaact	tgcctcaggc	atgtcgggtg	aagagattgc	cgtagagctg	660
ggattgtcgc	caaagaccgt	tcacgttcat	cgcgccaacc	tgatggaaaa	actcaacgtc	720
agtaacgatg	tcgagctggc	gcgcgcgtatg	tttgacagct	ggcaatga		768

<210> 3825

<211> 1320
 <212> DNA
 <213> Enterobacter cloacae

<400> 3825

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ctgtttctact	ttaccogcaa	aagcttcaac	gccgcgcgcg	cggagatcct	cgcgagcggc	180
gtgatgaccc	gcaccgacat	cggcctgctg	gcgacgctgt	ttacatcac	ctacggcctg	240
togaagttct	tctccggcat	cgtcagcgat	cgtcccaacg	cgcgttattt	tatgggcgtc	300
gggtgatcg	ccaccggcgt	ggtgaatatt	ctgtttggct	tctccacctc	gctctgggcc	360
ttcgccctgc	tgtgggcgct	gaacgccttt	ttccagggt	ggggcgcgcg	ggtctgcgcc	420
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accgcgcata	acgtcggcgg	ggcgtgatc	ccgatggtgg	tgggtgccgc	ggcgtgcac	540
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gcgcgggtga	tgcacatctg	gcactggagc	gggttcttcg	cggtgatcgc	catcgcggcg	1260
ggcatctccg	ccctgctttt	actgccgttt	ttgcacgcgc	aggcaccgcg	cgaagcgtga	1320

<210> 3826
 <211> 1524
 <212> DNA
 <213> Enterobacter cloacae

<400> 3826

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agtaaaccaa	ccatgctggc	cttcttaaac	cagggtgcga	agccgaccct	ggatctgccg	180
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atctcgacct	acgggctgag	catgacccaa	ctggggatga	ttggcctggg	cttttccatc	360
acctacggcg	tggggaaaac	ggttgtgtcc	tactacgcgg	acggcaaaaa	caccaagcag	420
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cagagtaccg	gcgggtcgtg	cagctactcc	accattacca	aatggacccc	acgccgcaag	600
cgtggttcc	acctcggcat	gtggaacatc	tcccacaacc	tcggcggagc	gggcgcggct	660
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atcgtcctga	tggcgatggt	agcgggtgctg	gaagaacgta	aaattcgccg	tgagaatcgt	1500
gcgcagaaat	taaaagtagc	ctga				1524

<210> 3827
 <211> 315
 <212> DNA
 <213> Enterobacter cloacae

<400> 3827
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 cagtccccga gcctgtgctt tgaagccctg cacgcggcgc gtcagggcaa ccttgacgag 120
 gccaaaagcc tgctgcgcga agccgacggc tacgcgcgcc aggcgcacaa gatgcagacc 180
 aaactgattg agcaggacgc gggcgaagcc cgcagccga tgacattaat tatggtgcac 240
 gcgcaggatc atttaatgaa ttcgctatta gcgcgtgaat tatctgaaga gattattcat 300
 ttatatcaga gatag 315

<210> 3828
 <211> 1407
 <212> DNA
 <213> Enterobacter cloacae

<400> 3828
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 atcgacgcca ttgtggcgaa agcgggtgat aaagccctgg ccgagcgta ggctaaaatg 180
 gatgcggcgg tcgcgaaaaa agcggacgtg gtgaccgagc cgcagagcgc ggcgcaatcc 240
 ccggatatgg cgatcccgtt cgggggttaa tttaccggct acgcccgtca cggcgcgcac 300
 ttccaggctg ccgatcagaa atacgtggct gtcgatggct cctacaacgg cgcgtccgcg 360
 atcggtcgtc tgggtaacga aggcaacggc ggcgagttcc agctctccaa agctttcaag 420
 ggcgaaaacg gcgccatctg ggacatcaac gtgatgatcg accactgggg cgacgaagtt 480
 aacctcaaga aagcctacgc cggcgtgacc aacattatgg cctccaaccc gaacgcctac 540
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 gccacctcta aaatccacgg catgaagctc ggtccgctgg atctggagct gtacgccaac 840
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 aattctgaca acagcgtgtt caataaaaacc gaagacctga ccacggtcta cgccagcttc 1020
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 tacgacaacg gcggcgacaa caagggtctg aagctgaccc tgtcgcagaa catgtctatc 1260
 gccatggggc cggagttccg cccgatgctg cgcttctacg tgaccggcgg caagggtgat 1320
 aacgaacgca ccgcgcgcgt gaacaacacc aaagatgaga cgctggacga cttcaacgtc 1380
 ggcgcgatgt gggaggcgtg gttctaa 1407

<210> 3829
 <211> 1050
 <212> DNA
 <213> Enterobacter cloacae

<400> 3829
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 aacgacaaca taacagggga gaacatgggt tccacacgca aagggatgct caacgtcctg 180
 atcgccgcgg ttttatgggg cagttccggg gtttgccgc agtacatcat ggagaaaagc 240
 cacatttctt cgccttacct gacctgggt cgtctgctgt ttaccggcgt gatcctgttg 300
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 ctacgcctgc tgtttttctc gctgggttgg cgcctcaccc tgcagctcac cttcctgtg 420
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 atcgtggcat ggtttgcgct ggcgcggaaa acgcgtcccg gcataattgt cttatccgcg 540
 attttcacgt cgtttgtggg taccttccct ctgggtaccc acggcgaccc gacgtcgtc 600
 tccatctcgc ctgcgcgcgt gttcttcggt atcgccctcag cgtttgccgc ggcgttttac 660

accacctatc	catcgacgct	gattgcccgc	tacggcacgc	tgccgattgt	cggtctggagt	720
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atcgacggcg	gcctgctgct	ggcgtttttc	tacctggtgg	tgattggcac	cgcgctgacg	840
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tgcgccgaac	cgctgagcag	cgcgctgctg	tcggtggtgt	tgctgggggt	ggcattcacc	960
ctgccggact	ggctggggac	gctgttgatt	gtgtcgtcgg	tggtgttgat	ttcgatggat	1020
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<210> 3830

<211> 912

<212> DNA

<213> Enterobacter cloacae

<400> 3830

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gccgtgagcg	gcatgctcaa	ccgcctgcgg	gactacttcg	acgatccgct	ctttatccgc	180
gccccgcacg	gcatggtgcc	aaccacgcgc	gcggaagcgc	tgcccgctcc	ggtgaagcgc	240
attctcgcg	atctcgacgt	gctgcttcag	cccgttgcc	ttgacccaaa	taccgctcgc	300
ctcaccttca	ctcttgccgc	tacggattat	gcacttcggg	cggttgttgt	gcggtttatc	360
gccgccctta	aaacacaggc	gcctggcata	cgcgtgcgcg	tggtgcccgt	tacccccggt	420
agccttgta	gccagcttga	gcagggcgct	attgacgtag	cgttatcac	ccccacacc	480
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<210> 3831

<211> 1341

<212> DNA

<213> Enterobacter cloacae

<400> 3831

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gttggcgcga	tgatggggat	gagcccgcgt	gatatggtta	acgccattga	gagcgggatt	180
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cacggtcttg	gctctatcgc	caacattttg	ctgattatcg	gtgcggggcg	ggcgttcaac	960
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atgcacccta	tccttctcgc	ctggctggtg	gcactggtgc	tgacgcgcgc	cgtgggttcg	1080
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aacgtaagcc	cggagatcat	caccattgcc	atcgggtccg	gcgctattgg	ctgcacgatc	1200
gtgaccgatt	ctctcttctg	gctggttaag	cagtactcgc	gcgcgacct	gaatgagacc	1260
ttcaaatact	atacgacggc	gacgtttatc	gcctcgggtg	ttgcacttgg	cggcacattc	1320
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<210> 3832
 <211> 756
 <212> DNA
 <213> Enterobacter cloacae

<400> 3832
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 gagtttggcg tagcccgat gaccgtccgc aaagcgtggt atctgctggt aagctggggg 180
 ctggttgaac gtcgacacgg tagcgggacg ttctgtggcg gcaaagacgt tcatcatgaa 240
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 tattccgtga tggtccggaa cacaagcgat taccagggtg actaccatct gggcggtatc 720
 caccgggaag acttattagc ccattcccca gaatag 756

<210> 3833
 <211> 342
 <212> DNA
 <213> Enterobacter cloacae

<400> 3833
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 cagtacgggt tattttctct ttacctcagc cggaatgcgt ga 342

<210> 3834
 <211> 1368
 <212> DNA
 <213> Enterobacter cloacae

<400> 3834
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 cgagaggggt aaaccacgtg ggactactgg tttgcccgcg agccgaaccg ttttcacaac 120
 ggcgtggggc cgcagcacac ctccacgttt tatcagcact ggaaaacgga cattcagctg 180
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 gacggcatcg gtgaagtga cccggacgcg gtgcattttt acaatcaggt cattgatgag 300
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 cagatatgct tcgagctgtt cggcgacgcg gtgctgcact gggttacctt caacgagccg 480
 atcgtgccgg ttgaaggcgg ttatctgtac gacttccact accccaacgt agtgatttc 540
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1368

<210> 3835

<211> 855

<212> DNA

<213> Enterobacter cloacae

<400> 3835

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<210> 3836

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 3836

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<210> 3837

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 3837

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<210> 3838

<211> 1446

<212> DNA

<213> *Enterobacter cloacae*

<400> 3838

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<210> 3839

<211> 1059

<212> DNA

<213> *Enterobacter cloacae*

<400> 3839

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<210> 3840

<211> 291

<212> DNA

<213> *Enterobacter cloacae*

<400> 3840

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<210> 3841

<211> 1230

<212> DNA

<213> Enterobacter cloacae

<400> 3841

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<210> 3842

<211> 1389

<212> DNA

<213> Enterobacter cloacae

<400> 3842

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<210> 3843

<211> 1983

<212> DNA

<213> Enterobacter cloacae

<400> 3843

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<211> 1680

<212> DNA

<213> Enterobacter cloacae

<400> 3844

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<210> 3845

<211> 1203

<212> DNA

<213> Enterobacter cloacae

<400> 3845

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gaagccctgt	cactgattta	caacaaagac	ctggtgccaa	acccaccgaa	aacctgggaa	480
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gcaagcggtc	gccagactgt	cgatgcgcga	ctgaaagatg	ctcagggccg	tattactaag	1200
taa						1203

<210> 3846

<211> 909

<212> DNA

<213> Enterobacter cloacae

<220>

<221> unsure

<222> (744)

<400> 3846

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aaagggttaa						909

<210> 3847

<211> 282

<212> DNA

<213> Enterobacter cloacae

<400> 3847

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cgttttcac	gaaagcgagc	accacaaaca	gttgcggacc	atcgttttag	tgcagtact	180
ggctggcata	cgccatgttc	tgaagtctg	catcggtcag	atgcacgcc	ggcgtgccga	240
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<210> 3848

<211> 348

<212> DNA

<213> Enterobacter cloacae

<400> 3848

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tccatcatca	tgttaattat	ctacgtcggc	tttattctgc	tgatcgctt	tgcgccgcac	180
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<210> 3849

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 3849

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ctgtcgcaca	gcgcgcaggg	gtggttgcaa	tgtgtgagg	ggttttgggt	gccctga	897

<210> 3850

<211> 240

<212> DNA

<213> Enterobacter cloacae

<400> 3850

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cagcggccca	tttttgatat	cgcaatggat	ctgggctatg	tgtcgcagca	gaccttttcc	180
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<210> 3851

<211> 333

<212> DNA

<213> Enterobacter cloacae

<400> 3851

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gccagcacgt	taaacattca	gttcgaaag	tccgactacg	caggtcttgc	tgtgattagc	180
accctgttag	ggtttaggcg	cgcagctctg	ttcgcaacag	gtttgctcgg	tattacgctg	240
gtggatatag	ccgccgtctg	ggaaaacatt	aaagtgggtga	tggttgaagc	catgagccac	300
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<210> 3852

<211> 2823

<212> DNA

<213> Enterobacter cloacae

<400> 3852

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<210> 3853

<211> 303

<212> DNA

<213> Enterobacter cloacae

<400> 3853

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cggggagtac	gtttttttgc	cgccgcagaa	accggggctg	gagaagagaa	cggtatcgtc	240
aatatcgaag	cccacggcca	tccgcggcgc	accgcgcagg	ctgttttcaa	tttgtgccac	300
tga						303

<210> 3854

<211> 1110

<212> DNA

<213> Enterobacter cloacae

<400> 3854

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<210> 3855

<211> 2502

<212> DNA

<213> Enterobacter cloacae

<400> 3855

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<210> 3856

<211> 1557

<212> DNA

<213> Enterobacter cloacae

<400> 3856

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<210> 3857

<211> 552

<212> DNA

<213> Enterobacter cloacae

<400> 3857

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cacgcgctgg	acgttgctgg	catcagacc	cgcacgcac	atacggccgc	tgccgatcag	180
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gttcggcggg	ctggagtaga	tacggcggac	cgtcgccttc	agctggccga	gtacgcgtcc	480
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<210> 3858

<211> 522

<212> DNA

<213> Enterobacter cloacae

<400> 3858

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<210> 3859

<211> 552

<212> DNA

<213> Enterobacter cloacae

<400> 3859

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<210> 3860

<211> 216

<212> DNA

<213> Enterobacter cloacae

<400> 3860

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<210> 3861

<211> 2139

<212> DNA

<213> Enterobacter cloacae

<400> 3861

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<210> 3862

<211> 468

<212> DNA

<213> *Enterobacter cloacae*

<400> 3862

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<210> 3863

<211> 570

<212> DNA

<213> *Enterobacter cloacae*

<400> 3863

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<210> 3864

<211> 882

<212> DNA

<213> *Enterobacter cloacae*

<400> 3864

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<210> 3865

<211> 381

<212> DNA

<213> *Enterobacter cloacae*

<400> 3865

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<210> 3866

<211> 633

<212> DNA

<213> Enterobacter cloacae

<400> 3866

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<210> 3867

<211> 1380

<212> DNA

<213> Enterobacter cloacae

<400> 3867

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<210> 3868

<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 3868

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<210> 3869

<211> 1089

<212> DNA

<213> Enterobacter cloacae

<400> 3869

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<210> 3870

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 3870

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<210> 3871

<211> 225

<212> DNA

<213> Enterobacter cloacae

<400> 3871

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tgggtgcggg	cgccccgaac	ttcgatctta	tccattcacc	tttcccgggt	ggaacacgga	180
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<210> 3872

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3872

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aaaagtatcc	gtaacgccgg	aaaccagcgg	cgctacacgc	gcgatgtgct	ccgctacgtg	180
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ggctgcattg	gttgccgggtg	tttatcacgt	agcgattgcc	cgctgcgtaa	cccgggtgac	420
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<210> 3873

<211> 1794

<212> DNA

<213> Enterobacter cloacae

<400> 3873

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gagcgtgccg	agctgtatca	cctgcgcgcg	acgcggcaga	tcagtaacga	gacgctgcaa	1740
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<210> 3874

<211> 756
 <212> DNA
 <213> Enterobacter cloacae

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 tttgccaaca agcgccctgta tcgcgccttt cgcgcgctgc cgctgatgcc gttggtcttt 180
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 tttgggatgg cggtgggcga tatgctgttt ctgcggcttt ctattcggga aggaatggcc 600
 aaaggcgctg gatttgccgc ggctgcgcac ggcgcgggca cggcacgttc ctatgagctg 660
 ggacagcagg agggcggtgt cgcgagcctg gtgatgatgc tgcggggcgt cacgatggtg 720
 ctgatcgcac cgttggtggc gtggatgatg ttttaa 756

<210> 3875
 <211> 1260
 <212> DNA
 <213> Enterobacter cloacae

<400> 3875
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 tcataccctt tcagtatgtc tccatattca tgcagttttg atggtgcgga gatttcattg 180
 aggaagtcat tttctatgaa aaatttgaaa gtcagcctgg cctggcagat cctgctggcc 240
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<210> 3876
 <211> 840
 <212> DNA
 <213> Enterobacter cloacae

<400> 3876
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<210> 3877

<211> 369

<212> DNA

<213> Enterobacter cloacae

<400> 3877

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caacttattt	ttggcatgat	tcttgtaacg	atcgcagcat	cattcgggaa	ctcgtgggag	120
agcaccatgc	ttgaactact	ttttgtgatt	ggtttcttta	tcattgctgat	ggtcacgggc	180
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ggtttatttg	ccttgacgat	taaactcttg	ccgtgggttac	ttctggcgat	tgcggttgta	300
tgggcgatac	gggcgattaa	atcgccaaaa	ctgcccagtt	atcagcgtaa	taaccgcttc	360
cgttactaa						369

<210> 3878

<211> 1209

<212> DNA

<213> Enterobacter cloacae

<400> 3878

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<210> 3879

<211> 549

<212> DNA

<213> Enterobacter cloacae

<400> 3879

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<210> 3880

<211> 1476

<212> DNA

<213> Enterobacter cloacae

<400> 3880

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<210> 3881

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 3881

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<210> 3882

<211> 1419

<212> DNA

<213> Enterobacter cloacae

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<210> 3883
 <211> 1893
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3883
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<210> 3884

<211> 681

<212> DNA

<213> Enterobacter cloacae

<400> 3884

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ctgtgggaca	gcatgttcgg	cacgcggggc	gtgcatctga	ccgatgacga	acttcagaac	180
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<210> 3885

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 3885

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gaagaggggtg	ccacattcgc	tatcggtttg	ccgccagagc	gttgccatct	gttccgtgag	1080
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<210> 3886

<211> 1353

<212> DNA

<213> Enterobacter cloacae

<400> 3886

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gacttttaag	gttatgtctg	ttccggcatt	ggctggaccg	gaagtggcgg	tgaacaacaa	180
tgtttccagg	caacaggcgc	acaaagtaaa	taccgtctcg	gtaacgaatg	tgaaccttac	240
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<210> 3887

<211> 996

<212> DNA

<213> Enterobacter cloacae

<400> 3887

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<210> 3888

<211> 225

<212> DNA

<213> Enterobacter cloacae

<400> 3888

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aaagcgaaaag	aacagtgggg	taagctgaca	gatgacgata	tgaccgtcat	tgaaggtaag	120
cgcgatcagc	tggtaggtaa	aatccaggag	cgctacgggt	acgaaaaaga	tcaggcgga	180
aacgaagtca	aagactggga	aaccgcgaac	gactaccgct	ggtaa		225

<210> 3889

<211> 1452

<212> DNA

<213> Enterobacter cloacae

<400> 3889

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cactcgattg	aagcgggaaca	gtcgggtgttg	ggcgggttta	tgctggataa	cgaacgctgg	180
gacgacgtcg	ccgagcgcgt	tgctcgggaa	gacttctata	cccgcgcgca	ccgccacatc	240
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<210> 3890

<211> 738

<212> DNA

<213> Enterobacter cloacae

<400> 3890

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<210> 3891

<211> 384

<212> DNA

<213> Enterobacter cloacae

<400> 3891

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<210> 3892

<211> 588

<212> DNA

<213> *Enterobacter cloacae*

<400> 3892

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<210> 3893

<211> 1650

<212> DNA

<213> *Enterobacter cloacae*

<400> 3893

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<210> 3894

<211> 477

<212> DNA

<213> *Enterobacter cloacae*

<400> 3894

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<210> 3898

<211> 1122

<212> DNA

<213> Enterobacter cloacae

<400> 3898

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<210> 3899

<211> 984

<212> DNA

<213> Enterobacter cloacae

<400> 3899

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<210> 3900

<211> 621

<212> DNA

<213> Enterobacter cloacae

<400> 3900

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cogettaatt	atggttttct	tctgcgcggc	catggcttaa	cctgctgggg	acgcgacgtg	540
gccgaagccc	gccgtcatct	ggaaggttta	gaattcttat	ttgaatgcga	aatgcgttta	600
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<210> 3901

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 3901

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<210> 3902

<211> 1113

<212> DNA

<213> Enterobacter cloacae

<400> 3902

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<210> 3903

<211> 801

<212> DNA

<213> Enterobacter cloacae

<400> 3903

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<210> 3904

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 3904

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<210> 3905

<211> 891

<212> DNA

<213> Enterobacter cloacae

<400> 3905

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<210> 3906

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 3906

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<210> 3907

<211> 2457

<212> DNA

<213> Enterobacter cloacae

<400> 3907

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<210> 3908

<211> 426

<212> DNA

<213> Enterobacter cloacae

<400> 3908

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<210> 3909

<211> 684

<212> DNA

<213> Enterobacter cloacae

<400> 3909

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<210> 3910

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 3910

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<210> 3911

<211> 831

<212> DNA

<213> Enterobacter cloacae

<400> 3911

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<210> 3912

<211> 444

<212> DNA

<213> Enterobacter cloacae

<400> 3912

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<210> 3913

<211> 261

<212> DNA

<213> Enterobacter cloacae

<400> 3913

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gccagcgtgt	tgtcttcttt	gaaggctact	ttcggcgaca	gctcagcaat	ctctgtcagc	180
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<210> 3914

<211> 1281

<212> DNA

<213> Enterobacter cloacae

<400> 3914

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tggacgctta	acaattttctc	cagggtctgc	gtttcctttt	ccgggtggaaa	agattctacc	180
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<210> 3915

<211> 723

<212> DNA

<213> Enterobacter cloacae

<400> 3915

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<210> 3916

<211> 528

<212> DNA

<213> Enterobacter cloacae

<400> 3916

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<210> 3917

<211> 1644

<212> DNA

<213> *Enterobacter cloacae*

<400> 3917

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<210> 3918

<211> 1068

<212> DNA

<213> *Enterobacter cloacae*

<400> 3918

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<210> 3919

<211> 1083

<212> DNA

<213> *Enterobacter cloacae*

<400> 3919

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<210> 3920

<211> 621

<212> DNA

<213> *Enterobacter cloacae*

<400> 3920

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<210> 3921

<211> 732

<212> DNA

<213> *Enterobacter cloacae*

<400> 3921

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<210> 3922
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 <212> DNA
 <213> Enterobacter cloacae

<400> 3922
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<210> 3923
 <211> 996
 <212> DNA
 <213> Enterobacter cloacae

<400> 3923
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<210> 3924
 <211> 1310
 <212> DNA

<213> *Enterobacter cloacae*

<400> 3924

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<210> 3925

<211> 1620

<212> DNA

<213> *Enterobacter cloacae*

<400> 3925

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<210> 3926

<211> 822

<212> DNA

<213> Enterobacter cloacae

<400> 3926

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<210> 3927

<211> 1098

<212> DNA

<213> Enterobacter cloacae

<400> 3927

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<210> 3928

<211> 1305

<212> DNA

<213> Enterobacter cloacae

<400> 3928

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<210> 3929

<211> 2124

<212> DNA

<213> Enterobacter cloacae

<400> 3929

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<210> 3930

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 3930

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<210> 3931

<211> 2139

<212> DNA

<213> Enterobacter cloacae

<400> 3931

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<210> 3932

<211> 312

<212> DNA

<213> Enterobacter cloacae

<400> 3932

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ccggattacg	acaactacgt	cgagcatatg	cgcgtaacc	acccggacca	gacgcccatg	240
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<210> 3933

<211> 1035

<212> DNA

<213> Enterobacter cloacae

<400> 3933

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ctgaccgtcg	tcgcgctgg	ggcgttttt	ggcctggcgt	cggacagctt	cctcgatccg	180
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<210> 3934

<211> 1242

<212> DNA

<213> Enterobacter cloacae

<400> 3934

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aatctcggca	cgacgatatt	tacgcagatg	agcgccctgg	cgcagcagca	caacgccatt	180
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<210> 3935

<211> 1605

<212> DNA

<213> Enterobacter cloacae

<400> 3935

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<210> 3936

<211> 1266

<212> DNA

<213> Enterobacter cloacae

<400> 3936

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<210> 3937

<211> 234

<212> DNA

<213> Enterobacter cloacae

<400> 3937

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cagcgtacgg	gtgagctcct	cgccggtggt	caggtttgcg	aacttcacct	ggctgttcat	180
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<210> 3938

<211> 336

<212> DNA

<213> Enterobacter cloacae

<400> 3938

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<210> 3939

<211> 1188

<212> DNA

<213> Enterobacter cloacae

<400> 3939

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<210> 3940
 <211> 1002
 <212> DNA
 <213> *Enterobacter cloacae*

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<210> 3941
 <211> 477
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3941
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 tgogaatcct gcggtgttga aatcgggtatt cgtgcgcctg aagcgcgtcc aacagccgat 420
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<210> 3942
 <211> 903
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3942
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 gaaattatcg ctctggctga acaggcgtcg aacgagaaag gtcttcgtgc tgacgacgtt 780
 caaattcggg atgccgatac gcttctggcg cttacagaga ccagcaagcg tgcggttaatt 840
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 tag 903

<210> 3943
 <211> 615
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3943
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 tctaataaca cctgtaaagt atccctggat cagaagattg accaggatgg taatgatttt 180
 gacgttaacc tggataccgt gtttgtaaaa gacttcgcta atgcgctggg taccaccagc 240
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 caggcatccg ctcagtttga ttcttggcg ggttcttctt caacttcggg cggctctgctg 360
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 ggcaactccg ctaccgatca gatcaaaact gatcagacca acaataccca gaaagcaacg 480
 attgatacca caggcgcagg cgcactttac taccgtgtag cgtataccca aggtcagaac 540
 tgggatgcgg ccaacaaccc agtgcagct ggtgtggttc aggcacaagc tgcattcacc 600
 atgatctacg agtaa 615

<210> 3944
 <211> 627
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3944
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 gctgcggcag ccgatctcaa tgttaacttt actgccaaata tccgcgaaac cacctgcgat 180
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 gtggccacct tacgtgaaac acaggaaaac aggatgacca taggtgattt tcaggccgtg 600
 gcgacctttg aatttatcta cgagtga 627

<210> 3945
 <211> 1122
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3945
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 agccactcct gctgggcagc tgatttgtgc atgaataatg gaaaaggcgg cacaaccacg 180
 ctgatcaatt ccgaatactc aggtggcacc gtacgtcttc cccctccggg taattatgcc 240
 agtactcttt ttaacgttaa cctgacacgg ggcattcagg ccgaatgtgg tccagggaac 300
 gatggtttta acctcgtctc acaaaacaaac ccgaccttgc taaaggggag cagttatggc 360
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 gaaagtgatg gaggcattgg tggtattttc gctatgaata ctactgactg gactaccgtt 480
 gcatcctccg gaaattctga tccctgggat gaaaaatgga taaacacctc agttcaaatt 540
 tatattgatg cagggttacag aggcaccccg aacaaagaaa cctcaatcag acccaaacc 600
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1122

<210> 3946

<211> 1803

<212> DNA

<213> Enterobacter cloacae

<400> 3946

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catcatgctc	atcaccccag	gcatggcgat	ttccgtctac	ctgatcccgg	tctggattgc	180
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aatgttttct	cgctgtactc	gcggttgccg	gtacagcgctc	ttgttacctt	cctcacaat	300
tcgcgccaac	agcaaaatcc	tccatatcac	cgcctttata	ttgcaacgca	tatatctggt	360
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gtacgtctgc	tgaagtggga	ccgtgagacc	atgaagcaga	tccagtcgga	tctggaaaag	1740
cgtcgacca	actatcgcca	gctgaacgat	tatcaggaac	tcaaagccgc	tgagactaaa	1800
taa						1803

<210> 3947

<211> 987

<212> DNA

<213> Enterobacter cloacae

<400> 3947

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caccgacgtg	acgcgcttct	ggaacgtatt	aatagtata	tcccgcaag	cgttgcccat	180
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cogtcccgcg	tcttgtctgac	tgggtgaacgc	accgcgctca	attttgtgca	aacgctctct	480
ggcgttgcca	gtgaagtacg	ccgctacgtt	gacctgctgg	caggcacccg	cacgcagctg	540
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acaaacggcc	aggcgcagct	tgaggtgtcc	ggcaacgtga	cgttcgacac	catccgcgaa	900

tttgcgtgaaa cgggcgtcga ttacatctcc gtaggcgccc tgaccaagca cgtccgcgcc 960
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<210> 3948

<211> 1224

<212> DNA

<213> Enterobacter cloacae

<400> 3948

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cgtaacgcag	cttacacggc	tctggtgctt	aaacagctgc	acccgctggc	gctaaaaacgc	180
tgccagcagc	accaccgatg	gcaagtgcag	cactgctacg	atatttttgc	ccagctcgcc	240
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cctttgcagc	actggcaggc	gctgctgcac	agtcttgctg	atgacctgag	cgaagggttc	360
gctctgtcag	aggccatgaa	gaaatggcca	gaggtgttta	gcccccttta	tgtctcgatg	420
gtgaagacgg	gtgaactgac	gggtaagctc	gaagcctgct	gocgtcagct	tgcgcagcaa	480
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accggagaag	tgtcgggttc	actggatgtc	atgctgatga	atctggcccg	ccatcatacg	1080
gaacagacat	ttcagcaggc	agacaatctg	gcggcgcttc	ttgagccctt	gctactggtc	1140
gtgacaggtc	tgattattgg	cacgctggtg	gtggcaatgt	atctgccgat	tttccatctg	1200
gggatgcaa	tgagcgcggg	gtaa				1224

<210> 3949

<211> 639

<212> DNA

<213> Enterobacter cloacae

<400> 3949

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attgcccgctc	atgtggtaga	acccaatata	ccgccttaaa	acgccatcga	agcgcatttt	180
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gaaactcagc	gtcaaattgc	cgcagcccg	tgcacctatg	tgttggtggg	cgtcccgtta	360
ctggtggaaa	atcagcttca	gaataaaagca	gacagaacgc	tggtgattga	cgtttcccg	420
gaaacgcaaa	tccagagaa	catggcgcg	gaccatgttt	cacgcgaaca	tgctgaacaa	480
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aataacggcg	caccagatgc	cattgcacgc	gatgttgctc	gtctgcacgc	gcagtatctg	600
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<210> 3950

<211> 585

<212> DNA

<213> Enterobacter cloacae

<400> 3950

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acttcgcggc	gcagtgcaga	cgtatacgat	attgttcagc	ctccggcgte	cagttcagta	180
cgtcagccc	tttttccga	atgccattca	gcacgcctg	gtgtaactct	tcctccgacg	240
gcttcgccc	cggtttgcgc	cgcagcgtca	gtttgccaat	ctggctacga	cggaaacgct	300
tcagcgtgcc	ctgggtatca	tcccattcca	cgatgtcaga	ttgctgaagc	agctgcgggc	360

aggcacgcgt	caggaggtca	atatccacgg	caaccgcctg	taaaatacgc	gcgtccgggg	420
agtggctgcc	ctggagtaag	agcggcgcca	tcagccattc	atgacgcgtc	agggcgctcat	480
cgctgtccag	catcgcgccc	atcccatttg	ccagctgata	gcgaccatcc	agccccgcgac	540
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<210> 3951

<211> 714

<212> DNA

<213> Enterobacter cloacae

<400> 3951

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accggcgcca	tgaccggttg	cgccacgcgg	ggtgacacgg	tctggtatcc	cacatcagaa	180
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tacgcgcaat	tgttgaatga	ggcacaaaag	cagggggtag	agatttttgc	ttataaagcg	660
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<210> 3952

<211> 489

<212> DNA

<213> Enterobacter cloacae

<400> 3952

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cagggttaacg	ctgccgtgca	ggcgcgtggg	gagatccgc	aaagccgcct	cgctcgcgctg	120
tcttcatttt	accgtacgcc	gccgcctcgg	ccgcaggatc	agcctgatta	tctgaacgcc	180
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cgctggtaaa						489

<210> 3953

<211> 831

<212> DNA

<213> Enterobacter cloacae

<400> 3953

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<210> 3954

<211> 393

<212> DNA

<213> *Enterobacter cloacae*

<400> 3954

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gaagcacgtc	gctggcagcc	taaagtggcc	tactttgaag	gcgataatga	gatgaaacgt	360
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<210> 3955

<211> 840

<212> DNA

<213> *Enterobacter cloacae*

<400> 3955

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<210> 3956

<211> 2598

<212> DNA

<213> *Enterobacter cloacae*

<400> 3956

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<210> 3957

<211> 651

<212> DNA

<213> Enterobacter cloacae

<400> 3957

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cctggcgtag	gccaggcaag	ctcaggatta	gacgtaaata	ttaccgctaa	cattgttaat	180
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acgcctttta	agatccatgt	agatgattgc	tatggagaca	gcagtacggc	taaaaagctg	360
agtttttagct	tttcgccgca	gtcgggtttc	tggccaggac	aaaatcagggt	tttcaaaagt	420
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<210> 3958

<211> 897

<212> DNA

<213> Enterobacter cloacae

<400> 3958

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<210> 3959

<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 3959

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<210> 3960

<211> 1392

<212> DNA

<213> Enterobacter cloacae

<400> 3960

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<210> 3961

<211> 999

<212> DNA

<213> Enterobacter cloacae

<400> 3961

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tactttatcg	cctccgtacc	ggagtacgat	cggctggcga	tccgcgcgcg	ggactcgcctg	180
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ccgctttacg	atcccaatcg	ccatactcgc	ctgaaactca	tccgctggaa	cgaaaacggg	960
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<210> 3962

<211> 213

<212> DNA

<213> Enterobacter cloacae

<400> 3962

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cctggcatgg	tgcagccacc	gtcgcgtgat	atctggccgc	ccagaccgtg	cgcagcgtca	180
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<210> 3963

<211> 924

<212> DNA

<213> Enterobacter cloacae

<400> 3963

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<210> 3964

<211> 1440

<212> DNA

<213> Enterobacter cloacae

<400> 3964

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aatttttgcc	gtaaagtgtc	gagccgcgaa	gagagcatgg	cgaacgacgc	tattgcacag	120

ccacacatgt	cggctcattcc	gcgtgagcag	cacaatattt	cccgc aaaaga	tatcagt gaa	180
aatgccctca	aggtgctcta	tcgtctgaat	aaagcaggct	acgaggccta	tctcgctggc	240
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<210> 3965

<211> 606

<212> DNA

<213> Enterobacter cloacae

<400> 3965

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<210> 3966

<211> 768

<212> DNA

<213> Enterobacter cloacae

<400> 3966

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acactcatca	gcaacaatgc	actatggtca	aaaatgctgg	tggaggaaga	ccccgattt	180
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<210> 3967
 <211> 2424
 <212> DNA
 <213> *Enterobacter cloacae*

<220>
 <221> unsure
 <222> (1605)

<400> 3967
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<210> 3968
 <211> 636
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3968
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agctaccgtg	atttaagcgg	tattggcatt	cccactgcta	aaaaatgcaa	agcgtctggct	600
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<210> 3969

<211> 1554

<212> DNA

<213> Enterobacter cloacae

<400> 3969

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caaattctga	tggcctcaac	ctatccggcg	agcgtgattc	aggccgccc	gtgggtcaaag	360
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gccagcgtga	aatcgctggg	cgcctttccg	cagttaatgt	cgtgatggg	ggaaaacccg	480
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cagcgcgggc	tgcaaaagccg	ccagcacgcg	tcgctgaaca	gtgagcagcg	tgccagcttc	1500
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<210> 3970

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 3970

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gcgctcaccg	atatgctgca	aacgttcac	ccctaccgca	ccgccattga	gctttgcgcc	180
ctggatcgtg	gtgggtgtgga	tcgctgcgac	gcaggcacca	atggcatccc	ctccccgaca	240
accacacggt	acgttttcagc	gatgagcgtg	gcgaagggga	tcgtatcggt	aacagggcag	300
gaaagccotta	acggacttga	agtgtctcat	acaccgatct	ggagcgacgg	taacggtatg	360
acgggctgga	cgcgtgactg	caaaatttgcg	tccgacacgg	cgtctagaca	agcctgtgaa	420
gatgttttcc	gcttcgacaa	caactga				447

<210> 3971

<211> 1392

<212> DNA

<213> Enterobacter cloacae

<400> 3971

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ctgatggaag	cgttacgctt	cgccacgcag	aaacgtattg	atattgagtg	ctggacggct	180
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<210> 3972

<211> 837

<212> DNA

<213> Enterobacter cloacae

<400> 3972

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ccgcttaacg	aaaaaatgcg	tacctggcta	cgcatagaat	ttcttattca	acagctttca	180
caacatctgc	ctgtcaacga	tcacgccacc	gcgtcgcatt	ttttccgcaa	cgtgggcgat	240
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cagcagcgta	aattacaggc	ctgggcccga	gtaccgggcg	tggatcaaag	tcgaattgac	360
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cagctttacc	cgcaaatttc	cggacataaa	agccgtttcg	cgatccgctt	tatgccgctg	780
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<210> 3973

<211> 204

<212> DNA

<213> Enterobacter cloacae

<400> 3973

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tggggagaag	tgagtccatt	tcgcccatte	tgctgcaagc	gctgtcagct	tatagacctg	120
ggcgaatggg	cggcggaaga	gaaacgcatt	ccgagcgaag	gcgatctctc	ggatagcgat	180
gactggagcg	aaaaccagca	gtaa				204

<210> 3974

<211> 2739

<212> DNA

<213> *Enterobacter cloacae*

<400> 3974

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ggataggaa	cggcgatgga	gaagctctct	gatgatgagc	tgaaagcgaa	aaccgcggag	180
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<210> 3975

<211> 450

<212> DNA

<213> *Enterobacter cloacae*

<400> 3975

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caacgtgccg	ccgatgcgca	catggccaac	aaatgggaat	tccccggcgg	gaaaatcgaa	180
tcaggtgaaa	cgcgggagca	ggcgtggtg	cgtgagcttc	aggaagaggt	ggggatcacc	240

ccgcttggcg	caacgctggt	cgataagctg	gagtaccagt	ttccggatcg	tcacatcacg	300
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<210> 3976

<211> 1098

<212> DNA

<213> Enterobacter cloacae

<400> 3976

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<210> 3977

<211> 579

<212> DNA

<213> Enterobacter cloacae

<400> 3977

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<210> 3978

<211> 2643

<212> DNA

<213> Enterobacter cloacae

<400> 3978

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<210> 3979

<211> 555

<212> DNA

<213> Enterobacter cloacae

<400> 3979

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<210> 3980

<211> 936

<212> DNA

<213> Enterobacter cloacae

<400> 3980

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<210> 3981

<211> 468

<212> DNA

<213> Enterobacter cloacae

<400> 3981

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<210> 3982

<211> 1311

<212> DNA

<213> Enterobacter cloacae

<400> 3982

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<210> 3983
 <211> 519
 <212> DNA
 <213> *Enterobacter cloacae*

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 <211> 483
 <212> DNA
 <213> *Enterobacter cloacae*

<400> 3985

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<210> 3986

<211> 2430

<212> DNA

<213> Enterobacter cloacae

<400> 3986

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<210> 3987

<211> 1956

<212> DNA

<213> *Enterobacter cloacae*

<400> 3987

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<210> 3988

<211> 522

<212> DNA

<213> *Enterobacter cloacae*

<400> 3988

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<210> 3989

<211> 864

<212> DNA

<213> *Enterobacter cloacae*

<400> 3989

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<210> 3990

<211> 795

<212> DNA

<213> Enterobacter cloacae

<400> 3990

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<210> 3991

<211> 2679

<212> DNA

<213> Enterobacter cloacae

<400> 3991

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<210> 3992

<211> 1434

<212> DNA

<213> Enterobacter cloacae

<400> 3992

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<210> 3993

<211> 447

<212> DNA

<213> Enterobacter cloacae

<400> 3993

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<210> 3994

<211> 1764

<212> DNA

<213> Enterobacter cloacae

<400> 3994

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<210> 3995

<211> 834

<212> DNA

<213> Enterobacter cloacae

<400> 3995

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<210> 3996

<211> 237

<212> DNA

<213> Enterobacter cloacae

<400> 3996

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cgtgagattg	gcctgaccgc	tgaacgtgtt	cgtcagattc	aggttgaagg	cctacgccgc	180
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<210> 3997

<211> 603

<212> DNA

<213> Enterobacter cloacae

<400> 3997

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<210> 3998

<211> 357

<212> DNA

<213> Enterobacter cloacae

<400> 3998

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<210> 3999

<211> 624

<212> DNA

<213> Enterobacter cloacae

<400> 3999

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<210> 4000

<211> 1827

<212> DNA

<213> Enterobacter cloacae

<400> 4000

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<210> 4001

<211> 807

<212> DNA

<213> Enterobacter cloacae

<400> 4001

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<210> 4002

<211> 465

<212> DNA

<213> Enterobacter cloacae

<400> 4002

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gacggcggca	gcgcgccgga	aaacgacgtg	gtcgccatcc	gtgaactgca	tccggacagg	180
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gtcgggtttt	attacccgat	gacgcgcgcg	gtgaaagagg	cgggtggacgt	ggtgtattca	420
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<210> 4003

<211> 1111

<212> DNA

<213> Enterobacter cloacae

<400> 4003

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ccgctgggca	atgttgacca	ggtgagcctg	ctgcgcctgg	atggtcttca	ccacggggct	1080
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<210> 4004

<211> 1521

<212> DNA

<213> Enterobacter cloacae

<400> 4004

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<210> 4005

<211> 495

<212> DNA

<213> Enterobacter cloacae

<400> 4005

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tgttc	agcgt	caatc	gctgt	ctatc	atgag	gatatt	ogcg	cta	acctg	ac	gatg	180
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gagatt	atga	atgaa	attct	ccctg	acttc	tttct	gtatc	cga	agaaaa	tctga	attat	420
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<210> 4006

<211> 630

<212> DNA

<213> Enterobacter cloacae

<400> 4006

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<210> 4007

<211> 948

<212> DNA

<213> Enterobacter cloacae

<400> 4007

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<210> 4008

<211> 1725

<212> DNA

<213> Enterobacter cloacae

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<210> 4009

<211> 552

<212> DNA

<213> Enterobacter cloacae

<400> 4009						
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<210> 4010

<211> 2373

<212> DNA

<213> Enterobacter cloacae

<400> 4010

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<210> 4011

<211> 1071

<212> DNA

<213> Enterobacter cloacae

<400> 4011


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<210> 4012

<211> 906

<212> DNA

<213> *Enterobacter cloacae*

<400> 4012

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<210> 4013

<211> 258

<212> DNA

<213> *Enterobacter cloacae*

<400> 4013

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<210> 4014

<211> 900

<212> DNA

<213> *Enterobacter cloacae*

<400> 4014

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<210> 4015

<211> 423

<212> DNA

<213> Enterobacter cloacae

<400> 4015

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<210> 4016

<211> 1053

<212> DNA

<213> Enterobacter cloacae

<400> 4016

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<210> 4017

<211> 582

<212> DNA

<213> Enterobacter cloacae

<400> 4017

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<210> 4018

<211> 1239

<212> DNA

<213> Enterobacter cloacae

<400> 4018

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<210> 4019

<211> 1599

<212> DNA

<213> Enterobacter cloacae

<400> 4019

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<210> 4020

<211> 849

<212> DNA

<213> Enterobacter cloacae

<400> 4020

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aaagtgccgc	tcaagcgcgg	gtgcgactat	caggacgtgc	tgaacatgct	gctgttttac	780
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<210> 4021

<211> 360

<212> DNA

<213> Enterobacter cloacae

<400> 4021

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gagtacgtca	cgtgctgtgc	atcgaaggta	cagcgtgtgc	cgcagtgcca	gagcagcggg	300
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<210> 4022

<211> 867

<212> DNA

<213> Enterobacter cloacae

<400> 4022

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gacattgaga	tccctgctgt	ttccgcacag	cgcggcgagc	ggatggacgc	ctggctgaac	840
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<210> 4023

<211> 2109

<212> DNA

<213> Enterobacter cloacae

<400> 4023

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gcactgagcg	atgccttgac	gcggctggtc	aggcaatctg	cgctggcgga	cagcgccgcc	180
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<210> 4024

<211> 330

<212> DNA

<213> Enterobacter cloacae

<400> 4024

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agaaagcgtc	atgaagatcg	taaaaccaag	atcccaacgc	gttacagcgt	acacgcagcc	180
ctgaatctga	aaggggactg	gctcgaaaaa	gcaggccttt	taaccatttc	gcaggttcgg	240

gtggagggtcg ggccggggtaa aataattatc gaactcatta aagagccgga tgatggacat 300
cccggccatg tcgttcagcg agagcagtaa 330

<210> 4025

<211> 990

<212> DNA

<213> Enterobacter cloacae

<400> 4025

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accgcgggca	cgcgcccggc	gacgtctgac	aagttgcgcg	agctgaccgg	ctgggaagcg	180
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<210> 4026

<211> 375

<212> DNA

<213> Enterobacter cloacae

<400> 4026

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gaagagtttt	gctttatcca	ctgccacggc	gagctgaacg	gcgagctgaa	ggccggaagc	180
cagctggagc	tgggcaaggc	gcgctatgcg	gtaaccggcg	tcgggtgacg	cgccgagcaa	240
aacctgcgcg	agctggggca	tatcacccctg	cgtttcgcgc	gccagccgca	ggcggagtat	300
cccggcacgg	ttcacgttga	gggtccggtt	ccgcaggctg	tcaccccagg	ctgcacgtta	360
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<210> 4027

<211> 372

<212> DNA

<213> Enterobacter cloacae

<400> 4027

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aagggaacgc	tcggcgctcg	gcgttccggg	ggcgctttta	agccgcgcgt	ggtggttgcc	180
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gatgtgatct	tccccatga	ttactctgt	cagaatgcac	tatcatttag	gcttaattctg	360
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<210> 4028

<211> 837

<212> DNA

<213> Enterobacter cloacae

<400> 4028

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tgctcggtag	aggatctggc	ccactacttt	gacaccaccg	gcacgacaat	acgcaaggac	180
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ggcagtactg	tcctacagat	gatcccgctg	ctcagccgct	ttaataacat	caccgtgatg	420
accaacagcc	tgcacatcgt	caatgcctcg	tcagagttcg	acagcgagca	gaccatcctg	480
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<210> 4029

<211> 1152

<212> DNA

<213> Enterobacter cloacae

<400> 4029

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<210> 4030

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 4030

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ccggatgggc	atcgcacacc	acacgctctg	gctggaaagc	gtagatctcc	tgcacgtcgc	180
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tcagcaccgc	ctggttgcca	cgtaccaggc	agaagggtatt	tttcatctcc	gcgcgggtgc	300
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<210> 4031

<211> 1014

<212> DNA

<213> Enterobacter cloacae

<400> 4031

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cgcattgocg	tctcaaccct	caccgcacac	ggtgacaggc	tggcgttctc	taccgacagc	180
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<210> 4032

<211> 765

<212> DNA

<213> Enterobacter cloacae

<400> 4032

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<210> 4033

<211> 1230

<212> DNA

<213> Enterobacter cloacae

<400> 4033

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<210> 4034

<211> 2583

<212> DNA

<213> Enterobacter cloacae

<400> 4034

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<210> 4035

<211> 264

<212> DNA

<213> Enterobacter cloacae

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 cgggtgcttca tcaatatcct tctgcgtcat gcggaacgct tccgggtaat gctcgcggct 180
 ggtacggcgc agcggttcgg tatcgcgcca ggtatacaga cagtgcgtgac actgatatac 240
 cgtccagaca cctttcaccg gtga 264

<210> 4036

<211> 594

<212> DNA

<213> Enterobacter cloacae

<400> 4036
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 ctgcccctgc tgatcagcct gctgggtgatc atgaacgcgc tgattaactt tatcgccag 180
 cagcgcattg agcgtctcgc ccagcgtgc gccggaacc cgtgtcccg ctacctgata 240
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 ggcttacca cgttggcct gccgctcggc ccgctggcgg tgagctacct gctggtcggg 480
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<210> 4037

<211> 978

<212> DNA

<213> Enterobacter cloacae

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 accattatcc actgcgaggg taaagtgatc gtggcgggta tcggtaaate cggtcataac 180
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<210> 4038

<211> 1461

<212> DNA

<213> Enterobacter cloacae

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 cgcgagttcg tgcagaacct gcgcagcgaa atcgatctga atgagatcga ctacattatc 240
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 gataccccga tctactgcac cactaacgcc attgactcca tcaacggcca ccaccaccat 360
 ccggagtgga acttccacac tgtgaaaacc ggcgacacgc tggatatcgg caacggcaaa 420

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<210> 4039

<211> 1497

<212> DNA

<213> Enterobacter cloacae

<400> 4039

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<210> 4040

<211> 1443

<212> DNA

<213> Enterobacter cloacae

<400> 4040

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<210> 4041

<211> 243

<212> DNA

<213> Enterobacter cloacae

<400> 4041

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ccggggctga	ggcattggca	tgcgccctgc	gcacccagcc	gtgcagcggg	attatcccg	180
ccagcaggcc	aaaaccgact	acgcccaca	gccagacgtc	ggtgcccagc	ggctggccgt	240
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<210> 4042

<211> 342

<212> DNA

<213> Enterobacter cloacae

<400> 4042

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gtgattaatg	aggaagaagc	ccgcgacacg	ctggacgcgc	tacagaatat	gtttgacgtc	300
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<210> 4043

<211> 1125

<212> DNA

<213> Enterobacter cloacae

<400> 4043

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<211> 1005

<212> DNA

<213> Enterobacter cloacae

<400> 4044

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<210> 4045

<211> 747

<212> DNA

<213> Enterobacter cloacae

<400> 4045

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<210> 4046

<211> 435

<212> DNA

<213> Enterobacter cloacae

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<210> 4047

<211> 1416

<212> DNA

<213> Enterobacter cloacae

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<210> 4048

<211> 1215

<212> DNA

<213> Enterobacter cloacae

<400> 4048
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